

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
17 October 2002 (17.10.2002)

PCT

(10) International Publication Number
WO 02/081638 A2

(51) International Patent Classification⁷: C12N

GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(21) International Application Number: PCT/US02/10824

(22) International Filing Date: 8 April 2002 (08.04.2002)

Declarations under Rule 4.17:

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/281,731 6 April 2001 (06.04.2001) US
60/281,732 6 April 2001 (06.04.2001) US

— as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)

(71) Applicant (for all designated States except US): ORIGENE TECHNOLOGIES, INC [US/US]; 6 Taft Court, Suite 100, Rockville, MD 20850 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): SUN, Zairen [CN/US]; 1083 Copperstone Court, Rockville, MD 20852 (US). JAY, Gilbert [US/US]; 5801 Nicholson Lane, North Bethesda, MD 20852 (US).

— as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)

— of inventorship (Rule 4.17(iv)) for US only

(74) Agent: LEOVITZ, Richard, M.; Origene Technologies, Inc., 6 Taft Court, Suite 100, Rockville, MD 20850 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

Published:

— without international search report and to be republished upon receipt of that report

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR,

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: PROSTATE CANCER EXPRESSION PROFILES

(57) Abstract: The present invention relates to all facets of novel polynucleotides, the polypeptides they encode, antibodies and specific binding partners thereto, and their applications to research, diagnosis, drug discovery, therapy, clinical medicine, forensic science and medicine, etc. The polynucleotides are differentially-regulated in prostate cancer and are therefore useful in variety of ways, including, but not limited to, as molecular markers, as drug targets, and for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, determining predisposition to, etc., diseases and conditions, to prostate cancer.

WO 02/081638 A2

PROSTATE CANCER EXPRESSION PROFILES

This application claims the benefit U.S. Provisional Application No. 60/281,731, filed April 6, 2001, and U.S. Provisional Application No. 60/281,732, filed April 6, 2001, which are hereby incorporated by reference in their entirety.

5

DESCRIPTION OF THE DRAWINGS

Tables 1 and 2 list genes differentially-regulated in prostate cancer. "DNA SEQ ID" and "Prt SEQ ID" refer to the corresponding DNA and protein sequences in the attached sequence listing. The genes can alternatively be referred to by GenBank accession number in the fifth column ("GI#") or the "identifier" in the third column. The genes listed in Table 1 are up-regulated, and those in Table 2 are down-regulated ("Exp" refers to the expression profile, U is up-regulated expression, and D is down-regulated expression). The characterization of the gene under the "description" heading is based on its listing in GenBank. 5', 3', genomic sequences, etc., which correspond to the genes can be retrieved routinely from Genbank, e.g., by searching the accession number. SEQ ID NOS 1-107 are DNA, and 108-211 are polypeptide. These sequences, and all information referenced to the accession number, are incorporated by reference in their entirety.

The polypeptide sequences was analyzed for the presence of functional domains using the publicly available Pfam program. This information is summarized in Table 3. Domains present in each polypeptide are listed under "domain." Any abbreviations are those used in Pfam. The start of the domain is indicated by "seq-f" and the end of the domain by "seq-t." The "score" is the statistical score of this match to the domain in bits. In general, a higher score indicates a better match. "E" is the statistical score of this match in Evalve (frequentist) approach. The smaller score in this case shows a better match between the domain and the query sequence. For more information on the program and scoring, see, e.g., Sonnhammer et al., *Proteins: Structure, Function and Genetics* 28:405-420 (1997); Sonnhammer et al., *Nucleic Acids Research*, 26:320-322 (1998); Bateman et al., *Nucleic Acids Research*, 27:260-262 (1999); Bateman et al., *Nucleic Acids Research*, 28:263-266 (2000).

30

DESCRIPTION OF THE INVENTION

The present invention relates to all facets of novel polynucleotides, the polypeptides they encode, antibodies and specific binding partners thereto, and their applications to research, diagnosis, drug discovery, therapy, clinical medicine, forensic science and medicine, etc. The polynucleotides are differentially regulated in prostate cancer and are therefore useful in variety of ways, including, but not limited to, as molecular markers, as drug targets, and for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, determining predisposition to, etc., diseases and conditions,, especially relating to prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways, and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinical applications. The present invention also relates to methods of using the polynucleotides and related products (proteins, antibodies, etc.) in business and computer-related methods, e.g., advertising, displaying, offering, selling, etc., such products for sale, commercial use, licensing, etc.

Prostate cancer is the most common form of cancer diagnosed in the American male, occurring predominantly in males over age 50. The number of men diagnosed with prostate cancer has steadily increased as a result of the increasing population of older men. The American Cancer Society estimates that in the year 2000, about 180,000 American men were diagnosed with prostate cancer and about 32,000 died from the disease. In comparison, 1998 estimates for lung cancer in men were 171,500 cases and 160,100 deaths, and for colorectal cancer, the estimates were 131,600 cases and 56,000 deaths. Despite these high numbers, 89 percent of men diagnosed with the disease will survive at least five years and 63 percent will survive at least 10 years.

Patients having prostate cancer display a wide range of phenotypes. In some men, following detection, the tumor remains a latent histological tumor and does not become clinically significant. However, in other men, the tumor progresses rapidly, metastasizing and killing the patient in a relatively short time. Prostate cancer can be cured if the tumor is confined to a small region of the gland and is discovered at early stage. In such cases, radiation or surgical removal often results in complete elimination of the disease. Frequently, however, the prostate cancer has already spread to surrounding tissue and metastasized to

remote locations. In these cases, radiation and other therapies, are less likely to effect a complete cure.

Androgen deprivation is a conventional therapy to treat prostate cancer. Androgen blockade can be achieved through several different routes. Androgen suppressive drugs include, e.g., Lupron (leuprolide acetate), Casodex (bicalutamide), Eulexin (flutamide), Nilandron (nilutamide), Zoladex (goserelin acetate implant), and Viadur (leuprolide acetate), which act through several different mechanisms. While these drugs may offer remission and tumor regression in many cases, often the therapeutic effects are only temporary. Prostate tumors lose their sensitivity to such treatments, and become androgen-independent. Thus, new therapies are clearly needed.

The first clinical symptoms of prostate cancer are typically urinary disturbances, including painful and more frequent urination. Diagnosis for prostate cancer is usually accomplished using a combination of different procedures. Since the prostate is located next to the rectum, rectal digital examination allows the prostate to be examined manually for the presence of hyperplasia and abnormal tissue masses. Usually, this is the first line of detection. If a palpable mass is observed, a blood specimen can be assayed for prostate-specific antigen (PSA). Very little PSA is present in the blood of a healthy individual, but BPH and prostate cancer can cause large amounts of PSA to be released into the blood, indicating the presence of diseased tissue. Definitive diagnosis is generally accomplished by biopsy of the prostate tissue.

No single gene or protein has been identified which is responsible for the etiology of all prostate cancers. Although PSA is widely used as a diagnostic reagent, it has limitations in its sensitivity and its ability to detect early cancers. It is estimated that approximately 20% to 30% of tumors will be missed when PSA is used alone. It is likely that diagnostic and prognostic markers for prostate cancer disease will involve the identification and use of many different genes and gene products to reflect its multifactorial origin.

A continuing goal is to characterize the gene expression patterns of the various prostate cancers to genetically differentiate them, providing important guidance in preventing and treating cancers. Molecular pictures of cancer, such as the pattern of differentially-regulated genes identified herein, provide an important tool for molecularly dissecting and classifying cancer, identifying drug targets, providing prognosis and therapeutic information, etc. For instance, an array of polynucleotides corresponding to genes differentially regulated in prostate cancer can be used to screen tissue samples for the existence of cancer, to

categorize the cancer (e.g., by the particular pattern observed), to grade the cancer (e.g., by the number of differentially-regulated genes and their amounts of expression), to identify the source of a secondary tumor, to screen for metastatic cells, etc. These arrays can be used in combination with other markers, e.g., PSA, PMSA (prostate membrane specific antigen), or
5 any of the grading systems used in clinical medicine.

As indicated by these studies, cancer is a highly diverse disease. Although all cancers share certain characteristics, the underlying cause and disease progression can differ significantly from patient to patient. So far, over a dozen distinct genes have been identified which, when mutant, result in a cancer. In breast cancer, alone, a handful of different genes
10 have been isolated which either cause the cancer, or produce a predisposition to it. As a consequence, disease phenotypes for a particular cancer do not look all the same. In addition to the differences in the gene(s) responsible for the cancer, heterogeneity among individuals, e.g., in age, health, sex, and genetic background, can also influence the disease and its progression. Gene penetrance, in particular, can vary widely among population members.
15 Recent studies have shown tremendous diversity in gene expression patterns among cancer patients. For these and other reasons, one gene/polypeptide target alone can be insufficient to diagnose or treat a cancer. Even a gene which is highly differentially-expressed and penetrant in cancer patients may not be so highly expressed in all patients and at all stages of the cancer. By selecting a set of genes and/or the polypeptides they encode, cancer
20 diagnostics and therapeutics can be designed which effectively diagnose and treat a population of diseased individuals, rather than only a small handful when single genes are targeted.

Nucleic acids

25 In accordance with the present invention, genes have been identified which are differentially expressed in prostate cancer. Tables 1 and 2 list of genes which are differentially-regulated in the cancer. These genes can be further divided into groups based on additional characteristics of their expression and the tissues in which they are expressed. For instance, genes can be further subdivided based on the stage and/or grade of the cancer in
30 which they are expressed. Genes can also be grouped based on their penetrance in a prostate cancer, e.g., expressed in all prostate cancer examined, expressed in a certain percentage of prostate cancer examined, etc. Additionally, genes can be categorized by their function and/or the polypeptides they encode. This includes, but is not limited to, cellular

localization, functional activity (e.g., kinase, cytoskeletal element, or transcriptional factor), functional pathway (e.g., protein manufacture, cell signaling, cell movement, cell adhesion, responsivity to cAMP, energy production, etc.), etc. These groupings do not restrict or limit the use such genes in therapeutic, diagnostic, prognostic, etc., applications. For instance, a gene which is expressed in only some cancers (e.g., incompletely penetrant) may be useful in therapeutic applications to treat a subset of cancers. Similarly, a co-penetrant gene, or a gene which is expressed in prostate cancer and other normal tissues, may be useful as a therapeutic or diagnostic, even if its expression pattern is not highly prostate specific. Thus, the uses of the genes or their products are not limited by their patterns of expression.

For genes which are differentially-regulated, gene and protein replacement therapies can be used therapeutically to restore expression levels to normal. When a protein product is to be administered, secreted proteins are more likely to be targets for replacement therapy than intracellular and membrane-bound proteins. For the latter classes, gene therapy may be a more effective means of delivery, e.g., administering a gene which is expressed inside a cell on or on its surface.

By the phrase "differential expression," it is meant that the levels of expression of a gene, as measured by its transcription or translation product, are different depending upon the specific cell-type or tissue (e.g., in an averaging assay that looks at a population of cells). There are no absolute amounts by which the gene expression levels must vary, as long as the differences are measurable.

The phrase "down-regulated" indicates that an mRNA transcript or other nucleic acid corresponding to a polynucleotide of the present invention is expressed in lower amounts in a cancer as compared to the same transcript expressed in normal cells from which the cancer was derived. In general, down-regulation can be assessed by any suitable method, including any of the nucleic acid detection and hybridization methods mentioned below, as well as polypeptide-based methods. Down-regulation also includes going from substantially no expression in a normal tissue, from detectable expression in a normal tissue, from significant expression in a normal tissue, to higher levels in the cancer.

The phrase "up-regulated" indicates that an mRNA transcript or other nucleic acid corresponding to a polynucleotide of the present invention is expressed in larger amounts in a cancer as compared to the same transcript expressed in normal cells from which the cancer was derived. For instance, a gene's up-regulation can be determined by comparing its abundance per gram of RNA (e.g., total RNA, polyadenylated mRNA, etc.) extracted from a

cancer tissue in comparison to the corresponding normal tissue. The normal tissue can be from the same or different individual or source. For convenience, it can be supplied as a separate component or in a kit in combination with probes and other reagents for detecting genes. The quantity by which a nucleic acid is up-regulated can be any value, e.g., more than
5 10%, 50%, 2-fold, 5-fold, 10-fold, etc. Up-regulation also includes going from substantially no expression, to detectable expression, to significant or highly restricted expression, etc.

Differential regulation can be determined by any suitable method, e.g., by comparing its abundance per gram of RNA (e.g., total RNA, polyadenylated mRNA, etc.) extracted from a prostate tissue in comparison to the corresponding normal tissue. The normal tissue can be
10 from the same or different individual or source. For convenience, it can be supplied as a separate component or in a kit in combination with probes and other reagents for detecting genes. The quantity by which a nucleic acid is differentially-regulated can be any value, e.g., about 10% more or less of normal expression, about 50% more or less of normal expression, 2-fold more or less, 5-fold more or less, 10-fold more or less, etc.

The amount of transcript can also be compared to a different gene in the same sample, especially a gene whose abundance is known and substantially no different in its expression between normal and cancer cells (e.g., a "control" gene). If represented as a ratio, with the quantity of differentially-regulated gene transcript in the numerator and the control gene transcript in the denominator, the ratio would be larger, e.g., in breast cancer than in a sample
20 from normal breast tissue.

Differential-regulation can arise through a number of different mechanisms. The present invention is not bound by any specific way through which it occurs. Differential-regulation of a polynucleotide can occur, e.g., by modulating (1) transcriptional rate of the gene (e.g., increasing its rate, inducing or stimulating its transcription from a basal, low-level
25 rate, etc.), (2) the post-transcriptional processing of RNA transcripts, (3) the transport of RNA from the nucleus into the cytoplasm, (4) RNA nuclear and cytoplasmic turnover and polypeptide turnover (e.g., by virtue of having higher stability or resistance to degradation), and combinations thereof. See, e.g., Tollervey and Caceras, *Cell*, 103:703-709, 2000.

A differentially-regulated polynucleotide is useful in a variety of different
30 applications as described in greater details below. Because it is more abundant in cancer, it and its expression products can be used in a diagnostic test to assay for the presence of cancer, e.g., in tissue sections, in a biopsy sample, in total RNA, in lymph, in blood, etc. Differentially-regulated polynucleotides and polypeptides can be used individually, or in

-7-

groups, to assess the cancer, e.g., to determine the specific type of cancer, its stage of development, the nature of the genetic defect, etc., or to assess the efficacy of a treatment modality. How to use polynucleotides in diagnostic and prognostic assays is discussed below. In addition, the polynucleotides and the polypeptides they encode, can serve as a
5 target for therapy or drug discovery. A polypeptide, coded for by a differentially-regulated polynucleotide, which is displayed on the cell-surface, can be a target for immunotherapy to destroy, inhibit, etc., the diseased tissue. Differentially-regulated transcripts can also be used in drug discovery schemes to identify pharmacological agents which suppress, inhibit, etc., their differential-regulation, thereby preventing the phenotype associated with their
10 expression. Thus, a differentially-regulated polynucleotide and its expression products of the present invention have significant applications in diagnostic, therapeutic, prognostic, drug development, and related areas.

The expression patterns of the differentially expressed genes disclosed herein can be described as a "fingerprint" in that they are a distinctive pattern displayed by a cancer. Just
15 as with a fingerprint, an expression pattern can be used as a unique identifier to characterize the status of a tissue sample. The list of genes represented in Tables 1 and 2 provide an example of a cell expression profile for a prostate cancer. It can be used as a point of reference to compare and characterize unknown samples and samples for which further information is sought. Tissue fingerprints can be used in many ways, e.g., to classify an
20 unknown tissue as being a prostate cancer, to determine the origin of a particular cancer (e.g., the origin of metastatic cells), to determine the presence of a cancer in a biopsy sample, to assess the efficacy of a cancer therapy in a human patient or a non-human animal model, to detect circulating cancer cells in blood or a lymph node biopsy, etc. While the expression profile of the complete gene set represented in Tables 1 and 2 may be most informative, a
25 fingerprint containing expression information from less than the full collection can be useful, as well. In the same way that an incomplete fingerprint may contain enough of the pattern of whorls, arches, loops, and ridges, to identify the individual, a cell expression fingerprint containing less than the full complement may be adequate to provide useful and unique identifying and other information about the sample. Moreover, cancer is a multifactorial
30 disease, involving genetic aberrations in more than gene locus. This multifaceted nature may be reflected in different cell expression profiles associated with breast cancers arising in different individuals, in different locations in the same individual, or even within the same cancer locus. As a result, a complete match with a particular cell expression profile, as

shown herein, is not necessary to classify a cancer as being of the same type or stage. Similarity to one cell expression profile, e.g., as compared to another, can be adequate to classify cancer types, grades, and stages. SEQ ID NOS 1-211 are referred to generally as "genes" to indicate that they represent specific gene loci, and are not limited to the particular
5 nucleotide and polypeptide sequences disclosed herein. For example, fibronectin (SEQ ID NO 60 and 196) is up-regulated in prostate cancers. Probes to detect its up regulation can be selected from the attached specific sequences, as well as genomic, upstream, downstream, and intron sequences which are not in the attached sequence listing.

A mammalian polynucleotide, or fragment thereof, of the present invention is a
10 polynucleotide having a nucleotide sequence obtainable from a natural source. It therefore includes naturally-occurring normal, naturally-occurring mutant, and naturally-occurring polymorphic alleles (e.g., SNPs), differentially-spliced transcripts, splice-variants, etc. By the term "naturally-occurring," it is meant that the polynucleotide is obtainable from a natural source, e.g., animal tissue and cells, body fluids, tissue culture cells, forensic samples.
15 Natural sources include, e.g., living cells obtained from tissues and whole organisms, tumors, cultured cell lines, including primary and immortalized cell lines. Naturally-occurring mutations can include deletions (e.g., a truncated amino- or carboxy-terminus), substitutions, inversions, or additions of nucleotide sequence. These genes can be detected and isolated by polynucleotide hybridization according to methods which one skilled in the art would know,
20 e.g., as discussed below.

A polynucleotide according to the present invention can be obtained from a variety of different sources. It can be obtained from DNA or RNA, such as polyadenylated mRNA or total RNA, e.g., isolated from tissues, cells, or whole organism. The polynucleotide can be obtained directly from DNA or RNA, from a cDNA library, from a genomic library, etc. The
25 polynucleotide can be obtained from a cell or tissue (e.g., from an embryonic or adult tissues) at a particular stage of development, having a desired genotype, phenotype, disease status, etc.

The genes described in Tables 1 and 2 can be partial sequences that correspond to full-length, naturally-occurring transcripts. The present invention includes, as well, full-
30 length polynucleotides that comprise these partial sequences, e.g., genomic DNAs and polynucleotides comprising a start and stop codon, a start codon and a polyA tail, a transcription start and a polyA tail, etc. These sequences can be obtained by any suitable method, e.g., using a partial sequence as a probe to select a full-length cDNA from a library

containing full-length inserts. A polynucleotide which "codes without interruption" refers to a polynucleotide having a continuous open reading frame ("ORF") as compared to an ORF which is interrupted by introns or other noncoding sequences.

5 Genomic

The present invention also relates genomic DNA from which the polynucleotides of the present invention can be derived. A genomic DNA coding for a human, mouse, or other mammalian polynucleotide, can be obtained routinely, for example, by screening a genomic library (e.g., a YAC library) with a polynucleotide of the present invention, or by searching
10 nucleotide databases, such as GenBank and EMBL, for matches. Promoter and other regulatory regions can be identified upstream of coding and expressed RNAs, and assayed routinely for activity, e.g., by joining to a reporter gene (e.g., CAT, GFP, alkaline phosphatase, luciferase, galactosidase). A promoter obtained from a prostate selective gene can be used, e.g., in gene therapy to obtain tissue-specific expression of a heterologous gene
15 (e.g., coding for a therapeutic product or cytotoxin).

Constructs

A polynucleotide of the present invention can comprise additional polynucleotide sequences, e.g., sequences to enhance expression, detection, uptake, cataloging, tagging, etc.
20 A polynucleotide can include only coding sequence; a coding sequence and additional non-naturally occurring or heterologous coding sequence (e.g., sequences coding for leader, signal, secretory, targeting, enzymatic, fluorescent, antibiotic resistance, and other functional or diagnostic peptides); coding sequences and non-coding sequences, e.g., untranslated sequences at either a 5' or 3' end, or dispersed in the coding sequence, e.g., introns.
25 A polynucleotide according to the present invention also can comprise an expression control sequence operably linked to a polynucleotide as described above. The phrase "expression control sequence" means a polynucleotide sequence that regulates expression of a polypeptide coded for by a polynucleotide to which it is functionally ("operably") linked. Expression can be regulated at the level of the mRNA or polypeptide. Thus, the expression
30 control sequence includes mRNA-related elements and protein-related elements. Such elements include promoters, enhancers (viral or cellular), ribosome binding sequences, transcriptional terminators, etc. An expression control sequence is operably linked to a nucleotide coding sequence when the expression control sequence is positioned in such a

manner to effect or achieve expression of the coding sequence. For example, when a promoter is operably linked 5' to a coding sequence, expression of the coding sequence is driven by the promoter. Expression control sequences can include an initiation codon and additional nucleotides to place a partial nucleotide sequence of the present invention in-frame in order to produce a polypeptide (e.g., pET vectors from Promega have been designed to permit a molecule to be inserted into all three reading frames to identify the one that results in polypeptide expression). Expression control sequences can be heterologous or endogenous to the normal gene.

A polynucleotide of the present invention can also comprise nucleic acid vector sequences, e.g., for cloning, expression, amplification, selection, etc. Any effective vector can be used. A vector is, e.g., a polynucleotide molecule which can replicate autonomously in a host cell, e.g., containing an origin of replication. Vectors can be useful to perform manipulations, to propagate, and/or obtain large quantities of the recombinant molecule in a desired host. A skilled worker can select a vector depending on the purpose desired, e.g., to propagate the recombinant molecule in bacteria, yeast, insect, or mammalian cells. The following vectors are provided by way of example. Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pBS, pD10, Phagescript, phiX174, pBK Phagemid, pNH8A, pNH16a, pNH18Z, pNH46A (Stratagene); Bluescript KS+II (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR54 0, pRIT5 (Pharmacia). Eukaryotic: PWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene), pSVK3, PBPV, PMSG, pSVL (Pharmacia), pCR2.1/TOPO, pCRII/TOPO, pCR4/TOPO, pTrcHisB, pCMV6-XL4, etc. However, any other vector, e.g., plasmids, viruses, or parts thereof, may be used as long as they are replicable and viable in the desired host. The vector can also comprise sequences which enable it to replicate in the host whose genome is to be modified.

Hybridization

Polynucleotide hybridization, as discussed in more detail below, is useful in a variety of applications, including, in gene detection methods, for identifying mutations, for making mutations, to identify homologs in the same and different species, to identify related members of the same gene family, in diagnostic and prognostic assays, in therapeutic applications (e.g., where an antisense polynucleotide is used to inhibit expression), etc.

The ability of two single-stranded polynucleotide preparations to hybridize together is a measure of their nucleotide sequence complementarity, e.g., base-pairing between nucleotides, such as A-T, G-C, etc. The invention thus also relates to polynucleotides, and their complements, which hybridize to a polynucleotide comprising a nucleotide sequence as set forth in Tables 1 and 2 and genomic sequences thereof. A nucleotide sequence hybridizing to the latter sequence will have a complementary polynucleotide strand, or act as a template for one in the presence of a polymerase (i.e., an appropriate polynucleotide synthesizing enzyme). The present invention includes both strands of polynucleotide, e.g., a sense strand and an anti-sense strand.

Hybridization conditions can be chosen to select polynucleotides which have a desired amount of nucleotide complementarity with the nucleotide sequences set forth in Tables 1 and 2 and genomic sequences thereof. A polynucleotide capable of hybridizing to such sequence, preferably, possesses, e.g., about 70%, 75%, 80%, 85%, 87%, 90%, 92%, 95%, 97%, 99%, or 100% complementarity, between the sequences. The present invention particularly relates to polynucleotide sequences which hybridize to the nucleotide sequences set forth in Tables 1 and 2 or genomic sequences thereof, under low or high stringency conditions. These conditions can be used, e.g., to select corresponding homologs in non-human species.

Polynucleotides which hybridize to polynucleotides of the present invention can be selected in various ways. Filter-type blots (i.e., matrices containing polynucleotide, such as nitrocellulose), glass chips, and other matrices and substrates comprising polynucleotides (short or long) of interest, can be incubated in a prehybridization solution (e.g., 6X SSC, 0.5% SDS, 100 µg/ml denatured salmon sperm DNA, 5X Denhardt's solution, and 50% formamide), at 22-68°C, overnight, and then hybridized with a detectable polynucleotide probe under conditions appropriate to achieve the desired stringency. In general, when high homology or sequence identity is desired, a high temperature can be used (e.g., 65 °C). As the homology drops, lower washing temperatures are used. For salt concentrations, the lower the salt concentration, the higher the stringency. The length of the probe is another consideration. Very short probes (e.g., less than 100 base pairs) are washed at lower temperatures, even if the homology is high. With short probes, formamide can be omitted. See, e.g., *Current Protocols in Molecular Biology*, Chapter 6, Screening of Recombinant Libraries; Sambrook et al., *Molecular Cloning*, 1989, Chapter 9.

For instance, high stringency conditions can be achieved by incubating the blot overnight (e.g., at least 12 hours) with a long polynucleotide probe in a hybridization solution containing, e.g., about 5X SSC, 0.5% SDS, 100 µg/ml denatured salmon sperm DNA and 50% formamide, at 42°C. Blots can be washed at high stringency conditions that allow, e.g.,
5 for less than 5% bp mismatch (e.g., wash twice in 0.1% SSC and 0.1% SDS for 30 min at 65°C), i.e., selecting sequences having 95% or greater sequence identity.

Other non-limiting examples of high stringency conditions includes a final wash at 65°C in aqueous buffer containing 30 mM NaCl and 0.5% SDS. Another example of high stringent conditions is hybridization in 7% SDS, 0.5 M NaPO₄, pH 7, 1 mM EDTA at 50°C,
10 e.g., overnight, followed by one or more washes with a 1% SDS solution at 42°C.

Whereas high stringency washes can allow for less than 5% mismatch, reduced or low stringency conditions can permit up to 20% nucleotide mismatch. Hybridization at low stringency can be accomplished as above, but using lower formamide conditions, lower temperatures and/or lower salt concentrations, as well as longer periods of incubation time.

15 Hybridization can also be based on a calculation of melting temperature (T_m) of the hybrid formed between the probe and its target, as described in Sambrook et al..

Generally, the temperature T_m at which a short oligonucleotide (containing 18 nucleotides or fewer) will melt from its target sequence is given by the following equation: T_m =

(number of A's and T's) x 2°C + (number of C's and G's) x 4°C. For longer molecules,

20 $T_m = 81.5 + 16.6 \log_{10}[\text{Na}^+] + 0.41(\%GC) - 600/N$ where [Na⁺] is the molar concentration of sodium ions, %GC is the percentage of GC base pairs in the probe, and N is the length. Hybridization can be carried out at several degrees below this temperature to ensure that the probe and target can hybridize. Mismatches can be allowed for by lowering the temperature even further.

25 Stringent conditions can be selected to isolate sequences, and their complements, which have, e.g., at least about 90%, 95%, or 97%, nucleotide complementarity between the probe (e.g., a short polynucleotide of Tables 1 and 2 or genomic sequences thereof) and a target polynucleotide.

Other homologs of polynucleotides of the present invention can be obtained from
30 mammalian and non-mammalian sources according to various methods. For example, hybridization with a polynucleotide can be employed to select homologs, e.g., as described in Sambrook et al., *Molecular Cloning*, Chapter 11, 1989. Such homologs can have varying amounts of nucleotide and amino acid sequence identity and similarity to such

-13-

polynucleotides of the present invention. Mammalian organisms include, e.g., mice, rats, monkeys, pigs, cows, etc. Non-mammalian organisms include, e.g., vertebrates, invertebrates, zebra fish, chicken, *Drosophila*, *C. elegans*, *Xenopus*, yeast such as *S. pombe*, *S. cerevisiae*, roundworms, prokaryotes, plants, *Arabidopsis*, *artemia*, viruses, etc. The degree of nucleotide sequence identity between human and mouse can be about, e.g. 70% or more, 85% or more for open reading frames, etc.

Alignment

Alignments can be accomplished by using any effective algorithm. For pairwise alignments of DNA sequences, the methods described by Wilbur-Lipman (e.g., Wilbur and Lipman, *Proc. Natl. Acad. Sci.*, 80:726-730, 1983) or Martinez/Needleman-Wunsch (e.g., Martinez, *Nucleic Acid Res.*, 11:4629-4634, 1983) can be used. For instance, if the Martinez/Needleman-Wunsch DNA alignment is applied, the minimum match can be set at 9, gap penalty at 1.10, and gap length penalty at 0.33. The results can be calculated as a similarity index, equal to the sum of the matching residues divided by the sum of all residues and gap characters, and then multiplied by 100 to express as a percent. Similarity index for related genes at the nucleotide level in accordance with the present invention can be greater than 70%, 80%, 85%, 90%, 95%, 99%, or more. Pairs of protein sequences can be aligned by the Lipman-Pearson method (e.g., Lipman and Pearson, *Science*, 227:1435-1441, 1985) with k-tuple set at 2, gap penalty set at 4, and gap length penalty set at 12. Results can be expressed as percent similarity index, where related genes at the amino acid level in accordance with the present invention can be greater than 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, or more. Various commercial and free sources of alignment programs are available, e.g., MegAlign by DNA Star, BLAST (National Center for Biotechnology Information), BCM (Baylor College of Medicine) Launcher, etc.

Percent sequence identity can also be determined by other conventional methods, e.g., as described in Altschul et al., *Bull. Math. Bio.* 48: 603-616, 1986 and Henikoff and Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915-10919, 1992.

Specific polynucleotide probes

A polynucleotide of the present invention can comprise any continuous nucleotide sequence of Tables 1 and 2, sequences which share sequence identity thereto, or complements thereof. The term "probe" refers to any substance that can be used to detect,

identify, isolate, etc., another substance. A polynucleotide probe is comprised of nucleic acid can be used to detect, identify, etc., other nucleic acids, such as DNA and RNA.

These polynucleotides can be of any desired size that is effective to achieve the specificity desired. For example, a probe can be from about 7 or 8 nucleotides to several thousand nucleotides, depending upon its use and purpose. For instance, a probe used as a primer PCR can be shorter than a probe used in an ordered array of polynucleotide probes. Probe sizes vary, and the invention is not limited in any way by their size, e.g., probes can be from about 7-2000 nucleotides, 7-1000, 8-700, 8-600, 8-500, 8-400, 8-300, 8-150, 8-100, 8-75, 7-50, 10-25, 14-16, at least about 8, at least about 10, at least about 15, at least about 25, etc. The polynucleotides can have non-naturally-occurring nucleotides, e.g., inosine, AZT, 3TC, etc. The polynucleotides can have 100% sequence identity or complementarity to a sequence of Tables 1 and 2, or it can have mismatches or nucleotide substitutions, e.g., 1, 2, 3, 4, or 5 substitutions. The probes can be single-stranded or double-stranded.

In accordance with the present invention, a polynucleotide can be present in a kit, where the kit includes, e.g., one or more polynucleotides, a desired buffer (e.g., phosphate, tris, etc.), detection compositions, RNA or cDNA from different tissues to be used as controls, libraries, etc. The polynucleotide can be labeled or unlabeled, with radioactive or non-radioactive labels as known in the art. Kits can comprise one or more pairs of polynucleotides for amplifying nucleic acids specific for differentially-regulated genes of the present invention, e.g., comprising a forward and reverse primer effective in PCR. These include both sense and anti-sense orientations. For instance, in PCR-based methods (such as RT-PCR), a pair of primers are typically used, one having a sense sequence and the other having an antisense sequence.

Another aspect of the present invention is a nucleotide sequence that is specific to, or for, a selective polynucleotide. The phrases "specific for" or "specific to" a polynucleotide have a functional meaning that the polynucleotide can be used to identify the presence of one or more target genes in a sample. It is specific in the sense that it can be used to detect polynucleotides above background noise ("non-specific binding"). A specific sequence is a defined order of nucleotides which occurs in the polynucleotide, e.g., in the nucleotide sequences of Tables 1 and 2. A probe or mixture of probes can comprise a sequence or sequences that are specific to a plurality of target sequences, e.g., where the sequence is a consensus sequence, a functional domain, etc., e.g., capable of recognizing a family of related genes. Such sequences can be used as probes in any of the methods described herein or

incorporated by reference. Both sense and antisense nucleotide sequences are included. A specific polynucleotide according to the present invention can be determined routinely.

A polynucleotide comprising a specific sequence can be used as a hybridization probe to identify the presence of, e.g., human or mouse polynucleotide, in a sample comprising a mixture of polynucleotides, e.g., on a Northern blot. Hybridization can be performed under high stringent conditions (see, above) to select polynucleotides (and their complements which can contain the coding sequence) having at least 90%, 95%, 99%, etc., identity (i.e., complementarity) to the probe, but less stringent conditions can also be used. A specific polynucleotide sequence can also be fused in-frame, at either its 5' or 3' end, to various nucleotide sequences as mentioned throughout the patent, including coding sequences for enzymes, detectable markers, GFP, etc, expression control sequences, etc.

A polynucleotide probe, especially one that is specific to a polynucleotide of the present invention, can be used in gene detection and hybridization methods as already described. In one embodiment, a specific polynucleotide probe can be used to detect whether a particular tissue or cell-type is present in a target sample. To carry out such a method, a selective polynucleotide can be chosen which is characteristic of the desired target tissue. Such polynucleotide is preferably chosen so that it is expressed or displayed in the target tissue, but not in other tissues which are present in the sample. For instance, if detection of prostate is desired, it may not matter whether the selective polynucleotide is expressed in other tissues, as long as it is not expressed in cells normally present in blood, e.g., peripheral blood mononuclear cells. Starting from the selective polynucleotide, a specific polynucleotide probe can be designed which hybridizes (if hybridization is the basis of the assay) under the hybridization conditions to the selective polynucleotide, whereby the presence of the selective polynucleotide can be determined.

Probes which are specific for polynucleotides of the present invention can also be prepared using involve transcription-based systems, e.g., incorporating an RNA polymerase promoter into a selective polynucleotide of the present invention, and then transcribing anti-sense RNA using the polynucleotide as a template. See, e.g., U.S. Pat. No. 5,545,522.

Polynucleotide composition

A polynucleotide according to the present invention can comprise, e.g., DNA, RNA, synthetic polynucleotide, peptide polynucleotide, modified nucleotides, dsDNA, ssDNA, ssRNA, dsRNA, and mixtures thereof. A polynucleotide can be single- or double-stranded,

-16-

triplex, DNA:RNA, duplexes, comprise hairpins, and other secondary structures, etc.

Nucleotides comprising a polynucleotide can be joined via various known linkages, e.g., ester, sulfamate, sulfamide, phosphorothioate, phosphoramidate, methylphosphonate, carbamate, etc., depending on the desired purpose, e.g., resistance to nucleases, such as
5 RNase H, improved in vivo stability, etc. See, e.g., U.S. Pat. No. 5,378,825. Any desired nucleotide or nucleotide analog can be incorporated, e.g., 6-mercaptoguanine, 8-oxo-guanine, etc.

Various modifications can be made to the polynucleotides, such as attaching detectable markers (avidin, biotin, radioactive elements, fluorescent tags and dyes, energy
10 transfer labels, energy-emitting labels, binding partners, etc.) or moieties which improve hybridization, detection, and/or stability. The polynucleotides can also be attached to solid supports, e.g., nitrocellulose, magnetic or paramagnetic microspheres (e.g., as described in U.S. Pat. No. 5,411,863; U.S. Pat. No. 5,543,289; for instance, comprising ferromagnetic, supermagnetic, paramagnetic, superparamagnetic, iron oxide and polysaccharide), nylon,
15 agarose, diazotized cellulose, latex solid microspheres, polyacrylamides, etc., according to a desired method. See, e.g., U.S. Pat. Nos. 5,470,967, 5,476,925, and 5,478,893.

Polynucleotide according to the present invention can be labeled according to any desired method. The polynucleotide can be labeled using radioactive tracers such as ^{32}P , ^{35}S , ^3H , or ^{14}C , to mention some commonly used tracers. The radioactive labeling can be carried
20 out according to any method, such as, for example, terminal labeling at the 3' or 5' end using a radiolabeled nucleotide, polynucleotide kinase (with or without dephosphorylation with a phosphatase) or a ligase (depending on the end to be labeled). A non-radioactive labeling can also be used, combining a polynucleotide of the present invention with residues having immunological properties (antigens, haptens), a specific affinity for certain reagents
25 (ligands), properties enabling detectable enzyme reactions to be completed (enzymes or coenzymes, enzyme substrates, or other substances involved in an enzymatic reaction), or characteristic physical properties, such as fluorescence or the emission or absorption of light at a desired wavelength, etc.

30 Nucleic acid detection methods

Another aspect of the present invention relates to methods and processes for detecting differentially-regulated genes of the present invention. Detection methods have a variety of applications, including for diagnostic, prognostic, forensic, and research applications. To

accomplish gene detection, a polynucleotide in accordance with the present invention can be used as a "probe." The term "probe" or "polynucleotide probe" has its customary meaning in the art, e.g., a polynucleotide which is effective to identify (e.g., by hybridization), when used in an appropriate process, the presence of a target polynucleotide to which it is designed.

- 5 Identification can involve simply determining presence or absence, or it can be quantitative, e.g., in assessing amounts of a gene or gene transcript present in a sample. Probes can be useful in a variety of ways, such as for diagnostic purposes, to identify homologs, and to detect, quantitate, or isolate a polynucleotide of the present invention in a test sample.

Assays can be utilized which permit quantification and/or presence/absence detection
10 of a target nucleic acid in a sample. Assays can be performed at the single-cell level, or in a sample comprising many cells, where the assay is "averaging" expression over the entire collection of cells and tissue present in the sample. Any suitable assay format can be used, including, but not limited to, e.g., Southern blot analysis, Northern blot analysis, polymerase chain reaction ("PCR") (e.g., Saiki et al., *Science*, 241:53, 1988; U.S. Pat. Nos. 4,683,195,
15 4,683,202, and 6,040,166; *PCR Protocols: A Guide to Methods and Applications*, Innis et al., eds., Academic Press, New York, 1990), reverse transcriptase polymerase chain reaction ("RT-PCR"), anchored PCR, rapid amplification of cDNA ends ("RACE") (e.g., Schaefer in *Gene Cloning and Analysis: Current Innovations*, Pages 99-115, 1997), ligase chain reaction ("LCR") (EP 320 308), one-sided PCR (Ohara et al., *Proc. Natl. Acad. Sci.*, 86:5673-5677,
20 1989), indexing methods (e.g., U.S. Pat. No. 5,508,169), *in situ* hybridization, differential display (e.g., Liang et al., *Nucl. Acid. Res.*, 21:3269-3275, 1993; U.S. Pat. Nos. 5,262,311, 5,599,672 and 5,965,409; WO97/18454; Prashar and Weissman, *Proc. Natl. Acad. Sci.*, 93:659-663, and U.S. Pat. Nos. 6,010,850 and 5,712,126; Welsh et al., *Nucleic Acid Res.*, 20:4965-4970, 1992, and U.S. Pat. No. 5,487,985) and other RNA fingerprinting techniques,
25 nucleic acid sequence based amplification ("NASBA") and other transcription based amplification systems (e.g., U.S. Pat. Nos. 5,409,818 and 5,554,527; WO 88/10315), polynucleotide arrays (e.g., U.S. Pat. Nos. 5,143,854, 5,424,186; 5,700,637, 5,874,219, and 6,054,270; PCT WO 92/10092; PCT WO 90/15070), Qbeta Replicase (PCT/US87/00880), Strand Displacement Amplification ("SDA"), Repair Chain Reaction ("RCR"), nuclease
30 protection assays, subtraction-based methods, Rapid-Scan™, etc. Additional useful methods include, but are not limited to, e.g., template-based amplification methods, competitive PCR (e.g., U.S. Pat. No. 5,747,251), redox-based assays (e.g., U.S. Pat. No. 5,871,918), Taqman-based assays (e.g., Holland et al., *Proc. Natl. Acad. Sci.*, 88:7276-7280, 1991; U.S. Pat. Nos.

5,210,015 and 5,994,063), real-time fluorescence-based monitoring (e.g., U.S. Pat. 5,928,907), molecular energy transfer labels (e.g., U.S. Pat. Nos. 5,348,853, 5,532,129, 5,565,322, 6,030,787, and 6,117,635; Tyagi and Kramer, *Nature Biotech.*, 14:303-309, 1996). Any method suitable for single cell analysis of gene or protein expression can be
5 used, including in situ hybridization, immunocytochemistry, MACS, FACS, flow cytometry, etc. For single cell assays, expression products can be measured using antibodies, PCR, or other types of nucleic acid amplification (e.g., Brady et al., *Methods Mol. & Cell. Biol.* 2, 17-25, 1990; Eberwine et al., 1992, *Proc. Natl. Acad. Sci.*, 89, 3010-3014, 1992; U.S. Pat. No. 5,723,290). These and other methods can be carried out conventionally, e.g., as described in
10 the mentioned publications.

Many of such methods may require that the polynucleotide is labeled, or comprises a particular nucleotide type useful for detection. The present invention includes such modified polynucleotides that are necessary to carry out such methods. Thus, polynucleotides can be DNA, RNA, DNA:RNA hybrids, PNA, etc., and can comprise any modification or
15 substituent which is effective to achieve detection.

Detection can be desirable for a variety of different purposes, including research, diagnostic, prognostic, and forensic. For diagnostic purposes, it may be desirable to identify the presence or quantity of a polynucleotide sequence in a sample, where the sample is obtained from tissue, cells, body fluids, etc. In a preferred method as described in more
20 detail below, the present invention relates to a method of detecting a polynucleotide comprising, contacting a target polynucleotide in a test sample with a polynucleotide probe under conditions effective to achieve hybridization between the target and probe; and detecting hybridization.

Any test sample in which it is desired to identify a polynucleotide or polypeptide
25 thereof can be used, including, e.g., blood, urine, saliva, stool (for extracting nucleic acid, see, e.g., U.S. Pat. No. 6,177,251), swabs comprising tissue, biopsied tissue, tissue sections, cultured cells, etc.

Detection can be accomplished in combination with polynucleotide probes for other genes, e.g., genes which are expressed in other disease states, tissues, cells, such as brain,
30 heart, kidney, spleen, thymus, liver, stomach, small intestine, colon, muscle, lung, testis, placenta, pituitary, thyroid, skin, adrenal gland, pancreas, salivary gland, uterus, ovary, prostate gland, peripheral blood cells (T-cells, lymphocytes, etc.), embryo, normal breast fat,

adult and embryonic stem cells, specific cell-types, such as endothelial, epithelial, myocytes, adipose, luminal epithelial, basoepithelial, myoepithelial, stromal cells, etc.

Polynucleotides can be used in wide range of methods and compositions, including for detecting, diagnosing, staging, grading, assessing, prognosticating, etc. diseases and disorders associated with differentially-regulated genes of the present invention, for monitoring or assessing therapeutic and/or preventative measures, in ordered arrays, etc. Any method of detecting genes and polynucleotides of Tables 1 and 2 can be used; certainly, the present invention is not to be limited how such methods are implemented.

Along these lines, the present invention relates to methods of detecting differentially-regulated genes described herein in a sample comprising nucleic acid. Such methods can comprise one or more the following steps in any effective order, e.g., contacting said sample with a polynucleotide probe under conditions effective for said probe to hybridize specifically to nucleic acid in said sample, and detecting the presence or absence of probe hybridized to nucleic acid in said sample, wherein said probe is a polynucleotide which is Tables 1 and 2, a polynucleotide having, e.g., about 70%, 80%, 85%, 90%, 95%, 99%, or more sequence identity thereto, effective or specific fragments thereof, or complements thereto. The detection method can be applied to any sample, e.g., cultured primary, secondary, or established cell lines, tissue biopsy, blood, urine, stool, and other bodily fluids, for any purpose.

Contacting the sample with probe can be carried out by any effective means in any effective environment. It can be accomplished in a solid, liquid, frozen, gaseous, amorphous, solidified, coagulated, colloid, etc., mixtures thereof, matrix. For instance, a probe in an aqueous medium can be contacted with a sample which is also in an aqueous medium, or which is affixed to a solid matrix, or vice-versa.

Generally, as used throughout the specification, the term "effective conditions" means, e.g., the particular milieu in which the desired effect is achieved. Such a milieu, includes, e.g., appropriate buffers, oxidizing agents, reducing agents, pH, co-factors, temperature, ion concentrations, suitable age and/or stage of cell (such as, in particular part of the cell cycle, or at a particular stage where particular genes are being expressed) where cells are being used, culture conditions (including substrate, oxygen, carbon dioxide, etc.). When hybridization is the chosen means of achieving detection, the probe and sample can be combined such that the resulting conditions are functional for said probe to hybridize specifically to nucleic acid in said sample.

The phrase "hybridize specifically" indicates that the hybridization between single-stranded polynucleotides is based on nucleotide sequence complementarity. The effective conditions are selected such that the probe hybridizes to a preselected and/or definite target nucleic acid in the sample. For instance, if detection of a gene set forth in Tables 1 and 2 is
5 desired, a probe can be selected which can hybridize to such target gene under high stringent conditions, without significant hybridization to other genes in the sample. To detect homologs of a gene set forth in Tables 1 and 2, the effective hybridization conditions can be less stringent, and/or the probe can comprise codon degeneracy, such that a homolog is detected in the sample.

10 As already mentioned, the methods can be carried out by any effective process, e.g., by Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, *in situ* hybridization, etc., as indicated above. When PCR based techniques are used, two or more probes are generally used. One probe can be specific for a defined sequence which is characteristic of a selective polynucleotide, but the other probe can be
15 specific for the selective polynucleotide, or specific for a more general sequence, e.g., a sequence such as polyA which is characteristic of mRNA, a sequence which is specific for a promoter, ribosome binding site, or other transcriptional features, a consensus sequence (e.g., representing a functional domain). For the former aspects, 5' and 3' probes (e.g., polyA, Kozak, etc.) are preferred which are capable of specifically hybridizing to the ends of
20 transcripts. When PCR is utilized, the probes can also be referred to as "primers" in that they can prime a DNA polymerase reaction.

In addition to testing for the presence or absence of polynucleotides, the present invention also relates to determining the amounts at which polynucleotides of the present invention are expressed in sample and determining the differential expression of such
25 polynucleotides in samples.. Such methods can involve substantially the same steps as described above for presence/absence detection, e.g., contacting with probe, hybridizing, and detecting hybridized probe, but using more quantitative methods and/or comparisons to standards.

The amount of hybridization between the probe and target can be determined by any
30 suitable methods, e.g., PCR, RT-PCR, RACE PCR, Northern blot, polynucleotide microarrays, Rapid-Scan, etc., and includes both quantitative and qualitative measurements. For further details, see the hybridization methods described above and below. Determining by such hybridization whether the target is differentially expressed (e.g., up-regulated or

differentially-regulated) in the sample can also be accomplished by any effective means. For instance, the target's expression pattern in the sample can be compared to its pattern in a known standard, such as in a normal tissue, or it can be compared to another gene in the same sample. When a second sample is utilized for the comparison, it can be a sample of normal
5 tissue that is known not to contain diseased cells. The comparison can be performed on samples which contain the same amount of RNA (such as polyadenylated RNA or total RNA), or, on RNA extracted from the same amounts of starting tissue. Such a second sample can also be referred to as a control or standard. Hybridization can also be compared to a second target in the same tissue sample. Experiments can be performed that determine a
10 ratio between the target nucleic acid and a second nucleic acid (a standard or control), e.g., in a normal tissue. When the ratio between the target and control are substantially the same in a normal and sample, the sample is determined or diagnosed not to contain cells. However, if the ratio is different between the normal and sample tissues, the sample is determined to contain cancer cells. The approaches can be combined, and one or more second samples, or
15 second targets can be used. Any second target nucleic acid can be used as a comparison, including "housekeeping" genes, such as beta-actin, alcohol dehydrogenase, or any other gene whose expression does not vary depending upon the disease status of the cell.

Methods of identifying polymorphisms, mutations, etc., of a differentially-regulated gene
20 Polynucleotides of the present invention can also be utilized to identify mutant alleles, SNPs, gene rearrangements and modifications, and other polymorphisms of the wild-type gene. Mutant alleles, polymorphisms, SNPs, etc., can be identified and isolated from cancers that are known, or suspected to have, a genetic component. Identification of such genes can be carried out routinely (see, above for more guidance), e.g., using PCR, hybridization
25 techniques, direct sequencing, mismatch reactions (see, e.g., above), RFLP analysis, SSCP (e.g., Orita et al., *Proc. Natl. Acad. Sci.*, 86:2766, 1992), etc., where a polynucleotide having a sequence selected from Tables 1 and 2 is used as a probe, or genomic sequences thereof. The selected mutant alleles, SNPs, polymorphisms, etc., can be used diagnostically to determine whether a subject has, or is susceptible to a disorder associated with a
30 differentially-regulated gene, as well as to design therapies and predict the outcome of the disorder. Methods involve, e.g., diagnosing a disorder associated with a differentially-regulated gene or determining susceptibility to a disorder, comprising, detecting the presence of a mutation in a gene selected from Tables 1 and 2. The detecting can be carried out by any

-22-

effective method, e.g., obtaining cells from a subject, determining the gene sequence or structure of a target gene (using, e.g., mRNA, cDNA, genomic DNA, etc), comparing the sequence or structure of the target gene to the structure of the normal gene, whereby a difference in sequence or structure indicates a mutation in the gene in the subject.

- 5 Polynucleotides can also be used to test for mutations, SNPs, polymorphisms, etc., e.g., using mismatch DNA repair technology as described in U.S. Pat. No. 5,683,877; U.S. Pat. No. 5,656,430; Wu et al., *Proc. Natl. Acad. Sci.*, 89:8779-8783, 1992.

The present invention also relates to methods of detecting polymorphisms in a differentially-regulated gene, comprising, e.g., comparing the structure of: genomic DNA
10 comprising all or part of said gene, mRNA comprising all or part of said gene, cDNA comprising all or part of said gene, or a polypeptide comprising all or part of said gene, with the structure of said gene as set forth herein. The methods can be carried out on a sample from any source, e.g., cells, tissues, body fluids, blood, urine, stool, hair, egg, sperm, etc.

- 15 These methods can be implemented in many different ways. For example, "comparing the structure" steps include, but are not limited to, comparing restriction maps, nucleotide sequences, amino acid sequences, RFLPs, DNase sites, DNA methylation fingerprints (e.g., U.S. Pat. No. 6,214,556), protein cleavage sites, molecular weights, electrophoretic mobilities, charges, ion mobility, etc., between a standard gene
20 and a test gene. The term "structure" can refer to any physical characteristics or configurations which can be used to distinguish between nucleic acids and polypeptides. The methods and instruments used to accomplish the comparing step depends upon the physical characteristics which are to be compared. Thus, various techniques are contemplated, including, e.g., sequencing machines (both amino acid and polynucleotide),
25 electrophoresis, mass spectrometer (U.S. Pat. Nos. 6,093,541, 6,002,127), liquid chromatography, HPLC, etc.

- To carry out such methods, "all or part" of the gene or polypeptide can be compared. For example, if nucleotide sequencing is utilized, the entire gene can be sequenced, including promoter, introns, and exons, or only parts of it can be sequenced
30 and compared, e.g., exon 1, exon 2, etc.

Mutagenesis

Mutated polynucleotide sequences of the present invention are useful for various

purposes, e.g., to create mutations of the polypeptides they encode, to identify functional regions of genomic DNA, to produce probes for screening libraries, etc. Mutagenesis can be carried out routinely according to any effective method, e.g., oligonucleotide-directed (Smith, M., *Ann. Rev. Genet.* 19:423-463, 1985), degenerate oligonucleotide-directed (Hill et al., *Method Enzymology*, 155:558-568, 1987), region-specific (Myers et al., *Science*, 229:242-246, 1985; Derbyshire et al., *Gene*, 46:145, 1986; Ner et al., *DNA*, 7:127, 1988), linker-scanning (McKnight and Kingsbury, *Science*, 217:316-324, 1982), directed using PCR, recursive ensemble mutagenesis (Arkin and Yourvan, *Proc. Natl. Acad. Sci.*, 89:7811-7815, 1992), random mutagenesis (e.g., U.S. Pat. Nos. 5,096,815; 5,198,346; and 5,223,409), site-directed mutagenesis (e.g., Walder et al., *Gene*, 42:133, 1986; Bauer et al., *Gene*, 37:73, 1985; Craik, *Bio Techniques*, January 1985, 12-19; Smith et al., *Genetic Engineering: Principles and Methods*, Plenum Press, 1981), phage display (e.g., Lowman et al., *Biochem.* 30:10832-10837, 1991; Ladner et al., U.S. Pat. No. 5,223,409; Huse, WIPO Publication WO 92/06204), etc. Desired sequences can also be produced by the assembly of target sequences using mutually priming oligonucleotides (Uhlmann, *Gene*, 71:29-40, 1988). For directed mutagenesis methods, analysis of the three-dimensional structure of a polypeptide can be used to guide and facilitate making mutants which effect polypeptide activity. Sites of substrate-enzyme interaction or other biological activities can also be determined by analysis of crystal structure as determined by such techniques as nuclear magnetic resonance, crystallography or photoaffinity labeling. See, for example, de Vos et al., *Science* 255:306-312, 1992; Smith et al., *J. Mol. Biol.* 224:899-904, 1992; Wlodaver et al., *FEBS Lett.* 309:59-64, 1992.

In addition, libraries of differentially-regulated genes and fragments thereof can be used for screening and selection of gene variants. For instance, a library of coding sequences can be generated by treating a double-stranded DNA with a nuclease under conditions where the nicking occurs, e.g., only once per molecule, denaturing the double-stranded DNA, renaturing it to for double-stranded DNA that can include sense/antisense pairs from different nicked products, removing single-stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting DNAs into an expression vecore. By this method, expression libraries can be made comprising "mutagenized" differentially-regulated genes. The entire coding sequence or parts thereof can be used.

Polynucleotide expression, polypeptides produced thereby, and specific-binding partners thereto.

A polynucleotide according to the present invention can be expressed in a variety of different systems, in vitro and in vivo, according to the desired purpose. For example, a
5 polynucleotide can be inserted into an expression vector, introduced into a desired host, and cultured under conditions effective to achieve expression of a polypeptide coded for by the polynucleotide, to search for specific binding partners. Effective conditions include any culture conditions which are suitable for achieving production of the polypeptide by the host cell, including effective temperatures, pH, medium, additives to the media in which the host
10 cell is cultured (e.g., additives which amplify or induce expression such as butyrate, or methotrexate if the coding polynucleotide is adjacent to a dhfr gene), cycloheximide, cell densities, culture dishes, etc. A polynucleotide can be introduced into the cell by any effective method including, e.g., naked DNA, calcium phosphate precipitation, electroporation, injection, DEAE-Dextran mediated transfection, fusion with liposomes,
15 association with agents which enhance its uptake into cells, viral transfection. A cell into which a polynucleotide of the present invention has been introduced is a transformed host cell. The polynucleotide can be extrachromosomal or integrated into a chromosome(s) of the host cell. It can be stable or transient. An expression vector is selected for its compatibility with the host cell. Host cells include, mammalian cells, e.g., COS, CV1, BHK, CHO, HeLa,
20 LTK, NIH 3T3, PC-3 (CRL-1435), LNCaP (CRL-1740), CA-HPV-10 (CRL-2220), PZ-HPV-7 (CRL-2221), MDA-PCa 2b (CRL-2422), 22Rv1 (CRL2505), NCI-H660 (CRL-5813), HS 804.Sk (CRL-7535), LNCaP-FGF (CRL-10995), RWPE-1 (CRL-11609), RWPE-2 (CRL-11610), PWR-1E (CRL 11611), rat MAT-Ly-LuB-2 (CRL-2376), and other prostate cells, insect cells, such as Sf9 (*S. frugipeda*) and *Drosophila*, bacteria, such as
25 *E. coli*, *Streptococcus*, *Bacillus*, yeast, such as *Sacharomyces*, *S. cerevisiae*, fungal cells, plant cells, embryonic or adult stem cells (e.g., mammalian, such as mouse or human).

Expression control sequences are similarly selected for host compatibility and a desired purpose, e.g., high copy number, high amounts, induction, amplification, controlled expression. Other sequences which can be employed include enhancers such as from SV40,
30 CMV, RSV, inducible promoters, cell-type specific elements, or sequences which allow selective or specific cell expression. Promoters that can be used to drive its expression, include, e.g., the endogenous promoter, MMTV, SV40, trp, lac, tac, or T7 promoters for bacterial hosts; or alpha factor, alcohol oxidase, or PGH promoters for yeast. RNA

promoters can be used to produced RNA transcripts, such as T7 or SP6. See, e.g., Melton et al., *Polynucleotide Res.*, 12(18):7035-7056, 1984; Dunn and Studier. *J. Mol. Bio.*, 166:477-435, 1984; U.S. Pat. No. 5,891,636; Studier et al., *Gene Expression Technology, Methods in Enzymology*, 85:60-89, 1987. In addition, as discussed above, translational signals (including
5 in-frame insertions) can be included.

When a polynucleotide is expressed as a heterologous gene in a transfected cell line, the gene is introduced into a cell as described above, under effective conditions in which the gene is expressed. The term "heterologous" means that the gene has been introduced into the cell line by the "hand-of-man." Introduction of a gene into a cell line is discussed above.
10 The transfected (or transformed) cell expressing the gene can be lysed or the cell line can be used intact.

For expression and other purposes, a polynucleotide can contain codons found in a naturally-occurring gene, transcript, or cDNA, for example, e.g., as set forth in Tables 1 and 2, or it can contain degenerate codons coding for the same amino acid sequences. For
15 instance, it may be desirable to change the codons in the sequence to optimize the sequence for expression in a desired host. See, e.g., U.S. Pat. Nos. 5,567,600 and 5,567,862.

A polypeptide according to the present invention can be recovered from natural sources, transformed host cells (culture medium or cells) according to the usual methods, including, detergent extraction (e.g., non-ionic detergent, Triton X-100, CHAPS,
20 octylglucoside, Igepal CA-630), ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxyapatite chromatography, lectin chromatography, gel electrophoresis. Protein refolding steps can be used, as necessary, in completing the configuration of the mature protein. Finally, high performance liquid chromatography
25 (HPLC) can be employed for purification steps. Another approach is express the polypeptide recombinantly with an affinity tag (Flag epitope, HA epitope, myc epitope, 6xHis, maltose binding protein, chitinase, etc) and then purify by anti-tag antibody-conjugated affinity chromatography.

The present invention also relates to antibodies, and other specific-binding partners,
30 which are specific for polypeptides encoded by polynucleotides of the present invention. Antibodies, e.g., polyclonal, monoclonal, recombinant, chimeric, humanized, single-chain, Fab, and fragments thereof, can be prepared according to any desired method. See, also, screening recombinant immunoglobulin libraries (e.g., Orlandi et al., *Proc. Natl. Acad. Sci.*,

86:3833-3837, 1989; Huse et al., *Science*, 256:1275-1281, 1989); in vitro stimulation of lymphocyte populations; Winter and Milstein, *Nature*, 349: 293-299, 1991. The antibodies can be IgM, IgG, subtypes, IgG2a, IgG1, etc. Antibodies, and immune responses, can also be generated by administering naked DNA See, e.g., U.S. Pat. Nos. 5,703,055; 5,589,466; 5,580,859. Antibodies can be used from any source, including, goat, rabbit, mouse, chicken (e.g., IgY; see, Duan, W0/029444 for methods of making antibodies in avian hosts, and harvesting the antibodies from the eggs). An antibody specific for a polypeptide means that the antibody recognizes a defined sequence of amino acids within or including the polypeptide. Other specific binding partners include, e.g., aptamers and PNA, can be prepared against specific epitopes or domains of differentially regulated genes.

The preparation of polyclonal antibodies is well-known to those skilled in the art. See, for example, Green et al., Production of Polyclonal Antisera, in IMMUNOCHEMICAL PROTOCOLS (Manson, ed.), pages 1-5 (Humana Press 1992); Coligan et al., Production of Polyclonal Antisera in Rabbits, Rats, Mice and Hamsters, in CURRENT PROTOCOLS IN IMMUNOLOGY, section 2.4.1 (1992). The preparation of monoclonal antibodies likewise is conventional. See, for example, Kohler & Milstein, *Nature* 256:495 (1975); Coligan et al., sections 2.5.1-2.6.7; and Harlow et al., ANTIBODIES: A LABORATORY MANUAL, page 726 (Cold Spring Harbor Pub. 1988).

Antibodies can also be humanized, e.g., where they are to be used therapeutically. Humanized monoclonal antibodies are produced by transferring mouse complementarity determining regions from heavy and light variable chains of the mouse immunoglobulin into a human variable domain, and then substituting human residues in the framework regions of the murine counterparts. The use of antibody components derived from humanized monoclonal antibodies obviates potential problems associated with the immunogenicity of murine constant regions. General techniques for cloning murine immunoglobulin variable domains are described, for example, by Orlandi et al., *Proc. Nat'l Acad. Sci. USA* 86:3833 (1989), which is hereby incorporated in its entirety by reference. Techniques for producing humanized monoclonal antibodies are described, for example, in U.S. Pat. No. 6,054,297, Jones et al., *Nature* 321: 522 (1986); Riechmann et al., *Nature* 332: 323 (1988); Verhoeven et al., *Science* 239: 1534 (1988); Carter et al., *Proc. Nat'l Acad. Sci. USA* 89: 4285 (1992); Sandhu, *Crit. Rev. Biotech.* 12: 437 (1992); and Singer et al., *J. Immunol.* 150: 2844 (1993).

Antibodies of the invention also may be derived from human antibody fragments isolated from a combinatorial immunoglobulin library. See, for example, Barbas et al.,

METHODS: A COMPANION TO METHODS IN ENZYMOLOGY, VOL. 2, page 119 (1991); Winter et al., Ann. Rev. Immunol. 12: 433 (1994). Cloning and expression vectors that are useful for producing a human immunoglobulin phage library can be obtained commercially, for example, from STRATAGENE Cloning Systems (La Jolla, Calif.).

5 In addition, antibodies of the present invention may be derived from a human monoclonal antibody. Such antibodies are obtained from transgenic mice that have been "engineered" to produce specific human antibodies in response to antigenic challenge. In this technique, elements of the human heavy and light chain loci are introduced into strains of mice derived from embryonic stem cell lines that contain targeted disruptions of the
10 endogenous heavy and light chain loci. The transgenic mice can synthesize human antibodies specific for human antigens and can be used to produce human antibody-secreting hybridomas. Methods for obtaining human antibodies from transgenic mice are described, e.g., in Green et al., Nature Genet. 7:13 (1994); Lonberg et al., Nature 368:856 (1994); and Taylor et al., Int. Immunol. 6:579 (1994).

15 Antibody fragments of the present invention can be prepared by proteolytic hydrolysis of the antibody or by expression in E. coli of nucleic acid encoding the fragment. Antibody fragments can be obtained by pepsin or papain digestion of whole antibodies by conventional methods. For example, antibody fragments can be produced by enzymatic cleavage of antibodies with pepsin to provide a 5S fragment denoted F(ab')₂. This fragment can be
20 further cleaved using a thiol reducing agent, and optionally a blocking group for the sulfhydryl groups resulting from cleavage of disulfide linkages, to produce 3.5S Fab' monovalent fragments. Alternatively, an enzymatic cleavage using pepsin produces two monovalent Fab' fragments and an Fc fragment directly. These methods are described, for example, by Goldenberg, U.S. Pat. No. 4,036,945 and No. 4,331,647, and references
25 contained therein. These patents are hereby incorporated in their entireties by reference. See also Nisoihoff et al., Arch. Biochem. Biophys. 89:230 (1960); Porter, Biochem. J. 73:119 (1959); Edelman et al., METHODS IN ENZYMOLOGY, VOL. 1, page 422 (Academic Press 1967); and Coligan et al. at sections 2.8.1-2.8.10 and 2.10.1-2.10.4.

Other methods of cleaving antibodies, such as separation of heavy chains to form
30 monovalent light-heavy chain fragments, further cleavage of fragments, or other enzymatic, chemical, or genetic techniques can also be used. For example, Fv fragments comprise an association of V_H and V_L chains. This association may be noncovalent, as described in Inbar et al., Proc. Nat'l Acad. Sci. USA 69:2659 (1972). Alternatively, the

variable chains can be linked by an intermolecular disulfide bond or cross-linked by chemicals such as glutaraldehyde. See, e.g., Sandhu, *supra*. Preferably, the Fv fragments comprise V.sub.H and V.sub.L chains connected by a peptide linker. These single-chain antigen binding proteins (sFv) are prepared by constructing a structural gene comprising
5 nucleic acid sequences encoding the V.sub.H and V.sub.L domains connected by an oligonucleotide. The structural gene is inserted into an expression vector, which is subsequently introduced into a host cell such as *E. coli*. The recombinant host cells synthesize a single polypeptide chain with a linker peptide bridging the two V domains. Methods for producing sFvs are described, for example, by Whitlow et al., *METHODS: A
10 COMPANION TO METHODS IN ENZYMOLOGY*, VOL. 2, page 97 (1991); Bird et al., *Science* 242:423-426 (1988); Ladner et al., U.S. Pat. No. 4,946,778; Pack et al., *Bio/Technology* 11: 1271-77 (1993); and Sandhu, *supra*.

Another form of an antibody fragment is a peptide coding for a single complementarity-determining region (CDR). CDR peptides ("minimal recognition units") can
15 be obtained by constructing genes encoding the CDR of an antibody of interest. Such genes are prepared, for example, by using the polymerase chain reaction to synthesize the variable region from RNA of antibody-producing cells. See, for example, Larrick et al., *METHODS: A COMPANION TO METHODS IN ENZYMOLOGY*, VOL. 2, page 106 (1991).

The term "antibody" as used herein includes intact molecules as well as fragments
20 thereof, such as Fab, F(ab')₂, and Fv which are capable of binding to an epitopic determinant present in Bin1 polypeptide. Such antibody fragments retain some ability to selectively bind with its antigen or receptor. The term "epitope" refers to an antigenic determinant on an antigen to which the paratope of an antibody binds. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains
25 and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. Antibodies can be prepared against specific epitopes or polypeptide domains.

Antibodies which bind to a differentially-regulated polypeptide of the present invention can be prepared using an intact polypeptide or fragments containing small peptides
30 of interest as the immunizing antigen. For example, it may be desirable to produce antibodies that specifically bind to the N- or C-terminal domains of said polypeptide. The polypeptide or peptide used to immunize an animal which is derived from translated cDNA or chemically synthesized which can be conjugated to a carrier protein, if desired. Such commonly used

carriers which are chemically coupled to the immunizing peptide include keyhole limpet hemocyanin (KLH), thyroglobulin, bovine serum albumin (BSA), and tetanus toxoid.

Polyclonal or monoclonal antibodies can be further purified, for example, by binding to and elution from a matrix to which the polypeptide or a peptide to which the antibodies
5 were raised is bound. Those of skill in the art will know of various techniques common in the immunology arts for purification and/or concentration of polyclonal antibodies, as well as monoclonal antibodies (See for example, Coligan, et al., Unit 9, *Current Protocols in Immunology*, Wiley Interscience, 1994, incorporated by reference).

Anti-idiotypic technology can also be used to produce invention monoclonal
10 antibodies which mimic an epitope. For example, an anti-idiotypic monoclonal antibody made to a first monoclonal antibody will have a binding domain in the hypervariable region which is the "image" of the epitope bound by the first monoclonal antibody.

Methods of detecting polypeptides

15 Polypeptides coded for by a differentially-regulated gene of the present invention can be detected, visualized, determined, quantitated, etc. according to any effective method. useful methods include, e.g., but are not limited to, immunoassays, RIA (radioimmunoassay), ELISA, (enzyme-linked-immunosorbent assay), immunofluorescence, flow cytometry, histology, electron microscopy, light microscopy, in situ assays, immunoprecipitation,
20 Western blot, etc.

Immunoassays may be carried in liquid or on biological support. For instance, a sample (e.g., blood, stool, urine, cells, tissue, body fluids, etc.) can be brought in contact with and immobilized onto a solid phase support or carrier such as nitrocellulose, or other solid support that is capable of immobilizing cells, cell particles or soluble proteins. The support
25 may then be washed with suitable buffers followed by treatment with the detectably labeled differentially-regulated gene specific antibody. The solid phase support can then be washed with a buffer a second time to remove unbound antibody. The amount of bound label on solid support may then be detected by conventional means.

A "solid phase support or carrier" includes any support capable of binding an antigen,
30 antibody, or other specific binding partner. Supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, and magnetite. A support material can have any structural or physical configuration. Thus, the support configuration may be spherical, as in a bead, or cylindrical,

as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads

One of the many ways in which gene peptide-specific antibody can be detectably
5 labeled is by linking it to an enzyme and using it in an enzyme immunoassay (EIA). See,
e.g., Voller, A., "The Enzyme Linked Immunosorbent Assay (ELISA)," 1978, Diagnostic
Horizons 2, 1-7, Microbiological Associates Quarterly Publication, Walkersville, Md.);
Voller, A. et al., 1978, J. Clin. Pathol. 31, 507-520; Butler, J. E., 1981, Meth. Enzymol. 73,
482-523; Maggio, E. (ed.), 1980, Enzyme Immunoassay, CRC Press, Boca Raton, Fla.. The
10 enzyme which is bound to the antibody will react with an appropriate substrate, preferably a
chromogenic substrate, in such a manner as to produce a chemical moiety that can be
detected, for example, by spectrophotometric, fluorimetric or by visual means. Enzymes that
can be used to detectably label the antibody include, but are not limited to, malate
dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol
15 dehydrogenase, .alpha.-glycerophosphate, dehydrogenase, triose phosphate isomerase,
horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, .beta.-
galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase,
glucoamylase and acetylcholinesterase. The detection can be accomplished by colorimetric
methods that employ a chromogenic substrate for the enzyme. Detection may also be
20 accomplished by visual comparison of the extent of enzymatic reaction of a substrate in
comparison with similarly prepared standards.

Detection may also be accomplished using any of a variety of other immunoassays.
For example, by radioactively labeling the antibodies or antibody fragments, it is possible to
detect differentially-regulated peptides through the use of a radioimmunoassay (RIA). See,
25 e.g., Weintraub, B., Principles of Radioimmunoassays, Seventh Training Course on
Radioligand Assay Techniques, The Endocrine Society, March, 1986. The radioactive
isotope can be detected by such means as the use of a gamma counter or a scintillation
counter or by autoradiography.

It is also possible to label the antibody with a fluorescent compound. When the
30 fluorescently labeled antibody is exposed to light of the proper wave length, its presence can
then be detected due to fluorescence. Among the most commonly used fluorescent labeling
compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin,
allophycocyanin, o-phthaldehyde and fluorescamine. The antibody can also be detectably

-31-

labeled using fluorescence emitting metals such as those in the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as diethylenetriaminepentacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA).

5 The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of useful chemiluminescent labeling compounds are luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

10 Likewise, a bioluminescent compound may be used to label the antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

15

Tissue and Disease

The prostate is a secretory organ surrounding the neck of the bladder and urethra. Its primary function is to produce fluids and other materials necessary for sperm transport and maintenance. Structurally, it has both glandular and nonglandular components. The glandular component is predominantly comprised of ducts and acini responsible for the production and transport prostatic fluids. Epithelial cells are the main identifiable cell found in these regions, primarily of the basal and secretory types, but also endocrine-paracrine and transitional epithelial. The non-glandular component contains the capsular and muscle tissues, which, respectively, hold the organ together and function in fluid discharge. See, 25 e.g., Histology for Pathologists, Sternberg, S.S., editor, Raven Press, NY, 1992, Chapter 40.

The major diseases of the prostate include, e.g., prostatic hyperplasia (BPH), prostatitis, and prostate cancer (e.g., prostatic adenocarcinoma). BPH is a benign, proliferative disease of the prostatic epithelial cells. While it may cause urinary tract obstruction in some patients, for the most part, it is generally asymptomatic. Prostate cancer, 30 on the other hand, is the most common form of cancer in white males in the United States, occurring predominantly in males over age 50. The prevalence of prostate diseases, such as prostate cancer, has made the discovery of prostate selective markers and gene expression patterns of great importance.

The most common scale of assessing prostate pathology is the Gleason grading system. See, e.g., Bostwick, *Am. J. Clin. Path.*, 102: s38-s56, 1994. Once the cancer is identified, staging can assess the size, location, and extent of the cancer. Several different staging scales are commonly used, including stages A-D, and Tumor-Nodes-Metastases (TNM). For treatment, diagnosis, staging, etc., of prostate conditions, methods can be carried out analogously to, and in combination with, U.S. Pat. Nos. 6,107,090; 6,057,116; 6,034,218; 6,004,267; 5,919,638; 5,882,864; 5,763,202; 5,747,264; 5,688,649; 5,552,277.

In addition, the present invention relates to methods of assessing a therapeutic or preventative intervention in a subject having a prostate cancer, comprising, e.g., detecting the expression levels of differentially-regulated target genes, wherein the target genes comprise a gene which is represented by a sequence selected from Tables 1 and 2, or, a gene represented by a sequence having 95% sequence identity or more to a sequence selected from Tables 1 and 2. By "therapeutic or preventative intervention," it is meant, e.g., a drug administered a patient, surgery, radiation, chemotherapy, and other measures taken to prevent a cancer or treat a cancer.

Grading, staging, comparing, assessing, methods and compositions

The present invention also relates to methods and compositions for staging and grading cancers. As already defined, staging relates to determining the extent of a cancer's spread, including its size and the degree to which other tissues, such as lymph nodes are involved in the cancer. Grading refers to the degree of a cell's retention of the characteristics of the tissue of its origin. A lower grade cancer comprises tumor cells that more closely resemble normal cells than a medium or higher grade cancer. Grading can be a useful diagnostic and prognostic tool. Higher grade cancers usually behave more aggressively than lower grade cancers. Thus, knowledge of the cancer grade, as well as its stage, can be a significant factor in the choice of the appropriate therapeutic intervention for the particular patient, e.g., surgery, radiation, chemotherapy, etc. Staging and grading can also be used in conjunction with a therapy to assess its efficacy, to determine prognosis, to determine effective dosages, etc.

Various methods of staging and grading cancers can be employed in accordance with the present invention. A "cell expression profile" or "cell expression fingerprint" is a representation of the expression of various different genes (e.g., polynucleotide sequences of SEQ ID NOS 1-107) in a given cell or sample comprising cells. These cell expression

profiles can be useful as reference standards. The cell expression fingerprints can be used alone for grading, or in combination with other grading methods.

The present invention also relates to methods and compositions for diagnosing a prostate cancer, or determining susceptibility to a prostate cancer, using polynucleotides, polypeptides, and specific-binding partners of the present invention to detect, assess, 5 determine, etc., differentially-regulated genes of the present invention. In such methods, the gene can serve as a marker for prostate cancer, e.g., where the gene, when mutant, is a direct cause of the prostate cancer; where the gene is affected by another gene(s) which is directly responsible for the prostate cancer, e.g., when the gene is part of the same signaling pathway 10 as the directly responsible gene; and, where the gene is chromosomally linked to the gene(s) directly responsible for the prostate cancer, and segregates with it. Many other situations are possible. To detect, assess, determine, etc., a probe specific for the gene can be employed as described above and below. Any method of detecting and/or assessing the gene can be used, including detecting expression of the gene using polynucleotides, antibodies, or other 15 specific-binding partners.

The present invention relates to methods of diagnosing a disorder associated with prostate cancer, or determining a subject's susceptibility to such prostate cancer, comprising, e.g., assessing the expression of a differentially-regulated gene in a tissue sample comprising tissue or cells suspected of having prostate cancer (e.g., where the sample 20 comprises prostate). The phrase "diagnosing" indicates that it is determined whether the sample has a prostate cancer cells. "Determining a subject's susceptibility to a prostate cancer" indicates that the subject is assessed for whether s/he is predisposed to get such a disease or disorder, where the predisposition is indicated by abnormal expression of the gene (e.g., gene mutation, gene expression pattern is not normal, etc.). Predisposition or 25 susceptibility to a disease may result when a such disease is influenced by epigenetic, environmental, etc., factors.

By the phrase "assessing expression of a differentially-regulated gene," it is meant that the functional status of the gene is evaluated. This includes, but is not limited to, measuring expression levels of said gene, determining the genomic structure of said gene, 30 determining the mRNA structure of transcripts from said gene, or measuring the expression levels of polypeptide coded for by said gene. Thus, the term "assessing expression" includes evaluating the all aspects of the transcriptional and translational machinery of the gene. For instance, if a promoter defect causes, or is suspected of

causing, the disorder, then a sample can be evaluated (i.e., "assessed") by looking (e.g., sequencing or restriction mapping) at the promoter sequence in the gene, by detecting transcription products (e.g., RNA), by detecting translation product (e.g., polypeptide). Any measure of whether the gene is functional can be used, including, polypeptide, 5 polynucleotide, and functional assays for the gene's biological activity.

In making the assessment, it can be useful to compare the results to a normal gene, e.g., a gene which is not associated with the disorder. The nature of the comparison can be determined routinely, depending upon how the assessing is accomplished. If, for example, the mRNA levels of a sample is detected, then the mRNA levels of a normal can 10 serve as a comparison, or a gene which is known not to be affected by the disorder. Methods of detecting mRNA are well known, and discussed above, e.g., but not limited to, Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, etc. Similarly, if polypeptide production is used to evaluate the gene, then the polypeptide in a normal tissue sample can be used as a comparison, or, polypeptide 15 from a different gene whose expression is known not to be affected by the disorder. These are only examples of how such a method could be carried out.

Assessing the effects of therapeutic and preventative interventions (e.g., administration of a drug, chemotherapy, radiation, etc.) on prostate cancer is a major effort in drug discovery, clinical medicine, and pharmacogenomics. The evaluation of 20 therapeutic and preventative measures, whether experimental or already in clinical use, has broad applicability, e.g., in clinical trials, for monitoring the status of a patient, for analyzing and assessing animal models, and in any scenario involving cancer treatment and prevention. Analyzing the expression profiles of polynucleotides of the present invention can be utilized as a parameter by which interventions are judged and measured. Treatment 25 of a disorder can change the expression profile in some manner which is prognostic or indicative of the drug's effect on it. Changes in the profile can indicate, e.g., drug toxicity, return to a normal level, etc. Accordingly, the present invention also relates to methods of monitoring or assessing a therapeutic or preventative measure (e.g., chemotherapy, radiation, anti-neoplastic drugs, antibodies, etc.) in a subject having 30 prostate cancer, or, susceptible to such a disorder, comprising, e.g., detecting the expression levels of one or more differentially-regulated genes of the present invention. A subject can be a cell-based assay system, non-human animal model, human patient, etc. Detecting can be accomplished as described for the methods above and below. By

"therapeutic or preventative intervention," it is meant, e.g., a drug administered to a patient, surgery, radiation, chemotherapy, and other measures taken to prevent, treat, or diagnose prostate cancer.

Expression can be assessed in any sample comprising any tissue or cell type, body fluid, etc., as discussed for other methods of the present invention, including cells from prostate can be used, or cells derived from prostate. By the phrase "cells derived from prostate," it is meant that the derived cells originate from prostate, e.g., when metastasis from a primary tumor site has occurred, when a progenitor-type or pluripotent cell gives rise to other cells, etc.

10

Identifying agent methods

The present invention also relates to methods of identifying agents, and the agents themselves, which modulate prostate cancer genes. These agents can be used to modulate the biological activity of the polypeptide encoded for the gene, or the gene, itself. Agents which regulate the gene or its product are useful in variety of different environments, including as medicinal agents to treat or prevent disorders associated with prostate cancer genes and as research reagents to modify the function of tissues and cell.

Methods of identifying agents generally comprise steps in which an agent is placed in contact with the gene, transcription product, translation product, or other target, and then a determination is performed to assess whether the agent "modulates" the target. The specific method utilized will depend upon a number of factors, including, e.g., the target (i.e., is it the gene or polypeptide encoded by it), the environment (e.g., in vitro or in vivo), the composition of the agent, etc.

For modulating the expression of a prostate cancer gene, a method can comprise, in any effective order, one or more of the following steps, e.g., contacting a prostate cancer gene (e.g., in a cell population) with a test agent under conditions effective for said test agent to modulate the expression of the prostate cancer, and determining whether said test agent modulates said gene. An agent can modulate expression of a gene at any level, including transcription, translation, and/or perdurance of the nucleic acid (e.g., degradation, stability, etc.) in the cell. For modulating the biological activity of prostate cancer polypeptides, a method can comprise, in any effective order, one or more of the following steps, e.g., contacting a polypeptide (e.g., in a cell, lysate, or isolated) with a test agent under conditions

effective for said test agent to modulate the biological activity of said polypeptide, and determining whether said test agent modulates said biological activity.

Contacting a gene or polypeptide with the test agent can be accomplished by any suitable method and/or means that places the agent in a position to functionally control its expression or biological activity. Functional control indicates that the agent can exert its physiological effect on the gene or polypeptide through whatever mechanism it works. The choice of the method and/or means can depend upon the nature of the agent and the condition and type of environment in which the gene or polypeptide is presented, e.g., lysate, isolated, or in a cell population (such as, *in vivo*, *in vitro*, organ explants, etc.). For instance, if the cell population is an *in vitro* cell culture, the agent can be contacted with the cells by adding it directly into the culture medium. If the agent cannot dissolve readily in an aqueous medium, it can be incorporated into liposomes, or another lipophilic carrier, and then administered to the cell culture. Contact can also be facilitated by incorporation of agent with carriers and delivery molecules and complexes, by injection, by infusion, etc.

After the agent has been administered in such a way that it can gain access to the gene or polypeptide, it can be determined whether the test agent modulates the gene or polypeptide expression or biological activity. Modulation can be of any type, quality, or quantity, e.g., increase, facilitate, enhance, up-regulate, stimulate, activate, amplify, augment, induce, decrease, down-regulate, diminish, lessen, reduce, etc. The modulatory quantity can also encompass any value, e.g., 1%, 5%, 10%, 50%, 75%, 1-fold, 2-fold, 5-fold, 10-fold, 100-fold, etc. To modulate gene expression means, e.g., that the test agent has an effect on its expression, e.g., to effect the amount of transcription, to effect RNA splicing, to effect translation of the RNA into polypeptide, to effect RNA or polypeptide stability, to effect polyadenylation or other processing of the RNA, to effect post-transcriptional or post-translational processing, etc. To modulate biological activity means, e.g., that a functional activity of the polypeptide is changed in comparison to its normal activity in the absence of the agent. This effect includes, increase, decrease, block, inhibit, enhance, etc.

A test agent can be of any molecular composition, e.g., chemical compounds, biomolecules, such as polypeptides, lipids, nucleic acids (e.g., antisense to a polynucleotide sequence selected from Tables 1 and 2, or genomic sequences thereof), carbohydrates, antibodies, ribozymes, double-stranded RNA, aptamers, etc. For example, if a polypeptide to be modulated is a cell-surface molecule, a test agent can be an antibody that specifically recognizes it and, e.g., causes the polypeptide to be internalized, leading to its down

regulation on the surface of the cell. Such an effect does not have to be permanent, but can require the presence of the antibody to continue the down-regulatory effect. Antibodies can also be used to modulate the biological activity a polypeptide in a lysate or other cell-free form. Antisense can also be used as test agents to modulate gene expression.

5

Markers

The polynucleotides of the present invention can be used with other markers, especially prostate and prostate cancer markers to identity, detect, stage, diagnosis, determine, prognosticate, treat, etc., tissue, diseases and conditions, etc, of the prostate.

10 Markers can be polynucleotides, polypeptides, antibodies, ligands, specific binding partners, etc.

A number of genes and gene products have been identified which are associated with prostate cancer metastasis and/or progression, e.g., PSA, KAI1 (shows decreased expression in metastatic cells; Dong et al., *Science*, 268:884-6, 1995), D44 isoforms (differentially-
15 regulated during carcinoma progression; Noordzij et al., *Clin. Cancer Res.*, 3:805-15, 1997), p53 (Effert et al., *J. Urol.*, 150:257-61, 1993), Rb, CDKN2, E-cadherin, PTEN (Hamilton et al., *Br. J. Cancer*, 82:1671-6, 2000; Dong et al., *Clin. Cancer Res.*, 7:304-308, 2001), bcl-2, prostatic acid phosphatase (PAP), prostate specific membrane antigen (e.g., U.S. Pat. Nos. 5,538,866 and 6,107,090), Smad3 (e.g., Kang et al., *Proc. Natl. Acad. Sci.*, 98:3018-3023,
20 2001), TGF-beta, and other oncogenes and tumor suppressor genes. See, also, Myers and Grizzle, *Eur. Urol.*, 30:153-166, 1996, for other biomarkers associated with prostatic carcinoma, such as PCNA, p185-erbB-2, p180erbB-3, TAG-72, nm23-H1 and FASE. Such markers can be used in combination with the methods of the present invention to facilitate identifying, grading, staging, prognostication, etc, of conditions and diseases of the prostate.

25

Therapeutics

Selective polynucleotides, polypeptides, and specific-binding partners thereto, can be utilized in therapeutic applications, especially to treat prostate cancer. Useful methods include, but are not limited to, immunotherapy (e.g., using specific-binding partners to
30 polypeptides), vaccination (e.g., using a selective polypeptide or a naked DNA encoding such polypeptide), protein or polypeptide replacement therapy, gene therapy (e.g., germ-line correction, antisense), etc.

Various immunotherapeutic approaches can be used. For instance, unlabeled

antibody that specifically recognizes a tissue-specific antigen can be used to stimulate the body to destroy or attack the cancer, to cause down-regulation, to produce complement-mediated lysis, to inhibit cell growth, etc., of target cells which display the antigen, e.g., analogously to how c-erbB-2 antibodies are used to treat breast cancer. In addition, antibody
5 can be labeled or conjugated to enhance its deleterious effect, e.g., with radionuclides and other energy emitting entities, toxins, such as ricin, exotoxin A (ETA), and diphtheria, cytotoxic or cytostatic agents, immunomodulators, chemotherapeutic agents, etc. See, e.g., U.S. Pat. No. 6,107,090.

An antibody or other specific-binding partner can be conjugated to a second molecule,
10 such as a cytotoxic agent, and used for targeting the second molecule to a tissue-antigen positive cell (Vitetta, E. S. et al., 1993, Immunotoxin therapy, in DeVita, Jr., V. T. et al., eds, Cancer: Principles and Practice of Oncology, 4th ed., J. B. Lippincott Co., Philadelphia, 2624-2636). Examples of cytotoxic agents include, but are not limited to, antimetabolites, alkylating agents, anthracyclines, antibiotics, anti-mitotic agents, radioisotopes and
15 chemotherapeutic agents. Further examples of cytotoxic agents include, but are not limited to ricin, doxorubicin, daunorubicin, taxol, ethidium bromide, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicine, dihydroxy anthracin dione, actinomycin D, 1-dehydrotestosterone, diphtheria toxin, Pseudomonas exotoxin (PE) A, PE40, abrin, elongation factor-2 and glucocorticoid. Techniques for conjugating therapeutic agents to antibodies are
20 well.

In addition to immunotherapy, polynucleotides and polypeptides can be used as targets for non-immunotherapeutic applications, e.g., using compounds which interfere with function, expression (e.g., antisense as a therapeutic agent), assembly, etc. RNA interference can be used in vitro and in vivo to silence differentially-expressed genes when its
25 expression contributes to a disease (but also for other purposes, e.g., to identify the gene's function to change a developmental pathway of a cell, etc.). See, e.g., Sharp and Zamore, *Science*, 287:2431-2433, 2001; Grishok et al., *Science*, 287:2494, 2001.

Delivery of therapeutic agents can be achieved according to any effective method, including, liposomes, viruses, plasmid vectors, bacterial delivery systems, orally,
30 systemically, etc. Therapeutic agents of the present invention can be administered in any form by any effective route, including, e.g., oral, parenteral, enteral, intraperitoneal, topical, transdermal (e.g., using any standard patch), ophthalmic, nasally, local, non-oral, such as aerosol, inhalation, subcutaneous, intramuscular, buccal, sublingual, rectal, vaginal, intra-

arterial, and intrathecal, etc. They can be administered alone, or in combination with any ingredient(s), active or inactive.

In addition to therapeutics, *per se*, the present invention also relates to methods of treating prostate cancer showing altered expression of differentially-regulated genes, such as Tables 1 and 2, comprising, e.g., administering to a subject in need thereof a therapeutic agent which is effective for regulating expression of said genes and/or which is effective in treating said disease. The term "treating" is used conventionally, e.g., the management or care of a subject for the purpose of combating, alleviating, reducing, relieving, improving the condition of, etc., of a disease or disorder. By the phrase "altered expression," it is meant that the disease is associated with a mutation in the gene, or any modification to the gene (or corresponding product) which affects its normal function. Thus, expression of a differentially-regulated gene refers to, e.g., transcription, translation, splicing, stability of the mRNA or protein product, activity of the gene product, differential expression, etc.

Any agent which "treats" the disease can be used. Such an agent can be one which regulates the expression of the gene. Expression refers to the same acts already mentioned, e.g. transcription, translation, splicing, stability of the mRNA or protein product, activity of the gene product, differential expression, etc. For instance, if the condition was a result of a complete deficiency of the gene product, administration of gene product to a patient would be said to treat the disease and regulate the gene's expression. Many other possible situations are possible, e.g., where the gene is aberrantly expressed, and the therapeutic agent regulates the aberrant expression by restoring its normal expression pattern.

25 Antisense

Antisense polynucleotide (e.g., RNA) can also be prepared from a polynucleotide according to the present invention, preferably an anti-sense to a gene of Tables 1 and 2. Antisense polynucleotide can be used in various ways, such as to regulate or modulate expression of the polypeptides they encode, e.g., inhibit their expression, for in situ hybridization, for therapeutic purposes, for making targeted mutations (in vivo, triplex, etc.) etc. For guidance on administering and designing anti-sense, see, e.g., U.S. Pat. Nos. 6,200,960, 6,200,807, 6,197,584, 6,190,869, 6,190,661, 6,187,587, 6,168,950, 6,153,595, 6,150,162, 6,133,246, 6,117,847, 6,096,722, 6,087,343, 6,040,296, 6,005,095, 5,998,383,

5,994,230, 5,891,725, 5,885,970, and 5,840,708. An antisense polynucleotides can be operably linked to an expression control sequence. A total length of about 35 bp can be used in cell culture with cationic liposomes to facilitate cellular uptake, but for *in vivo* use, preferably shorter oligonucleotides are administered, e.g. 25 nucleotides.

5 Antisense polynucleotides can comprise modified, nonnaturally-occurring nucleotides and linkages between the nucleotides (e.g., modification of the phosphate-sugar backbone; methyl phosphonate, phosphorothioate, or phosphorodithioate linkages; and 2'-O-methyl ribose sugar units), e.g., to enhance *in vivo* or *in vitro* stability, to confer nuclease resistance, to modulate uptake, to modulate cellular distribution and compartmentalization, etc. Any
10 effective nucleotide or modification can be used, including those already mentioned, as known in the art, etc., e.g., disclosed in U.S. Pat. Nos. 6,133,438; 6,127,533; 6,124,445; 6,121,437; 5,218,103 (e.g., nucleoside thiophosphoramidites); 4,973,679; Sproat et al., "2'-O-Methyloligoribonucleotides: synthesis and applications," *Oligonucleotides and Analogs A Practical Approach*, Eckstein (ed.), IRL Press, Oxford, 1991, 49-86; Iribarren et al., "2'-O-
15 Alkyl Oligoribonucleotides as Antisense Probes," *Proc. Natl. Acad. Sci. USA*, 1990, 87, 7747-7751; Cotton et al., "2'-O-methyl, 2'-O-ethyl oligoribonucleotides and phosphorothioate oligodeoxyribonucleotides as inhibitors of the *in vitro* U7 snRNP-dependent mRNA processing event," *Nucl. Acids Res.*, 1991, 19, 2629-2635.

20 Arrays

 The present invention also relates to an ordered array of polynucleotide probes and specific-binding partners (e.g., antibodies) for detecting the expression of differentially-regulated genes in a sample, comprising, one or more polynucleotide probes or specific binding partners associated with a solid support, wherein each probe is specific for said
25 genes, and the probes comprise a nucleotide sequence of Tables 1 and 2 which is specific for said gene, a nucleotide sequence having sequence identity to Tables 1 and 2 which is specific for said gene or polynucleotide, or complements thereto, or a specific-binding partner which is specific for said genes.

 The phrase "ordered array" indicates that the probes are arranged in an identifiable or
30 position-addressable pattern, e.g., such as the arrays disclosed in U.S. Pat. Nos. 6,156,501, 6,077,673, 6,054,270, 5,723,320, 5,700,637, WO9919711, WO00023803. The probes are associated with the solid support in any effective way. For instance, the probes can be bound to the solid support, either by polymerizing the probes on the substrate, or by attaching a

probe to the substrate. Association can be, covalent, electrostatic, noncovalent, hydrophobic, hydrophilic, noncovalent, coordination, adsorbed, absorbed, polar, etc. When fibers or hollow filaments are utilized for the array, the probes can fill the hollow orifice, be absorbed into the solid filament, be attached to the surface of the orifice, etc. Probes can be of any effective size, sequence identity, composition, etc., as already discussed.

Ordered arrays can further comprise polynucleotide probes or specific-binding partners which are specific for other genes, including genes specific for prostate or disorders associated with prostate, such as prostate cancer.

10 Transgenic animals

The present invention also relates to transgenic animals comprising differentially-regulated genes of the present invention. Such genes, as discussed in more detail below, include, but are not limited to, functionally-disrupted genes, mutated genes, ectopically or selectively-expressed genes, inducible or regulatable genes, etc. These transgenic animals can be produced according to any suitable technique or method, including homologous recombination, mutagenesis (e.g., ENU, Rathkolb et al., *Exp. Physiol.*, 85(6):635-644, 2000), and the tetracycline-regulated gene expression system (e.g., U.S. Pat. No. 6,242,667). The term "gene" as used herein includes any part of a gene, i.e., regulatory sequences, promoters, enhancers, exons, introns, coding sequences, etc. The nucleic acid present in the construct or transgene can be naturally-occurring wild-type, polymorphic, or mutated.

Along these lines, polynucleotides of the present invention can be used to create transgenic animals, e.g. a non-human animal, comprising at least one cell whose genome comprises a functional disruption of a differentially-regulated gene. By the phrases "functional disruption" or "functionally disrupted," it is meant that the gene does not express a biologically-active product. It can be substantially deficient in at least one functional activity coded for by the gene. Expression of a polypeptide can be substantially absent, i.e., essentially undetectable amounts are made. However, polypeptide can also be made, but which is deficient in activity, e.g., where only an amino-terminal portion of the gene product is produced.

The transgenic animal can comprise one or more cells. When substantially all its cells contain the engineered gene, it can be referred to as a transgenic animal "whose genome comprises" the engineered gene. This indicates that the endogenous gene loci of the animal has been modified and substantially all cells contain such modification.

Functional disruption of the gene can be accomplished in any effective way, including, e.g., introduction of a stop codon into any part of the coding sequence such that the resulting polypeptide is biologically inactive (e.g., because it lacks a catalytic domain, a ligand binding domain, etc.), introduction of a mutation into a promoter or other regulatory sequence that is effective to turn it off, or reduce transcription of the gene, insertion of an exogenous sequence into the gene which inactivates it (e.g., which disrupts the production of a biologically-active polypeptide or which disrupts the promoter or other transcriptional machinery), deletion of sequences from the a differentially-regulated gene, etc. Examples of transgenic animals having functionally disrupted genes are well known, e.g., as described in U.S. Pat. Nos. 6,239,326, 6,225,525, 6,207,878, 6,194,633, 6,187,992, 6,180,849, 6,177,610, 6,100,445, 6,087,555, 6,080,910, 6,069,297, 6,060,642, 6,028,244, 6,013,858, 5,981,830, 5,866,760, 5,859,314, 5,850,004, 5,817,912, 5,789,654, 5,777,195, and 5,569,824. A transgenic animal which comprises the functional disruption can also be referred to as a "knock-out" animal, since the biological activity of its a differentially-regulated gene has been "knocked-out." Knock-outs can be homozygous or heterozygous.

For creating functional disrupted genes, and other gene mutations, homologous recombination technology is of special interest since it allows specific regions of the genome to be targeted. Using homologous recombination methods, genes can be specifically-inactivated, specific mutations can be introduced, and exogenous sequences can be introduced at specific sites. These methods are well known in the art, e.g., as described in the patents above. See, also, Robertson, *Biol. Reproduc.*, 44(2):238-245, 1991. Generally, the genetic engineering is performed in an embryonic stem (ES) cell, or other pluripotent cell line (e.g., adult stem cells, EG cells), and that genetically-modified cell (or nucleus) is used to create a whole organism. Nuclear transfer can be used in combination with homologous recombination technologies.

For example, a differentially-regulated gene locus can be disrupted in mouse ES cells using a positive-negative selection method (e.g., Mansour et al., *Nature*, 336:348-352, 1988). In this method, a targeting vector can be constructed which comprises a part of the gene to be targeted. A selectable marker, such as neomycin resistance genes, can be inserted into a differentially-regulated gene exon present in the targeting vector, disrupting it. When the vector recombines with the ES cell genome, it disrupts the function of the gene. The presence in the cell of the vector can be determined by expression of neomycin resistance. See, e.g., U.S. Pat. No. 6,239,326. Cells having at least one functionally disrupted gene can

be used to make chimeric and germline animals, e.g., animals having somatic and/or germ cells comprising the engineered gene. Homozygous knock-out animals can be obtained from breeding heterozygous knock-out animals. See, e.g., U.S. Pat. No. 6,225,525.

A transgenic animal, or animal cell, lacking one or more functional differentially-regulated genes can be useful in a variety of applications, including, as an animal model for cancer, for drug screening assays, as a source of tissues deficient in said gene activity, and any of the utilities mentioned in any issued U.S. Patent on transgenic animals, including, U.S. Pat. Nos. 6,239,326, 6,225,525, 6,207,878, 6,194,633, 6,187,992, 6,180,849, 6,177,610, 6,100,445, 6,087,555, 6,080,910, 6,069,297, 6,060,642, 6,028,244, 6,013,858, 5,981,830, 5,866,760, 5,859,314, 5,850,004, 5,817,912, 5,789,654, 5,777,195, and 5,569,824.

The present invention also relates to non-human, transgenic animal whose genome comprises recombinant a differentially-regulated gene nucleic acid operatively linked to an expression control sequence effective to express said coding sequence, e.g., in prostate. such a transgenic animal can also be referred to as a "knock-in" animal since an exogenous gene has been introduced, stably, into its genome.

A recombinant a differentially-regulated gene nucleic acid refers to a gene which has been introduced into a target host cell and optionally modified, such as cells derived from animals, plants, bacteria, yeast, etc. A recombinant a differentially-regulated gene includes completely synthetic nucleic acid sequences, semi-synthetic nucleic acid sequences, sequences derived from natural sources, and chimeras thereof. "Operable linkage" has the meaning used through the specification, i.e., placed in a functional relationship with another nucleic acid. When a gene is operably linked to an expression control sequence, as explained above, it indicates that the gene (e.g., coding sequence) is joined to the expression control sequence (e.g., promoter) in such a way that facilitates transcription and translation of the coding sequence. As described above, the phrase "genome" indicates that the genome of the cell has been modified. In this case, the recombinant a differentially-regulated gene has been stably integrated into the genome of the animal. The a differentially-regulated gene nucleic acid in operable linkage with the expression control sequence can also be referred to as a construct or transgene.

Any expression control sequence can be used depending on the purpose. For instance, if selective expression is desired, then expression control sequences which limit its expression can be selected. These include, e.g., tissue or cell-specific promoters, introns, enhancers, etc. For various methods of cell and tissue-specific expression, see, e.g., U.S. Pat.

Nos. 6,215,040, 6,210,736, and 6,153,427. These also include the endogenous promoter, i.e., the coding sequence can be operably linked to its own promoter. Inducible and regulatable promoters can also be utilized.

The present invention also relates to a transgenic animal which contains a functionally
5 disrupted and a transgene stably integrated into the animals genome. Such an animal can be constructed using combinations any of the above- and below-mentioned methods. Such animals have any of the aforementioned uses, including permitting the knock-out of the normal gene and its replacement with a mutated gene. Such a transgene can be integrated at the endogenous gene locus so that the functional disruption and "knock-in" are carried out in
10 the same step.

In addition to the methods mentioned above, transgenic animals can be prepared according to known methods, including, e.g., by pronuclear injection of recombinant genes into pronuclei of 1-cell embryos, incorporating an artificial yeast chromosome into embryonic stem cells, gene targeting methods, embryonic stem cell methodology, cloning
15 methods, nuclear transfer methods. See, also, e.g., U.S. Patent Nos. 4,736,866; 4,873,191; 4,873,316; 5,082,779; 5,304,489; 5,174,986; 5,175,384; 5,175,385; 5,221,778; Gordon et al., Proc. Natl. Acad. Sci., 77:7380-7384, 1980; Palmiter et al., Cell, 41:343-345, 1985; Palmiter et al., Ann. Rev. Genet., 20:465-499, 1986; Askew et al., Mol. Cell. Bio., 13:4115-4124, 1993; Games et al. Nature, 373:523-527, 1995; Valancius and Smithies, Mol. Cell. Bio.,
20 11:1402-1408, 1991; Stacey et al., Mol. Cell. Bio., 14:1009-1016, 1994; Hasty et al., Nature, 350:243-246, 1995; Rubinstein et al., Nucl. Acid Res., 21:2613-2617, 1993; Cibelli et al., Science, 280:1256-1258, 1998. For guidance on recombinase excision systems, see, e.g., U.S. Pat. Nos. 5,626,159, 5,527,695, and 5,434,066. See also, Orban, P.C., et al., "Tissue- and Site-Specific DNA Recombination in Transgenic Mice," Proc. Natl. Acad. Sci. USA,
25 89:6861-6865 (1992); O'Gorman, S., et al., "Recombinase-Mediated Gene Activation and Site-Specific Integration in Mammalian Cells," Science, 251:1351-1355 (1991); Sauer, B., et al., "Cre-stimulated recombination at loxP-Containing DNA sequences placed into the mammalian genome," Polynucleotides Research, 17(1):147-161 (1989); Gagneten, S. et al. (1997) Nucl. Acids Res. 25:3326-3331; Xiao and Weaver (1997) Nucl. Acids Res. 25:2985-
30 2991; Agah, R. et al. (1997) J. Clin. Invest. 100:169-179; Barlow, C. et al. (1997) Nucl. Acids Res. 25:2543-2545; Araki, K. et al. (1997) Nucl. Acids Res. 25:868-872; Mortensen, R. N. et al. (1992) Mol. Cell. Biol. 12:2391-2395 (G418 escalation method); Lakhani, P. P. et al. (1997) Proc. Natl. Acad. Sci. USA 94:9950-9955 ("hit and run"); Westphal and Leder

(1997) Curr. Biol. 7:530-533 (transposon-generated "knock-out" and "knock-in"); Templeton, N. S. et al. (1997) Gene Ther. 4:700-709 (methods for efficient gene targeting, allowing for a high frequency of homologous recombination events, e.g., without selectable markers); PCT International Publication WO 93/22443 (functionally-disrupted).

5 A polynucleotide according to the present invention can be introduced into any non-human animal, including a non-human mammal, mouse (Hogan et al., Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1986), pig (Hammer et al., Nature, 315:343-345, 1985), sheep (Hammer et al., Nature, 315:343-345, 1985), cattle, rat, or primate. See also, e.g., Church, 1987, Trends in
10 Biotech. 5:13-19; Clark et al., Trends in Biotech. 5:20-24, 1987); and DePamphilis et al., BioTechniques, 6:662-680, 1988. Transgenic animals can be produced by the methods described in U.S. Pat. No. 5,994,618, and utilized for any of the utilities described therein.

Database

15 The present invention also relates to electronic forms of polynucleotides, polypeptides, etc., of the present invention, including computer-readable medium (e.g., magnetic, optical, etc., stored in any suitable format, such as flat files or hierarchical files) which comprise such sequences, or fragments thereof, e-commerce-related means, etc. Along these lines, the present invention relates to methods of retrieving gene sequences from
20 a computer-readable medium, comprising, one or more of the following steps in any effective order, e.g., selecting a cell or gene expression profile, e.g., a profile that specifies that said gene is differentially expressed in prostate cancer, and retrieving said differentially expressed gene sequences, where the gene sequences consist of the genes represented by Tables 1 and 2.

25 A "gene expression profile" means the list of tissues, cells, etc., in which a defined gene is expressed (i.e, transcribed and/or translated). A "cell expression profile" means the genes which are expressed in the particular cell type. The profile can be a list of the tissues in which the gene is expressed, but can include additional information as well, including level of expression (e.g., a quantity as compared or normalized to a control gene), and
30 information on temporal (e.g., at what point in the cell-cycle or developmental program) and spatial expression. By the phrase "selecting a gene or cell expression profile," it is meant that a user decides what type of gene or cell expression pattern he is interested in retrieving, e.g., he may require that the gene is differentially expressed in a tissue, or he may require that the

gene is not expressed in blood, but must be expressed in prostate cancer. Any pattern of expression preferences may be selected. The selecting can be performed by any effective method. In general, "selecting" refers to the process in which a user forms a query that is used to search a database of gene expression profiles. The step of retrieving involves
5 searching for results in a database that correspond to the query set forth in the selecting step. Any suitable algorithm can be utilized to perform the search query, including algorithms that look for matches, or that perform optimization between query and data. The database is information that has been stored in an appropriate storage medium, having a suitable computer-readable format. Once results are retrieved, they can be displayed in any suitable
10 format, such as HTML.

For instance, the user may be interested in identifying genes that are differentially expressed in a prostate cancer. He may not care whether small amounts of expression occur in other tissues, as long as such genes are not expressed in peripheral blood lymphocytes. A query is formed by the user to retrieve the set of genes from the database having the desired
15 gene or cell expression profile. Once the query is inputted into the system, a search algorithm is used to interrogate the database, and retrieve results.

Advertising, licensing, etc., methods

The present invention also relates to methods of advertising, licensing, selling,
20 purchasing, brokering, etc., genes, polynucleotides, specific-binding partners, antibodies, etc., of the present invention. Methods can comprises, e.g., displaying a a differentially-regulated gene gene, a differentially-regulated gene polypeptide, or antibody specific for a differentially-regulated gene in a printed or computer-readable medium (e.g., on the Web or Internet), accepting an offer to purchase said gene, polypeptide, or antibody.

25

Other

A polynucleotide, probe, polypeptide, antibody, specific-binding partner, etc., according to the present invention can be isolated. The term "isolated" means that the material is in a form in which it is not found in its original environment or in nature, e.g.,
30 more concentrated, more purified, separated from component, etc. An isolated polynucleotide includes, e.g., a polynucleotide having the sequenced separated from the chromosomal DNA found in a living animal, e.g., as the complete gene, a transcript, or a cDNA. This polynucleotide can be part of a vector or inserted into a chromosome (by

specific gene-targeting or by random integration at a position other than its normal position) and still be isolated in that it is not in a form that is found in its natural environment. A polynucleotide, polypeptide, etc., of the present invention can also be substantially purified. By substantially purified, it is meant that polynucleotide or polypeptide is separated and is essentially free from other polynucleotides or polypeptides, i.e., the polynucleotide or polypeptide is the primary and active constituent. A polynucleotide can also be a recombinant molecule. By "recombinant," it is meant that the polynucleotide is an arrangement or form which does not occur in nature. For instance, a recombinant molecule comprising a promoter sequence would not encompass the naturally-occurring gene, but would include the promoter operably linked to a coding sequence not associated with it in nature, e.g., a reporter gene, or a truncation of the normal coding sequence.

The term "marker" is used herein to indicate a means for detecting or labeling a target. A marker can be a polynucleotide (usually referred to as a "probe"), polypeptide (e.g., an antibody conjugated to a detectable label), PNA, or any effective material.

The topic headings set forth above are meant as guidance where certain information can be found in the application, but are not intended to be the only source in the application where information on such topic can be found.

Reference materials

For other aspects of the polynucleotides, reference is made to standard textbooks of molecular biology. See, e.g., Hames et al., Polynucleotide Hybridization, IL Press, 1985; Davis et al., Basic Methods in Molecular Biology, Elsevier Sciences Publishing, Inc., New York, 1986; Sambrook et al., Molecular Cloning, CSH Press, 1989; Howe, Gene Cloning and Manipulation, Cambridge University Press, 1995; Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, Inc., 1994-1998.

The preceding description, utilize the present invention to its fullest extent. The preceding preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limiting the remainder of the disclosure in any way whatsoever. The entire disclosure of all applications, patents and publications, cited above and in the figures are hereby incorporated by reference in their entirety.

Claims:

1. A method for diagnosing a prostate cancer in a sample comprising prostate tissue, comprising:
 - determining the number of target genes which are differentially-regulated in said sample, wherein said target genes are selected from SEQ ID NO 1-211 of claim 26, whereby said number is indicative of the probability that said sample comprises prostate cancer.
2. A method of claim 1, wherein said determining is performed by Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, or *in situ* hybridization using polynucleotide probes specific for genes selected from SEQ ID NO 1-211 of claim 26.
3. A method of claim 1, wherein said determining is performed by:
 - contacting said sample with a polynucleotide probe under conditions effective for said probe to hybridize specifically to a target nucleic acid in said sample, and detecting the amount of hybridization between said probe and target nucleic acid, and
 - comparing the amount of hybridization in said sample with the amount of hybridization of said probe in a second sample comprising normal prostate tissue.
4. A method of claim 1, wherein said determining is performed by:
 - contacting said sample with a polynucleotide probe under conditions effective for said probe to hybridize specifically to a target nucleic acid in said sample, and detecting the amount of hybridization between said probe and target nucleic acid, and
 - comparing the amount of hybridization in said sample with the amount of hybridization between a second probe and its corresponding second target nucleic acid in said sample.

5. A method of claim 2, wherein said probe is a contiguous sequence of at least 8 nucleotides selected from a polynucleotide sequence selected from SEQ ID NOS 1-107 of claim 26, or a complement thereto.

5 6. A method of assessing a therapeutic or preventative intervention in a subject having a prostate cancer, comprising,

determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer,

wherein said target genes are selected from SEQ ID NO 1-211 of claim 26.

10 7. A method of claim 6, wherein the expression levels of at least 10 genes are determined.

8. A method of claim 6, wherein the determining is performed by Northern blot
15 analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, or *in situ* hybridization using polynucleotide probes specific for genes selected from SEQ IDS NO 1-211 of claim 26.

9. A method for identifying agents that modulate the expression of target
20 polynucleotides differentially-regulated in prostate cancer cells, comprising,

contacting a prostate cell population with a test agent under conditions effective for said test agent to modulate the expression of a target polynucleotide in said cell population, and

determining whether said test agent modulates said target polynucleotide expression,
25 wherein said target polynucleotide is selected from SEQ ID NOS 1-107 of claim 26.

10. A method of claim 9, wherein said agent is an antisense polynucleotide to said target polynucleotide sequence and which is effective to inhibit translation of said target polynucleotide.

11. A method for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, comprising,
contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for said test agent to modulate a biological activity of said polypeptide, and
5 determining whether said test agent modulates said biological activity, wherein said polypeptide is selected from SEQ ID NOS 108-211 of claim 26.

12. A method of treating prostate cancer, comprising,
10 administering to a subject in need thereof a therapeutic agent which is effective for regulating expression of at least one sequence selected from SEQ ID NOS 1-211 of claim 26.

13. A method of claim 12, wherein said agent is an antibody or an antisense
15 which is effective to inhibit translation of said gene.

14. A method of diagnosing a prostate cancer comprising:
assessing the expression of at least one gene selected from SEQ ID NO 1-211 of claim 26, wherein said gene is differentially-regulated in said cancer.

20 15. A method of claim 14, wherein assessing is:
measuring mRNA expression levels of said or measuring the expression levels of polypeptide coded for by said gene.

25 16. A method of claim 14, further comprising:
comparing said expression to the expression of said polynucleotide in a known normal tissue.

-51-

17. A method of claim 14, wherein said assessing detecting is performed by:
Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR,
RACE PCR, or *in situ* hybridization, and

5 using a polynucleotide probe specific for a polynucleotide sequence selected from
SEQ ID NOS 1-107 of claim 26.

18. A method of claim 14, wherein the expression of at least one up-regulated
polynucleotide and at least one down-regulated polynucleotide are assessed.

10 19. A method of claim 14, wherein the expression of at least five up-regulated
polynucleotides and at least five down-regulated polynucleotides are assessed.

20. A method of retrieving prostate cancer differentially-regulated gene
sequences from a computer-readable medium, comprising:

15 selecting a gene expression profile that specifies that said gene is differentially-
regulated in a prostate cancer, and retrieving prostate cancer differentially-regulated gene
sequences,

where the gene sequences consist of genes selected from SEQ ID NO 1-211 of claim
26.

20

21. An ordered array of polynucleotide probes for detecting the expression of
differentially-regulated prostate cancer genes in a sample, comprising:

polynucleotide probes associated with a solid support, wherein each probe is specific
for a different differentially-regulated prostate cancer gene, and the probes are specific for
25 genes selected from SEQ ID NO 1-211 of claim 26.

22. An array of claim 21, wherein said array comprises probes specific for up-
regulated and down-regulated polynucleotides.

30

23. A method of advertising for sale, commercial use, or licensing, comprising:
displaying at least one polynucleotide or polypeptide sequence selected from

-52-

SEQ ID NO 1-211 of claim 26, or a complement thereto.

24. A non-human, transgenic mammal having a functional disruption in at least one gene selected from SEQ ID NO 1-211 of claim 26, and which is susceptible to prostate cancer.

25. A cell expression profile consisting of the expression pattern of a prostate cancer tissue sample for differentially-regulated genes of claim 26.

26. A plurality of genes which are differentially regulated in a prostate cancer, selected from:

up-regulated genes having SEQ ID NOS 1-75 and 140-211; and
down-regulated genes having SEQ ID 76-107 and 108-139.

15

Table 1

DNA SEQ ID	Prt SEQ ID	Identifier	Exp	GI#	Gene Name and Description
1	140	PC030931U	U	337504	HUMRPS24A Human ribosomal protein S24 mRNA
2	141	PC010848U	U	3978243	Homo sapiens inhibitor of apoptosis protein-1 (MIHC) mRNA complete cds
3	142	PC010839U	U	6912451	AF070674 Homo sapiens inhibitor of apoptosis protein-1 (MIHC) mRNA complete cds
4	143	PC010957U	U	4557844	NM_001034.1 Homo sapiens ribonucleotide reductase M2 polypeptide (RRM2) mRNA
5	144	PC020728U	U	4503478	NM_001960.1 Homo sapiens eukaryotic translation elongation factor 1 delta
6	145	PC021342U	U	340057	HUMJUB Human poly-ubiquitin mRNA complete cds
7	146	PC030732U	U	4504374	Homo sapiens H factor 1 (complement) (HF1) mRNA
8	147	PC011348U	U	3093338	HSY17176 Homo sapiens mRNA for KIAA0976 protein complete cds
9	147	PC041029U	U	4589595	AB023193 Homo sapiens mRNA for KIAA0976 protein complete cds
10	148	PC040972U	U	4885132	Homo sapiens centromere protein F (400KD) (CENPF) mRNA
11	149	PC050853U	U	4503724	NM_000801.1 Homo sapiens FK506-binding protein 1A (12kD) (FKBP1A) mRNA
12	150	PC040158U	U	4826949	Homo sapiens kallikrein 7 (chymotryptic stratum corneum) (KLK7) mRNA
13	151	PC040441U	U	4826879	Homo sapiens oxidase (cytochrome c) assembly 1-like (OXA1L) mRNA
14	152	PC051210U	U	4506056	NM_002731.1 Homo sapiens protein kinase, cAMP-dependent, catalytic, beta
15	154	PC050296U	U	5453633	Homo sapiens dynein cytoplasmic light intermediate polypeptide 2 (DNCL2) mRNA
16	155	PC050151U	U	6715599	NM_002078.2 Homo sapiens golgi autoantigen, golgin subfamily a, 4
17	156	PC050149U	U	2217930	AB004884 Homo sapiens mRNA for PKU-alpha,
18	157	PC052095U	U	641957	HUMIMYHCB Human nonmuscle myosin heavy chain-B (MYH10) mRNA partial cds
19	158	PC052029U	U	5803218	Homo sapiens serine protease inhibitor Kazal type 5 (SPINK5) mRNA
20	159	PC050620U	U	4504580	NM_003641.1 Homo sapiens interferon induced transmembrane protein 1, (IFITM1), mRNA
21	160	PC041338U	U	8051620	Homo sapiens 2'-5'-oligoadenylate synthetase 1 (OAS1) transcript variant E18 mRNA
22	161	PC041980U	U	6735451	HSA271091 Homo sapiens mRNA for B-ind1 protein (B-ind1 gene)
23	162	PC060474U	U	4759321	Homo sapiens wingless-type MMTV integration site family member 2B (WNT2B) mRNA
24	163	PC060443U	U	4506730	Homo sapiens ribosomal protein S6 (RPS6) mRNA
25	164	PC060441U	U	1688257	HSU78045 Human collagenase and stromelysin genes, complete cds, and metalloelastase gene, partial cds
26	165	PC070152U	U	4506712	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
27	166	PC060529U	U	4503820	Homo sapiens FYN-binding protein (FYB-120130) (FYB) mRNA and translated products
28	167	PC080348U	U	9623360	AF261688 Homo sapiens DNA polymerase epsilon p12 subunit gene, complete cds
29	168	PC070544U	U	1679960	S42658 S3 ribosomal protein [human colon mRNA 826 nt]
30	169	PC070343U	U	4507210	Homo sapiens signal recognition particle 14kD (homologous Alu RNA-binding protein) (SRP14) mRNA
31	170	PC061477U	U	4506386	Homo sapiens RAD23 (S. cerevisiae) homolog B (RAD23B) mRNA
32	171	PC060940U	U	5052074	Homo sapiens PAPS synthetase-2 (PAPSS2) mRNA
33	172	PC061779U	U	4504766	Homo sapiens integrin beta 1 (fibronectin receptor beta polypeptide antigen CD29 includes MDF2 MSK12) (ITGB1) mRNA
34	173	PC061839U	U	8394498	Homo sapiens ubiquitin associated protein (UBAP) mRNA
35	174	PC061827U	U	7382495	Homo sapiens p21Cdc42Rac1-activated kinase 1 (fibronectin receptor beta polypeptide antigen CD29 includes MDF2 MSK12) (PAK1) mRNA
36	175	PC080511U	U	4504190	NM_000179.1 Homo sapiens muS (E. coli) homolog 6 (MSH6)
37	176	PC090754U	U	4503472	Homo sapiens eukaryotic translation elongation factor 1 alpha 1-like 14 (EEF1A1L14) mRNA
38	177	PC090842U	U	4557031	Homo sapiens lactate dehydrogenase B (LDHB) mRNA
39	178	PC091028U	U	7662425	Homo sapiens KIAA0976 protein (KIAA0976) mRNA
40		PC070890U	U	6531675	AF205588.1 AF205588 Homo sapiens ZNF01 and HUMORFKG1B genes
41		PC071851U	U	3090894	AF052497 Homo sapiens clone B18 unknown mRNA
42	179	PC070729U	U	8923790	Homo sapiens r1S beta protein (HSRTS8BETA) mRNA

Table 1

43	180	PC080742U	U	4507186	NM_003125.1	Homo sapiens small proline-rich protein 1B (corfilin)
44	181	PC100113U	U	6647292	AF166330.2	Homo sapiens stratum corneum chymotryptic enzyme gene
45		PC100356U	U	3093334	HSV17172	Homo sapiens mRNA from HIV-associated non-Hodgkin's lymphoma (clone H2-22)
46	182	PC100428U	U	4502980	NM_001861.1	Homo sapiens cytochrome c oxidase subunit IV (COX4)
47	183	PC090230U	U	3252910	AF056322	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA complete cds
48	184	PC090233U	U	4504192	Homo sapiens general transcription factor IIB (GTF2B) mRNA	
49	185	PC101863U	U	35037	HSNFIV	H.sapiens mRNA for nuclear factor IV
50	186	PC090625U	U	7706215	Homo sapiens H-2K binding factor-2 (LOC51580) mRNA	
51	187	PC101430U	U	609453	M69199.1	HUMG052A Human G0S2 protein gene, complete cds
52	188	PC091425U	U	4732025	AF118569	Homo sapiens angiotensin I converting enzyme precursor
53	189	PC101043U	U	4505374	NM_002499.1	Homo sapiens neogenin (chicken) homolog 1
54	190	PC101013U	U	7657203	Homo sapiens acidic 82 kDa protein mRNA (HSU15552) mRNA	
55	191	PC1010337U	U	6005813	Homo sapiens serine threonine protein kinase (NDR) mRNA	
56	192	PC1010336U	U	7662579	Homo sapiens PRO0644 protein (PRO0644) mRNA	
57	193	PC020185U	U	7669502	NM_013995.1	Homo sapiens lysosomal-associated membrane protein 2
58	194	PC020162U	U	4507164	NM_003113.1	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
59	195	PC030247U	U	348706	HUMCACTHBS	Homo sapiens cathepsin B mRNA 3' UTR with a stem-loop structure providing mRNA stability
60	196	PC030471U	U	31396	HSFIB1	Human mRNA for fibronectin (FN precursor)
61	197	PC030454U	U	4506678	Homo sapiens ribosomal protein S10 (RPS10) mRNA	
62	198	PC030326U	U	4507148	Homo sapiens superoxide dismutase 1 soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1) mRNA	
63	199	PC030425U	U	415818	HSMK167	H.sapiens mki67a mRNA (long type) for antigen of monoclonal antibody Ki-67
64	200	PC091527U	U	5803091	Homo sapiens methionine aminopeptidase; eIF-2-associated p67 (MNPEP) mRNA	
65	201	PC092004U	U	8922823	NM_018300.1	Homo sapiens hypothetical protein FLJ11015 (FLJ11015)
66	202	PC091888U	U	4757809	Homo sap/	ATP synthase H+ transporting mito. F1 complex alpha subunit isoform 1 cardiac muscle (ATP5A1) nuclear gene
67	203	PC091853U	U	31091	X16869.1	HSEFIAC Human mRNA for elongation factor 1-alpha
68	204	PC092052U	U	4505634	Homo sapiens BH-protocadherin (brain-heart) (9999DH7) mRNA	
69	205	PC091839U	U	7188646	AF222043	Homo sapiens ubiquitin-associated protein (NAG20) mRNA complete cds
70	206	PC111181U	U	7416940	AF139077	Homo sapiens M5-14 mRNA complete cds
71	207	PC111168U	U	4759283	NM_004181.1	Homo sapiens ubiquitin carboxyl-terminal esterase L1
72	208	PC120136U	U	7706728	Homo sapiens TBX3-iso protein (TBX3-iso) mRNA	
73	209	PC120331U	U	4504424	NM_002128.1	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1
74	210	PC121671U	U	7661635	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082) mRNA	
75	211	PC020741U	U	7657624	NM_014393.1	Homo sapiens staufen (Drosophila, RNA-binding protein) homolog 2
	153	PC051231U	U	4506600	Homo sapiens ribosomal protein L14 (RPL14) mRNA	
		PC020827U	U	8923949	Homo sapiens ovarian cancer related protein OVN9-3 (OVN9-3) mRNA	
		PC110927U	U	8923282	NM_017754.1	Homo sapiens hypothetical protein FLJ20302 (FLJ20302)

Table 2

DNA SEQ ID	Prt SEQ ID	Identifier	Exp	GI#	Gene Name and Description
76	108	PC040734D	D	5174656	NM_006096.1 Homo sapiens differentiation-related gene 1 nickel-specific induction protein
77	109	PC040156D	D	4505748	Homo sapiens phosphofructokinase muscle (PFKM) mRNA
78	110	PC051745D	D	4758751	Homo sapiens neuronal apoptosis inhibitory protein (NAIP) mRNA
79	111	PC042021D	D	4505986	Homo sapiens PTPRF interacting protein binding protein 1 (liprin beta 1) (PPFIBP1) mRNA and translated products
80	112	PC060144D	D	4758199	NM_004415.1 Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
81	113	PC080139D	D	7657159	NM_014362.1 Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH) mRNA
82	114	PC080435D	D	4758807	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
83	115	PC070436D	D	9790904	NM_001924.1 Homo sapiens growth arrest and DNA-damage-inducible
84	116	PC061342D	D	186485	HUMINT04 Human leukocyte adhesion protein p15095 alpha subunit gene exons 16-21
85	117	PC060793D	D	4507582	NM_000043.1 Homo sapiens tumor necrosis factor receptor superfamily
86	118	PC060743D	D	4557256	Homo sapiens adenylate cyclase 8 (brain) (ADCY8) mRNA
87	119	PC061528D	D	4506700	Homo sapiens ribosomal protein S23 (RPS23) mRNA
88	120	PC090788D	D	5031638	Homo sapiens cornichon-like (CNIL) mRNA
89	121	PC090722D	D	7670747	AF227906 Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 2 precursor mRNA complete cds
90	122	PC071770D	D	31441	HSFNRB Human mRNA for integrin beta 1 subunit
91	123	PC090677D	D	187701	HUMHBA123 Human MHC protein homologous to chicken B complex protein mRNA complete cds
92	124	PC101847D	D	5902021	Homo sapiens PL6 protein (PL6) mRNA
93	125	PC090622D	D	4506858	NM_002997.1 Homo sapiens syndecan 1 (SDC1) mRNA
94	126	PC010433D	D	4827043	Homo sapiens thyroid hormone receptor-associated protein 240 kDa subunit (TRAP240) mRNA
95	127	PC020238D	D	4503090	NM_001893.1 Homo sapiens casein kinase 1, delta (CSNK1D) mRNA
96	128	PC030301D	D	4506728	Homo sapiens ribosomal protein S5 (RPS5) mRNA
97	129	PC110249D	D	4759257	Homo sapiens Ac-like transposable element (ALTE) mRNA
98	130	PC110541D	D	5031778	Homo sapiens interferon gamma-inducible protein 16 (IFI16) mRNA
99		PC110431D	D	3885367	AB019564 Homo sapiens mRNA expressed only in placental villi clone SNAP47
100	131	PC110940D	D	4758949	NM_000942.1 Homo sapiens peptidylprolyl isomerase B (cyclophilin B)
101	132	PC111588D	D	4503412	Homo sapiens diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR) mRNA
102	133	PC111669D	D	7705822	Homo sapiens N-terminal acetyltransferase complex and subunit (LOC51126) mRNA
103	134	PC032046D	D	7657325	NM_014623.1 Homo sapiens male-enhanced antigen (MEA)
104	135	PC120741D	D	5174388	NM_005891.1 Homo sapiens acetyl-Coenzyme A acetyltransferase 2
105	136	PC120740D	D	311380	HSTCPI Human t-complex polypeptide 1 gene
106	137	PC010853D	D	4506660	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
107	139	PC030968D	D	4507668	Homo sapiens tumor protein translationally-controlled 1 (TPT1) mRNA
108	138	PC031146D	D	8924228	NM_018636.1 Homo sapiens hypothetical protein PRO2987 (PRO2987)

Table 3

Name	Serial No.	Expression	Protein Cl#	Classification	Domain	Domain description	Score	E	seq-f	seq-t
PC340	PC010139U	U	7657204		HM005apiensacidic82	RDalproteinmRNA(HSU05552)mRNA				
PC341	PC010139U	U	7657204		Ribosomal L2	Ribosomal Proteins L2	3.6	2.70E-01	197	217
PC342	PC010336U	U	7662580		HM005apiensPR0064	protein(PR0064)mRNA				
PC343	PC010336U	U	7662580							
PC344	PC010337U	U	6005814		HM005apienskinet	inretineinprotein kinase(NDR)mRNA				
PC345	PC010337U	U	6005814		kinase	Protein kinase domain	221.1	8.30E-64	89	359
PC346	PC010433D	D	4827044	Down-regulated	HM005apienshydrol	hormonereceptorassociatedprotein240	240	1.20E-01	176	238
PC347	PC010433D	D	4827044		Na K-ATPase	Sodium / potassium ATPase beta chain	2.5	3.50E-01	224	239
PC348	PC010433D	D	4827044		Chal stil symC	Chalcone and stilbene synthases, C-te	2.7	7.00E-01	1735	1752
PC349	PC010433D	D	4827044		A. deamin	Adenosine-deaminase (edifase) domain	1.2	9.10E-01	140	148
PC349	PC010434U	U	4505375		NM0024994	HM005apiensinogenin(chicken)homolog				
PC350	PC010434U	U	4505375		fn3	Fibronectin type III domain	367.4	7.70E-108	954	1044
PC351	PC010434U	U	4505375		ig	Immunoglobulin domain	131.9	1.20E-40	355	412
PC352	PC010434U	U	4505375		Ribosomal L23	Ribosomal protein L23	2.9	9.40E-01	662	676
PC353	PC010839U	U	6912452		NM0122893	HM005apiensKetchlikeEGF-associatedprotein(KIAA0195)				
PC354	PC010839U	U	6912452		Ketch	Ketch motif	271.7	5.10E-79	553	598
PC355	PC010839U	U	6912452		BTB	BTB/POZ domain	100.8	1.40E-27	61	179
PC356	PC010839U	U	6912452		PI3K p85B	PI3-kinase family, p85-binding domain	-21.1	8.20E-01	176	238
PC357	PC010849U	U	3978244		AF006748	HM005apiensinhibitorofapoptosisprotein1(MH10)mRNA-complexed				
PC358	PC010849U	U	3978244		CARD	Caspase recruitment domain	125.1	6.80E-35	440	529
PC359	PC010849U	U	3978244		Zf-C4	Zinc finger, C4 type (two domains)	3	7.40E-01	555	563
PC360	PC010853D	D	4506661	Down-regulated	HM005apiensribosomalprotein1(RP18P)mRNA					
PC361	PC010853D	D	4506661		Ribosomal L7Ae	Ribosomal protein L7Ae/L30e/S12e/Gad	103.9	1.60E-28	122	216
PC362	PC010853D	D	4506661		Ribosomal L39	Ribosomal protein L39 protein	-8.6	2.60E-01	211	244
PC363	PC010957U	U	4557845		NM0010344	HM005apiensribonucleotide reductase M20 polypeptide(RRM2)mRNA				
PC364	PC010957U	U	4557845		ribonuc red sm	Ribonucleotide reductase, small chain	598.8	1.70E-177	70	351
PC365	PC011348U	U	12005805		HS049173	HM005apiensRNaseH1Naseassociatednon-Histoneprotein(cloneH12266)				
PC366	PC020162U	U	4507165		oxidored q1	NADH-Ubiquinone/Plastoquinone (com)22.9	9.30E-07	82	108	
PC367	PC020162U	U	4507165		NM0031193	HM005apiensnucleotidyltransferase(SPL00)mRNA				
PC368	PC020162U	U	4507165							
PC369	PC020185U	U	7669503		NM0189954	HM005apienslysosomal-associatedmembrane protein2				
PC370	PC020185U	U	7669503		Lamp	Lysosome-associated membrane glycopol	767.3	3.20E-238	44	410
PC371	PC020238D	D	4503091	Down-regulated	NM0018999	HM005apienscasein1inase1delta(GSNK1D)mRNA				
PC372	PC020238D	D	4503091		kinase	Protein kinase domain	146.4	2.60E-41	9	239
PC373	PC020627U	U	14424570		HM005apiensclone MGGH166	HM005apiensclone MGGH166				
PC374	PC020627U	U	14424570							
PC375	PC020728U	U	4503479		NM0019602	HM005apiensleucylamylotranslationinhibitionfactor1delta				
PC376	PC020728U	U	4503479		EF1BD	EF-1 guanine nucleotide exchange domain	189.4	3.00E-54	195	281
PC377	PC020728U	U	4503479		bZIP	bZIP transcription factor	10.1	1.30E-02	79	114
PC378	PC020741U	U	7657625		NM0014393	HM005apiensstaufen2(rosophi)mRNA-binding protein(homolog2)				
PC379	PC020741U	U	7657625		dsrm	Double-stranded RNA binding motif	175.1	6.10E-50	276	341

Table 3

[illegible]

Table 3

PC059	PC0409720	U	4885133	Homo sapiens	transcriptome	protein	400kD	(GENEID)	mRNA	2930	2962
	bZIP			bZIP	transcription factor		68.1		4.80E-19	2930	2962
	M		4885133		M protein repeat		29.7		3.50E-06	2972	2992
	KID repeat		4885133		KID repeat		26.6		3.10E-05	2938	2948
	filament		4885133		Intermediate filament protein		13.2		8.80E-04	2810	2833
	Trp repressor		4885133		Trp repressor protein		-16.9		5.50E-02	1065	1157
	RNA pol L		4885133		RNA polymerase L / 13 to 16 kDa subunit		-28.7		9.90E-02	840	923
	Myosin tail		4885133		Myosin tail		4.3		1.40E-01	2283	2338
	DUF164		4885133		Uncharacterized ACR, COG1579		-91.7		1.80E-01	2560	2797
	HALZ		4885133		Homeobox associated leucine zipper		9		1.80E-01	2885	2928
	OSCP		4885133		ATP synthase delta (OSCP) subunit		4.1		2.10E-01	2283	2294
	K-box		4885133		K-box region		-40.4		3.10E-01	2440	2524
	HlyD		4885133		HlyD family secretion protein		-60.5		3.30E-01	2461	2730
	DUF38		4885133		Domain of unknown function DUF38		3.9		4.00E-01	1888	1914
	dynammin 2		4885133		Dynammin central region		-179.4		4.20E-01	991	1223
	HRI		4885133		Hr1 repeat motif		-4.4		4.70E-01	2201	2271
	Apolipoprotein		4885133		Apolipoprotein A1/A4/E family		-118.2		4.90E-01	2295	2547
	formyl transf		4885133		Formyl transferase		3		5.60E-01	3068	3081
	ERM		4885133		Ezrin/radixin/moesin family		-227.4		6.50E-01	2028	2290
	Tropomyosin		4885133		Tropomyosin		1.3		7.20E-01	2418	2451
	Borrelia orfA		4885133		Borrelia ORF-A		-107.4		7.40E-01	417	744
	PFEMP		4885133		Plasmodium falciparum erythrocyte membrane protein 1		-89.6		7.90E-01	2844	2950
	BglG antitermin		4885133		Transcriptional antiterminator bglG		-41.4		8.40E-01	2891	2967
	TFIIIE beta		4885133		TFIIIE beta subunit core domain		-15.1		8.40E-01	566	624
	TarH		4885133		Tar ligand binding domain homologue		-28.4		8.80E-01	2666	2793
	FLID		4885133		Flagellar hook-associated protein 2		-252.1		9.10E-01	2261	2712
PC057	ABO20038	U	4885956		ABO20038 protein						
	Laminin N1	U	4885956		Laminin N-terminal (Domain VI)		37		8.80E-14	50	295
	Laminin EGF	U	4885956		Laminin EGF-like (Domains III and V)		31.8		8.00E-07	297	341
	EGF	U	4885956		EGF-like domain		3.9		5.20E-01	299	326
PC104	PC0413380	U	8051621		Nucleoside transferase domain		0.3		4.10E-02	33	142
	PC0413380	U	8051621		Nucleoside transferase domain						
PC112	PC0419800	U	6735452		HSA02703 protein						
	PC0419800	U	6735452								
PC121	PC042021D	D	4505987		Down-regulated						
	PC042021D	D	4505987		SAM						
	PC042021D	D	4505987		integrate DNA						
	PC042021D	D	4505987		WHEP-TRS						
	PC042021D	D	4505987		DUF16						
	PC042021D	D	4505987		bZIP						
	PC042021D	D	4505987		STAT						
PC088	PC0501490	U	2217931		ABO20038 protein						
	PC0501490	U	2217931		Protein kinase domain		245.9		2.90E-71	409	688
	PC0501490	U	2217931		A2M		1.1		2.40E-01	471	493
	PC0501490	U	2217931		PC0501490 protein						

Table 3

PC050149U	U	2217931	DUF164	Uncharacterized ACR, COG1579	-99.2	5.10E-01	356	574	
PC050149U	U	2217931	Stathmin	Stathmin family	-22.4	8.40E-01	126	263	
PC050151U	U	6715600	GRIP	GRIP domain	77.2	1.70E-20	2171	2215	
PC050151U	U	6715600	M	M protein repeat	48.2	9.30E-12	2065	2085	
PC050151U	U	6715600	Involucrin	Involucrin repeat	14	4.20E-02	2005	2014	
PC050151U	U	6715600	Ribosomal L29	Ribosomal L29 protein	-7.7	8.80E-02	1263	1325	
PC050151U	U	6715600	DNA topoisomerase IV	DNA gyrase/topoisomerase IV, subunit	3.1	1.00E-01	1850	1882	
PC050151U	U	6715600	bZIP	bZIP transcription factor	6.7	1.20E-01	864	897	
PC050151U	U	6715600	DUF164	Uncharacterized ACR, COG1579	-89.1	1.20E-01	1559	1775	
PC050151U	U	6715600	Tropomyosin	Tropomyosin	3.4	1.50E-01	553	578	
PC050151U	U	6715600	Lipoprotein 7	Adhesin lipoprotein	-123	2.20E-01	725	1177	
PC050151U	U	6715600	DUF156	Uncharacterized BCR, COG1937	-9.6	3.90E-01	916	974	
PC050151U	U	6715600	UVR	UvrB/uvrC motif	-3.8	5.00E-01	363	397	
PC050151U	U	6715600	ATP-synt ab C	ATP synthase alpha/beta chain, C term	-21.2	5.10E-01	381	486	
PC050151U	U	6715600	ICL	Isocitrate lyase family	-1.6	5.90E-01	1963	1980	
PC050151U	U	6715600	CagE, TthE, VirB	CagE, TthE, VirB family, component of	-86.1	6.30E-01	1091	1290	
PC050151U	U	6715600	Borrelia orfA	Borrelia orfA	-107.4	7.40E-01	1366	1698	
PC050151U	U	6715600	SEA	SEA domain	-10.6	7.80E-01	1177	1299	
PC050151U	U	6715600	DUF28	Domain of unknown function DUF28	-167.8	8.00E-01	1248	1422	
PC050151U	U	6715600	Bac DNA binding	Bacterial DNA-binding protein	3.4	8.20E-01	2103	2118	
PC050151U	U	6715600	MSG	Major surface glycoprotein	-6.3	9.60E-01	1576	1635	
PC050151U	U	6715600	Transposase 8	Transposase	-21.9	9.70E-01	1150	1228	
PC085	PC050296U	U	Homologous to a prokaryotic cytoplasmic protein	Homologous to a prokaryotic cytoplasmic protein					
PC050296U	U	5453634	GTP CDC	Cell division protein	5.7	6.60E-02	56	71	
PC050296U	U	5453634	ABC tran	ABC transporter	-46	1.80E-01	54	291	
PC050296U	U	5453634	SRP54	SRP54-type protein, GTPase domain	4.2	2.20E-01	53	74	
PC101	PC050620U	U	Homologous to a prokaryotic membrane protein	Homologous to a prokaryotic membrane protein					
PC060	PC050853U	U	Homologous to a prokaryotic membrane protein	Homologous to a prokaryotic membrane protein					
PC050853U	U	4503725	FKBP	FKBP-type peptidyl-prolyl cis-trans isom	179.2	6.30E-55	11	105	
PC076	PC051210U	U	Homologous to a prokaryotic membrane protein	Homologous to a prokaryotic membrane protein					
PC051210U	U	4506057	kinase	Protein kinase domain	303.4	1.50E-88	44	298	
PC083	PC051231U	U	kinase C	Protein kinase C terminal domain	27.4	1.90E-08	299	330	
PC051231U	U	4506601	Ribosomal L14e	Ribosomal protein L14	120.1	2.20E-33	4	81	
PC051231U	U	4506601	Ribosomal L27e	Ribosomal L27e protein family	-62	1.60E-01	3	120	
PC90	PC051745D	D	Down-regulated	Down-regulated					
PC051745D	D	4758752	BIR	Inhibitor of Apoptosis domain	354.1	8.10E-104	281	346	
PC051745D	D	4758752	AAA	ATPase family associated with various	-45.7	4.00E-01	465	658	
PC051745D	D	4758752	Peptidase M29	Thermophilic metalloprotease (M29)	-0.4	6.20E-01	957	964	
PC051745D	D	4758752	ABC tran	ABC transporter	-72.9	6.40E-01	463	602	
PC051745D	D	4758752	NB-ARC	NB-ARC domain	1.5	7.70E-01	465	483	
PC100	PC052029U	U	Homologous to a prokaryotic membrane protein	Homologous to a prokaryotic membrane protein					

Table 3

PC093	PC052029U	U	5803219	kazal	Kazal-type serine protease inhibitor	172.5	3.70E-49	993	1046
	PC052029U	U	5803219	RNA POL M 15K	RNA polymerases M/15 Kd subunit	-7.8	6.40E-01	308	363
	PC052029U	U	5803219	DnaJ CXXCXXG	DnaJ central domain (4 repeats)	-51.3	6.50E-01	751	823
	PC052029U	U	5803219	Hirudin	Hirudin	-10.8	7.40E-01	380	441
	PC052029U	U	641958	Human myosin heavy chain B (NM_004416)	Human myosin heavy chain B (NM_004416)	1495.3	0.00E+00	87	771
	PC052029U	U	641958	Myosin head	Myosin head (motor domain)	788.7	1.20E-234	1073	1931
	PC052029U	U	641958	Myosin tail	Myosin tail	76.1	3.70E-20	1898	1918
	PC052029U	U	641958	M	M protein repeat	70.1	2.40E-18	33	77
	PC052029U	U	641958	Myosin N	Myosin N-terminal SH3-like domain	22.3	5.90E-04	787	807
	PC052029U	U	641958	IQ	IQ calmodulin-binding motif	-98.6	6.60E-02	1083	1318
PC129	PC052029U	U	641958	Apolipoprotein	Apolipoprotein A1/A4/E family	-86.6	8.70E-02	1018	1250
	PC052029U	U	641958	DUF164	Uncharacterized ACR, COG1579	7.2	8.80E-02	1788	1817
	PC052029U	U	641958	bZIP	bZIP transcription factor	-394.9	9.50E-02	171	425
	PC052029U	U	641958	Prismene	Prismene	-35.3	1.20E-01	965	1062
	PC052029U	U	641958	K-box	K-box region	0.1	1.30E-01	742	748
	PC052029U	U	641958	Tub	Tub family	3.2	1.80E-01	1863	1898
	PC052029U	U	641958	Tropomyosin	Tropomyosin	2.7	1.80E-01	1781	1809
	PC052029U	U	641958	Lipoprotein 1	Borrelia lipoprotein	-0.6	2.10E-01	1034	1108
	PC052029U	U	641958	HRI	HRI repeat motif	-414.1	2.20E-01	600	996
	PC052029U	U	641958	HSP70	Hsp70 protein	-38.3	2.70E-01	1488	1684
	PC052029U	U	641958	OEP	Outer membrane efflux protein	10.5	3.30E-01	1823	1832
	PC052029U	U	641958	Involucrin	Involucrin repeat	3.1	3.30E-01	1531	1548
	PC052029U	U	641958	kinesin	Kinesin motor domain	-47.4	4.00E-01	1062	1165
	PC052029U	U	641958	KE2	KE2 family protein	-65	5.30E-01	863	1220
	PC052029U	U	641958	HlyD	HlyD family secretion protein	2.5	5.40E-01	1107	1127
	PC052029U	U	641958	NAP family	Nucleosome assembly protein (NAP)	-4.5	6.10E-01	1043	1077
	PC052029U	U	641958	UVR	UvrB/uvrC motif	-36.2	7.30E-01	1232	1353
	PC052029U	U	641958	Bima VP5	Birnavirus VP5 protein	-110.7	7.90E-01	1325	1534
	PC052029U	U	641958	BAR	BAR domain	1	8.20E-01	1304	1317
	PC052029U	U	641958	Transaldolase	Transaldolase	0.5	9.60E-01	1182	1210
PC129	PC052029U	U	641958	PV RdRp	Viral RNA dependent RNA polymerase	537.6	4.50E-159	2724	2768
	PC060144D	D	4758200	Down-regulated	Down-regulated	23.9	1.60E-06	1702	1740
	PC060144D	D	4758200	Plectin repeat	Plectin repeat	24.2	1.60E-06	1060	1082
	PC060144D	D	4758200	bZIP	bZIP transcription factor	9.3	7.00E-03	1394	1416
	PC060144D	D	4758200	spectrin	Spectrin repeat	16.6	3.10E-02	1876	1896
	PC060144D	D	4758200	Myosin tail	Myosin tail	5.8	9.60E-02	1892	1908
	PC060144D	D	4758200	M	M protein repeat	-263.9	1.90E-01	1779	2352
	PC060144D	D	4758200	G-gamma	GGL domain	7.4	2.90E-01	1382	1426
	PC060144D	D	4758200	Exo70	Exo70 exocyst complex subunit	0.2	6.90E-01	2401	2413
	PC060144D	D	4758200	HALZ	Homeobox associated leucine zipper	-6.6	7.40E-01	1844	1918
PC060144D	PC060144D	D	4758200	RNA pol B	RNA polymerase beta subunit	1.5	7.50E-01	2713	2736
	PC060144D	D	4758200	HRI	Hrl repeat motif	-34.7	7.50E-01	1666	1818
	PC060144D	D	4758200	DNA pol B exo	DNA polymerase family B, exonuclease				
	PC060144D	D	4758200	Tropoin	Tropoin				

Table 3

PC060144D	D	4758200	phospholipase A2	3	7.70E-01	2553	2566		
PC060144D	D	4758200	Transposase		7.80E-01	1412	1720		
PC060144D	D	4758200	DNA binding domain of integrase	-7.2	8.80E-01	259	328		
PC060144D	D	4758200	Intermediate filament protein	1.8	8.80E-01	1552	1582		
PC060144D	D	4758200	Translin family	-86.4	9.90E-01	1283	1438		
PC060441U	U	1688258	Human collagenase and stromelysin complex	415.2	3.10E-122	37	204		
PC060441U	U	1688258	Matrixin	222.2	3.80E-64	426	466		
PC060441U	U	1688258	Hemopexin	-101.3	1.60E-02	107	264		
PC060441U	U	1688258	Asiacin (Peptidase family M12A)	-3.3	2.60E-02	27	91		
PC060441U	U	1688258	Putative peptidoglycan binding domain	1.9	8.40E-01	248	266		
PC060443U	U	4506731	UDPGP						
PC060443U	U	4506731	UTP-glucose-1-phosphate uridylyltran						
PC060443U	U	4506731	Homosapiens ribosomal protein S6	312.2	3.30E-91	1	127		
PC060443U	U	4506731	Ribosomal S6e						
PC060474U	U	4759322	Homosapiens wingless-type MMTV integrin alpha 2B (VNR2B) mRNA	656.5	1.00E-239	52	361		
PC060474U	U	4759322	wnt family	-87.2	8.50E-01	224	364		
PC060474U	U	4759322	Keratin, high sulfur B2 protein	-7	3.10E-02	514	570		
PC060529U	U	4503821	SH3						
PC060529U	U	4503821	vATP-synt E	-104.2	9.80E-01	464	645		
PC060743D	D	4557257	Down-regulated						
PC060743D	D	4557257	ATP synthase (E31 kDa) subunit	632	1.80E-187	973	1172		
PC060743D	D	4557257	guanylate cyc	-39.6	3.80E-01	292	347		
PC060743D	D	4557257	Bacterial export proteins, family 3	-92.8	5.50E-01	13	320		
PC060743D	D	4557257	GARS	-98.1	7.50E-01	52	268		
PC060743D	D	4557257	Prion protein	-223.6	9.40E-01	42	454		
PC060743D	D	4557257	Sodium transport protein						
PC060793D	D	4507583	Down-regulated						
PC060793D	D	4507583	TM6SF1	94.9	8.30E-26	129	165		
PC060793D	D	4507583	TNFR/c6	70.7	1.60E-18	231	314		
PC060793D	D	4507583	Death domain						
PC060940U	U	5052075	Homosapiens PAPSS2 mRNA	683.7	4.70E-203	284	612		
PC060940U	U	5052075	ATP-sulfurylase	395.1	3.60E-116	41	199		
PC060940U	U	5052075	APS kinase	-70	2.30E-01	47	207		
PC060940U	U	5052075	Thymidylate kin	-123.6	3.20E-01	30	223		
PC060940U	U	5052075	6-phosphofructo-2-kinase	3.1	3.90E-01	47	66		
PC060940U	U	5052075	PRK						
PC061342D	D	386831	Down-regulated						
PC061342D	D	386831	Phosphoribulokinase / Uridine kinase	239.3	2.80E-69	151	329		
PC061342D	D	386831	vva	200.6	1.30E-57	581	633		
PC061342D	D	386831	FG-GAP repeat	30.6	1.90E-06	1129	1143		
PC061342D	D	386831	Integrin alpha cytoplasmic region	1.3	6.10E-01	522	531		
PC061477U	U	4506387	Poliovirus coat protein	105.2	3.20E-29	1	78		
PC061477U	U	4506387	Ubiquitin family	71.5	9.40E-19	365	404		
PC061477U	U	4506387	UBA	6.2	4.10E-03	364	391		
PC061477U	U	4506387	Integrin B						
PC061528D	D	4506701	Down-regulated						
PC061528D	D	4506701	Homosapiens ribosomal protein S23 (RPS23) mRNA						

Table 3

	PC061528D	D	4506701	Ribosomal S12	Ribosomal protein S12	279.8	1.80E-81	7	142	
PC202	PC061779U	U	4504767	Homosapiens integrin beta-1 (fibronectin receptor type II polypeptide chain)	Integrins, beta chain	1121.8	0.00E+00	34	464	Human MSK2 (p408) mRNA
	PC061779U	U	4504767	Integrin B	Integrins, beta chain	1121.8	0.00E+00	34	464	
	PC061779U	U	4504767	EGF	EGF-like domain	21.3	1.20E-03	599	630	
	PC061779U	U	4504767	Plexin repeat	Plexin repeat	7.7	2.00E-02	26	76	
	PC061779U	U	4504767	PNTB	NAD(P) transhydrogenase beta subunit	4.1	1.40E-01	2	20	
	PC061779U	U	4504767	metallothionein	metallothionein	6.8	1.70E-01	594	667	
PC214	PC061827U	U	7382496	Homosapiens p21 (Cdc42Rac1 activator kinase 1 (yeast Slt2)-related)	Protein kinase domain	312.4	2.90E-91	270	521	
	PC061827U	U	7382496	kinase	Protein kinase domain	312.4	2.90E-91	270	521	
	PC061827U	U	7382496	PBD	P21-Rho-binding domain	127	1.80E-35	75	135	
	PC061827U	U	7382496	kinesin	Kinesin motor domain	3.4	2.70E-01	228	250	
	PC061827U	U	7382496	ABCI	ABCI family	57.1	1.00E+00	261	386	
PC208	PC061839U	U	8394499	Homosapiens tubulin associated protein (UBAP)	UBAP	23.1	3.50E-04	459	498	
	PC061839U	U	8394499	UBA	UBA/TS-N domain	23.1	3.50E-04	459	498	
PC147	PC070152U	U	4506713	Homosapiens ribosomal protein S27a (RPS27A)	ribosomal protein S27a	153.2	2.40E-43	1	74	
	PC070152U	U	4506713	ubiquitin	Ubiquitin family	153.2	2.40E-43	1	74	
	PC070152U	U	4506713	Ribosomal S27	Ribosomal protein S27a	121	1.10E-33	101	147	
	PC070152U	U	4506713	IBR	IBR domain	22.5	9.70E-01	103	156	
PC174	PC070343U	U	4507211	Homosapiens signal recognition particle 14kD (homologous to RNA binding protein) (SRP14)	Signal recognition particle 14kD prot	216.4	2.10E-62	4	94	
	PC070343U	U	4507211	Down-regulated	Signal recognition particle 14kD prot	216.4	2.10E-62	4	94	
PC175	PC070436D	D	4503287	Homosapiens growth arrest related DNA damage-inducible protein L7Ae	Ribosomal protein L7Ae/L30e/S12e/Gad	73.6	2.10E-19	21	123	
	PC070436D	D	4503287	SRP14	Ribosomal protein L7Ae/L30e/S12e/Gad	73.6	2.10E-19	21	123	
PC173	PC070544U	U	7765076	Homosapiens ribosomal protein human colonin RNA826m1	Ribosomal protein S3, C-terminal domain	112.8	1.30E-35	104	188	
	PC070544U	U	7765076	Ribosomal S3 C	Ribosomal protein S3, C-terminal domain	112.8	1.30E-35	104	188	
	PC070544U	U	7765076	KH domain	KH domain	24.7	1.10E-04	47	95	
PC257	PC070729U	U	8923791	Homosapiens ribosomal protein (HSR1TSBE1A)	ribosomal protein (HSR1TSBE1A)	144.5	2.40E-13	191	328	
	PC070729U	U	8923791	MR MLE	Mandelate racemase / muconate lactoni	17	1.50E-05	9	112	
	PC070729U	U	8923791	MR MLE N	Mandelate racemase / muconate lactoni	17	1.50E-05	9	112	
	PC070729U	U	8923791	Peptidase S26	Signal peptidase I	3.8	1.90E-01	54	84	
PC251	PC071170D	D	31442	Down-regulated	Signal peptidase I	3.8	1.90E-01	54	84	
	PC071170D	D	31442	Integrin B	Integrins, beta chain	1121.8	0.00E+00	34	464	
	PC071170D	D	31442	EGF	EGF-like domain	21.3	1.20E-03	599	630	
	PC071170D	D	31442	Plexin repeat	Plexin repeat	7.7	2.00E-02	26	76	
	PC071170D	D	31442	PNTB	NAD(P) transhydrogenase beta subunit	4.1	1.40E-01	2	20	
	PC071170D	D	31442	metallothionein	metallothionein	6.8	1.70E-01	594	667	
PC253	PC071851U	U	15297004	Homosapiens ribosomal protein B18 (unknown)	ribosomal protein B18 (unknown)	1121.8	0.00E+00	34	464	
	PC071851U	U	15297004	Down-regulated	ribosomal protein B18 (unknown)	1121.8	0.00E+00	34	464	
PC159	PC080139D	D	7657160	Homosapiens Enoyl-CoA hydratase/isomerase family	Enoyl-CoA hydratase/isomerase family	163.6	2.30E-16	142	213	
	PC080139D	D	7657160	ECH	Enoyl-CoA hydratase/isomerase family	163.6	2.30E-16	142	213	
	PC080139D	D	7657160	RNase HII	Ribonuclease HII	94.9	4.50E-01	205	357	
PC156	PC080348U	U	9623361	Homosapiens DNA polymerase epsilon (pol12)	DNA polymerase epsilon (pol12)	9.7	4.10E-03	39	106	
	PC080348U	U	9623361	CBFD NFYB HMI	Histone-like transcription factor (CBF)	9.7	4.10E-03	39	106	
	PC080348U	U	9623361	TAF	TATA box binding protein associated fa	14.3	1.10E-01	55	104	
PC163	PC080435D	D	4758808	Homosapiens ras GTPase activating protein like (NGAP)	ras GTPase activating protein like (NGAP)	1121.8	0.00E+00	34	464	

Table 3

PC080435D	D	4758808	RasGAP	GTase-activator protein for Ras-like	111.4	8.70E-31	348	520
PC080435D	D	4758808	PH	PH domain	19.9	1.90E-05	111	158
PC080435D	D	4758808	Respiratory-chain NADH dehydrogenase complex I 49Kd	Respiratory-chain NADH dehydrogenase	8.4	3.90E-04	351	359
PC080435D	D	4758808	DEAD	DEAD/DEAH box helicase	8.8	3.70E-03	950	992
PC080435D	D	4758808	C2	C2 domain	5.8	4.60E-02	171	251
PC080435D	D	4758808	FLID	Flagellar hook-associated protein 2	242	3.50E-01	603	1101
PC216	D	4504191	NM100019911	HomosapiensmutS(E60D)homolog(MSH6)	132.1	3.30E-94	1054	1316
PC080511U	U	4504191	MutS C	DNA mismatch repair proteins, mutS fa	127.1	2.00E-62	409	977
PC080511U	U	4504191	MutS N	MutS family, N-terminal putative DNA	127.1	1.60E-35	89	162
PC080511U	U	4504191	PWWP	PWWP domain	1.3	7.30E-01	753	768
PC080511U	U	4504191	SNF	Sodium:neurotransmitter symporter fam	1.3	7.30E-01	753	768
PC080742U	U	4504191	Luco ORF3	Luteovirus (ORF3) RNA-directed RNA-	0.3	8.60E-01	1304	1330
PC274	D	4507187	NM100312511	Homosapienssmallproteinhomolog(B) (comin)	57	2.10E-14	1	87
PC080742U	U	4507187	Comin	Comin (SPR) family	57	2.10E-14	1	87
PC299	D	3252911	AF056322	HomosapiensSP100FH(nucleolar antigen)(SP100)imRNA	180	2.10E-51	595	676
PC090230U	U	3252911	SAND	SAND domain	118.3	7.70E-33	769	837
PC090230U	U	3252911	HMG box	HMG (high mobility group) box	118.3	7.70E-33	769	837
PC302	D	4504193	Homosapiensgeneraltranscriptionfactor(B)(GTF2B)imRNA	Transcription factor TFIIB repeat	231.1	8.60E-67	215	285
PC090233U	U	4504193	transcript fac2	Transcription factor TFIIB repeat	231.1	8.60E-67	215	285
PC090233U	U	4504193	cyclin	Cyclin, N-terminal domain	26.6	8.30E-02	94	207
PC316	D	4506859	NM1009971	HomosapiensSyndecan(SDC1)imRNA	534.3	6.50E-187	3	308
PC090622D	D	4506859	Syndecan	Syndecan domain	534.3	6.50E-187	3	308
PC090625U	U	7706216	HomosapiensH2Akinbindingfactor2(BOG18.80)imRNA	IFT/TIG domain	55.5	6.20E-14	275	365
PC090625U	U	7706216	TIG	IFT/TIG domain	55.5	6.20E-14	275	365
PC090625U	U	7706216	Ig	Immunoglobulin domain	11.7	2.40E-03	165	221
PC310	D	307218	HM129H	HumanMHCproteinhomologus(orthocentB)complexproteinimRNA	200.3	1.60E-57	275	311
PC090677D	D	307218	WD40	WD domain, G-beta repeat	200.3	1.60E-57	275	311
PC239	D	7670748	AP2279060	HomosapiensUDP-glucose4-epimerase2 precursorimRNA	237.8	8.20E-69	4	175
PC230	D	4503473	Homosapiensleukocyte translaibindingfactor(Ta1ph)/Vitel14(EEH1A1H1)imRNA	Elongation factor Tu GTP binding domain	201.1	8.80E-58	269	378
PC090754U	U	4503473	GTP EFTU	Elongation factor Tu GTP binding domain	201.1	8.80E-58	269	378
PC090754U	U	4503473	GTP EFTU D3	Elongation factor Tu C-terminal domain	98.6	1.50E-27	187	263
PC090754U	U	4503473	GTP EFTU D2	Elongation factor Tu domain 2	98.6	1.50E-27	187	263
PC220	D	5031639	Homosapienscomichon-like(GN1)imRNA	Homosapienscomichon-like(GN1)imRNA				
PC233	D	5031639	Homosapienslactate dehydrogenase(B)(LDHB)imRNA	Homosapienslactate dehydrogenase(B)(LDHB)imRNA				
PC090842U	U	4557032	ldh C	lactate/malate dehydrogenase, alpha/het4297	297	1.20E-86	164	333
PC090842U	U	4557032	ldh	lactate/malate dehydrogenase, NAD binc	284.4	7.30E-83	19	162
PC236	D	7662426	HomosapiensKIAA0976protein(KIAA0976)imRNA	Laminin N-terminal (Domain VI)	37	8.80E-14	50	295
PC091028U	U	7662426	laminin Nterm	Laminin N-terminal (Domain VI)	37	8.80E-14	50	295
PC091028U	U	7662426	laminin EGF	Laminin EGF-like (Domains III and V)	31.8	8.00E-07	297	341
PC091028U	U	7662426	EGF	EGF-like domain	3.9	5.20E-01	299	326
PC324	D	4732026	NM108569	HomosapiensangiotensinII converting enzyme precursor	341.5	0.00E+00	634	1228
PC091425U	U	4732026	Peptidase M2	Angiotensin-converting enzyme	341.5	0.00E+00	634	1228
PC091425U	U	4732026	HupF HypC	HupF/HypC family	34	5.00E-01	1231	1286

Table 3

PC091425U	U	4732026	Phosphoprotein	Vesiculovirus phosphoprotein	0.1	7.10E-01	596	607	
PC091425U	U	4732026	MM CoA mutase	Methylmalonyl-CoA mutase	0.9	7.70E-01	192	221	
PC400	U	5803092	Homosapiensmetalloproteinase	Homosapiensmetalloproteinase (HSP)					
PC091527U	U	5803092	Peptidase M24	metallopeptidase family M24	319	2.80E-93	159	404	
PC091527U	U	5803092	PBP GOBP	PBP/GOBP family	-51.4	9.10E-01	127	254	
PC091839U	U	7188647	Homosapiens	Homosapiens					
PC405	U	31092	Homosapiens	Homosapiens					
PC091853U	U	31092	GTP EFTU	Elongation factor Tu GTP binding domain	378.7	3.00E-111	5	239	
PC091853U	U	31092	GTP EFTU D3	Elongation factor Tu C-terminal domain	212.7	3.00E-61	333	442	
PC091853U	U	31092	GTP EFTU D2	Elongation factor Tu domain 2	100.7	3.80E-28	251	327	
PC091853U	U	31092	pyr redox	Pyridine nucleotide-disulphide oxidoreductase	-99.3	6.10E-01	9	286	
PC091853U	U	31092	ATP-bind	Conserved hypothetical ATP binding protein	-138.3	9.80E-01	9	182	
PC402	U	4757810	Homosapiens	Homosapiens					
PC091888U	U	4757810	ATP-synt ab	ATP synthase alpha/beta family, nucleoside triphosphatase	554.9	2.80E-164	138	421	
PC091888U	U	4757810	ATP-synt ab C	ATP synthase alpha/beta family, C terminus	140.6	1.40E-39	423	531	
PC091888U	U	4757810	ATP-synt ab N	ATP synthase alpha/beta family, beta-b	76.5	2.80E-20	67	135	
PC091888U	U	4757810	FwdE	Tungsten formylmethanofuran dehydrogenase	-97.9	9.90E-01	230	408	
PC401	U	8922824	Homosapiens	Homosapiens					
PC092004U	U	8922824	zf-C2H2	Zinc finger, C2H2 type	455.9	1.80E-134	457	479	
PC092004U	U	8922824	zf-BED	BED zinc finger	4.8	2.00E-02	246	284	
PC092004U	U	8922824	LIM	LIM domain	-16.7	2.30E-01	431	483	
PC092004U	U	8922824	Bola	Bola-like protein	-24.5	2.70E-01	100	157	
PC092004U	U	8922824	zf-MIZ	MIZ zinc finger	-21.1	4.70E-01	354	412	
PC092004U	U	8922824	TFIS	Transcription factor S-II (TFIS)	-6.9	4.90E-01	289	327	
PC092004U	U	8922824	PHD	PHD-finger	-20.8	7.90E-01	122	185	
PC092004U	U	8922824	zf-ANI	ANI-like Zinc finger	-11.8	8.20E-01	123	169	
PC406	U	4505635	Homosapiens	Homosapiens					
PC092052U	U	4505635	cadherin	Cadherin domain	399.8	1.40E-117	749	840	
PC092052U	U	4505635	Adeno E3 CR2	Adenovirus E3 region protein CR2	-2.9	2.90E-01	873	912	
PC092052U	U	4505635	Hepes gE	Alphaherpesvirus glycoprotein E	-257.7	3.90E-01	552	948	
PC092052U	U	4505635	CBD 6	Cellulose binding domain	-23.5	6.10E-01	627	786	
PC279	U	5733684	Homosapiens	Homosapiens					
PC100113U	U	5733684	trypsin	Trypsin	277	1.90E-88	30	245	
PC100113U	U	5733684	toxin 4	Anenome neurotoxin	-3.3	4.70E-01	200	239	
PC285	U	13272790	Homosapiens	Homosapiens					
PC100356U	U	13272790	oxidored q1	NADH-ubiquinone/plastoquinone (complex 1)	344.3	6.80E-101	112	404	
PC100356U	U	13272790	oxidored q5 N	NADH-ubiquinone oxidoreductase chain 2	211.7	5.80E-61	1	109	
PC100356U	U	13272790	sugar tr	Sugar (and other) transporter	-201.8	6.50E-01	32	411	
PC100356U	U	13272790	DsbD	Cytochrome C biogenesis protein trans	-101.5	7.50E-01	126	305	
PC100356U	U	13272790	DUF6	Integral membrane protein DUF6	-29.6	9.80E-01	286	408	
PC294	U	4502981	Homosapiens	Homosapiens					
PC100428U	U	4502981	COX4	Cytochrome c oxidase subunit IV	242.1	4.00E-70	26	169	
PC323	U	182851	Homosapiens	Homosapiens					
PC101430U	U	182851							

SEQUENCE LISTING

<110> OriGene Technologies

<120> Prostate Cancer Expression Profiles

<130> 9U 206 PCT

<150> US 60/281,732

<151> 2001-04-06

<150> US 60/281,731

<151> 2001-04-06

<160> 211

<170> PatentIn version 3.1

<210> 1

<211> 620

<212> DNA

<213> Homo sapiens

<400> 1

```

gggtttatcg gaaaatgtgt ttattgagat ggtttccac tcattctgac tcagagtgt 60
tttagtgctg cttctctctg aaggaacatc cttctgtaag cttgctttt ctcctctggc 120
tgtctgaaga tagatcgcca tcatgaacga caccgtaact atccgcacta gaaagtcat 180
gaccaaccga ctacttcaga ggaaacaaat ggtcattgat gtccttcacc ccgggaaggc 240
gacagtgcct aagacagaaa ttcgggaaaa actagccaaa atgtacaaga ccacaccgga 300
tgtcatcttt gtatttggat tcagaactca ttttgggtgt ggcaagacaa ctggcttttg 360
catgatttat gattccctgg attatgcaaa gaaaaatgaa cccaaacata gacttgcaag 420
acatggcctg tatgagaaga aaaagacctc aagaaagcaa cgaaaggaac gcaagaacag 480
aatgaagaaa gtcaggggga ctgcaaaggc caatgttggg gctggcaaaa agccgaagga 540
gtaaaggtag tgcaatgatg ttagctgtgg ccaactgtga ttttctgcaa gaacattaat 600
aaactaaaaa cttcatgtgt 620

```

<210> 2

<211> 5212

<212> DNA

<213> Homo sapiens

<400> 2

```

ggccaggcga caggtgtcgc ttgaaaagac tgggcttgtc cttgctggtg catgcgtcgt 60
cggcctcttg gcagcaggtt tacaaaggag gaaaacgact tcttctagat ttttttttca 120
gtttcttcta taaatcaaaa catctcaaaa tggagacctc aaatccttaa agggacttag 180
tctaattctg ggaggtagtt ttgtgcatgg gtaaacaaat taagtattaa ctggtgtttt 240
actatccaaa gaatgctaata ttataaaca tgatcgagtt atataaggta taccataatg 300
agtttgattt tgaatttgat ttgtggaaat aaaggaaaag tgattctagc tggggcatat 360
tgttaagca tttttttcag agttggccag gcagtctcct actggcacat tctccatta 420
tgtagaatag aaatagtacc tgtgtttggg aaagatttta aaatgagtga cagttatttg 480
gaacaaagag ctaataatca atccactgca aattaaagaa acatgcagat gaaagttttg 540
acacattaaa atacttctac agtgacaaag aaaaatcaag aacaaagctt tttgatatgt 600
gcaacaaatt tagaggaagt aaaaagataa atgtgatgat tggtaagaa attatccagt 660
tatttacaag gccactgata ttttaaacgt ccaaaagttt gtttaaatgg gctgttaccg 720
ctgagaatga tgaggatgag aatgatggtt gaaggttaca ttttaggaaa tgaagaaact 780

```

```

tagaaaatta atataaagac agtgatgaat acaaagaaga tttttataac aatgtgtaaa 840
atttttggcc agggaaaagga atattgaagt tagatacaat tacttacctt tgagggaat 900
aattgttgggt aatgagatgt gatgtttctc ctgccacctg gaaacaaagc attgaagtct 960
gcagttgaaa agcccaacgt ctgtgagatc caggaaacca tgcttgcaaa ccactggtaa 1020
aaaaaaaaaa aaaaaaaaaa aaaaagccac agtgacttgc ttatttgtca ttgctagtat 1080
tactgactca gaacctcttt actaatggct agtaaatcat aattgagaaa ttctgaattt 1140
tgacaaggtc tctgtgttg aaatggtaaa tttattattt tttttgtcat gataaattct 1200
ggttcaaggt atgctatcca tgaaataatt tctgaccaa actaaattga tgcaatttga 1260
ttatccatct tagcctacag atggcatctg gtaacttttg actgttttaa aaataaatcc 1320
actatcagag tagatttgat gttggcttca gaaacatttt gaaaaacaaa agttcaaaaa 1380
tgttttcagg aggtgataag ttgaataact ctacaatgtt agttctttga gggggacaaa 1440
aaatttaaaa tctttgaaag gtcttatttt acagcccata tctaaattat cttagaaaa 1500
tttttaacaa agggaatgaa atatataatca tgattctctt tttccaaaag taacctgaat 1560
atagctatga agttcagttt tgttatttgt agtttgggca gagtctcttt ttgcagcacc 1620
tgttgtctac cataattaca gaggacattt ccatgttcta gccaagtata ctattagaat 1680
aaaaaaactt aacattgagt tgcttcaaca gcatgaaact gagtccaaaa gaccaaatga 1740
acaaacacat taatctctga ttattttatt taaatagaat atttaattgt gtaagatcta 1800
atagtatcat tatacttaag caatcatatt cctgatgatc tatgggaaat aactattatt 1860
taattaatat tgaaccagg ttttaagatg tgttagccag tcctgttact agtaaatctc 1920
tttatttggg gagaaatttt agattgtttt gttctcctta ttagaaggat tgtagaaaga 1980
aaaaaatgac taattggaga aaaattggg atatatcata tttcactgaa ttcaaatgt 2040
cttcagttgt aaatcttacc attattttac gtacctctaa gaaataaaag tgcttctaat 2100
taaaaatga tgtcattaat tatgaaatac ttcttgataa cagaagtttt aaaatagcca 2160
tcttagaatc agtgaaatat ggtaatgtat tattttctc ctttgagtta ggtcttgtgc 2220
ttttttttcc tggccactaa attcacaat ttccaaaag caaataaac atattctgaa 2280
tatttttgtc gtgaaacact tgacagcaga gctttccacc atgaaaagaa gttcatgag 2340
tcacacatta catctttggg ttgattgaat gccactgaaa cattctagta gcctggagaa 2400
gttgacctac ctgtggagat gcctgccatt aaatggcatc ctgatggctt aatacacatc 2460
actcttctgt gaagggtttt aattttcaac acagcttact ctgtagcatc atgtttacat 2520
tgtatgtata aagattatac aaaggtgcaa ttgtgtattt cttccttaa atgtatcagt 2580
ataggattta gaatctccat gttgaaactc taaatgcata gaaataaaaa taataaaaaa 2640
tttttcattt tggcttttca gcctagtatt aaaactgata aaagcaaagc catgcacaaa 2700
actacctccc tagagaaagg ctagtccctt ttcttcccca ttcatttcat tatgaacata 2760
gtagaaaaca gcatattctt atcaaatttg atgaaaagcg cctacacgtt tgaactgaaa 2820
tacgacttgt catgtgaact gtaccgaatg tctacgtatt ccacttttcc tgctggggtt 2880
cctgtctcag aaaggagtct tgctcgtgct ggtttctatt aactggtgt gaatgacaag 2940
gtcaaagtct tctgttgtg cctgatgctg gataactgga aaagaggaga cagtcctact 3000
gaaaagcata aaaagttgta tcctagctgc agattcgttc agagtctaaa ttccgttaac 3060
aacttgaag ctacctctca gcctactttt ccttcttcag taacaaattc cacacactca 3120
ttacttcggt gtacagaaaa cagtggatat ttccgtggct cttattcaaa ctctccatca 3180

```



```

aatcctgtaa actccagagc aaatcaagat ttttctgcct tgatgagaag ttcctaccac 3240
tgtgcaatga ataacgaaaa tgccagatta cttacttttc agacatggcc attgactttt 3300
ctgtcgccaa cagatctggc aaaagcaggc tttactaca taggacctgg agacagagtg 3360
gcttgctttg cctgtggtgg aaaattgagc aattgggaac cgaaggataa tgctatgtca 3420
gaacacctga gacattttcc caaatgccca tttatagaaa atcagcttca agacacttca 3480
agatacacag tttctaactc gagcatgcag acacatgcag cccgctttaa aacattcttt 3540
aactggccct ctagtgttct agttaatcct gagcagcttg caagtgcggg tttttattat 3600
gtgggtaaca gtgatgatgt caaatgcttt tgctgtgatg gtggactcag gtgttgggaa 3660
tctggagatg atccatgggt tcaacatgcc aagtggtttc caaggtgtga gtacttgata 3720
agaattaaag gacaggagtt catccgtcaa gttcaagcca gttaccctca tctacttgaa 3780
cagctgctat ccacatcaga cagcccagga gatgaaaatg cagagtcatc aattatccat 3840
tttgaacctg gagaagacca ttcagaagat gcaatcatga tgaatacccc tgtgattaat 3900
gctgccgtgg aaatgggctt tagtagaagc ctggtaaaac agacagtcca gagaaaaatc 3960
ctagcaactg gagagaatta tagactagtc aatgatcttg tgttagactt actcaatgca 4020
gaagatgaaa taagggaga ggagagagaa agagcaactg aggaaaaaga atcaaatgat 4080
ttattattaa tccggaagaa tagaatggca ctttttcaac atttgacttg tgaattcca 4140
atcctggata gtctactaac tgccggaatt attaatgaac aagaacatga tgttattaaa 4200
cagaagacac agacgtcttt acaagcaaga gaactgattg atacgatttt agtaaaagga 4260
aatattgcag ccactgtatt cagaaactct ctgcaagaag ctgaagctgt gttatatgag 4320
catttatatt tgcaacagga cataaaatat attcccacag aagatgtttc agatctacca 4380
gtggaagaac aattgcggag actacaagaa gaaagaacat gtaaagtgtg tatggacaaa 4440
gaagtgtcca tagtgtttat tccttgtggt catctagtag tatgcaagaa ttgtgtcctt 4500
tctttaagaa agtgtcctat ttgtaggagt acaatcaagg gtacagttcg tacatttctt 4560
tcataagaa gaacaaaaac atcatctaaa ctttagaatt aatttattaa atgtattata 4620
actttaactt ttatcctaatt ttggtttcct taaaattttt atttatttac aactcaaaaa 4680
acattgtttt gtgtaacata tttatatatg tatctaaacc atatgaacat atatttttta 4740
gaaactaaga gaatgatagg cttttgttct tatgaacgaa aaagaggtag cactacaaac 4800
acaatattca atcaaaatct cagcattatt gaaattgtaa gtgaagtaaa acttaagata 4860
tttgagttaa cctttaagaa ttttaatat tttggcattg tactaatacc gggaaacatga 4920
agccagggtg ggtggtatgt gcctgtagtc ccaggctgag gcaagagaat tacttgagcc 4980
caggagtttg aatccatcct gggcagcata ctgagaccct gcctttaaaa acaaacagaa 5040
caaaaacaaa acaccagga cacatttctc tgtctttttt gatcagtgtc ctatacatcg 5100
aagggtgtca tatatgttga atgacatttt agggacatgg tgtttttata aagaattctg 5160
tgagaaaaaa ttaataaag caacaaaaat tactcttaaa aaaaaaaaaa aa 5212

```

```

<210> 3
<211> 2513
<212> DNA
<213> Homo sapiens

```

```

<400> 3
cgcgcagcga tggaggcgcc ggggctcggg cggaggaggc ggagccggag cgcggccatg 60
gcgggggtccc tgagtgccag aggtggtggt gttgcttata ttctggaacc ccatgcagcc 120

```

agatcccagg cctagcgggg ctggggcctg ctgccgattc ctgcccctgc agtcacagtg 180
 ccctgagggg gcaggggagc cgtgatgta cgcctccact gattgcaagg cggagggtgac 240
 gccctcccag catggcaacc gcaccttcag ctacaccctg gaggatcata ccaagcaggc 300
 ctttggtatc atgaacgagc tgcggctcag ccagcagctg tgtgacgtca cactgcaggc 360
 caagtaccag gatgcaccgg ccgcccagtt catggcccac aagggtgtgc tggcctcacc 420
 cagccctgtt ttcaaggcca tgttcaccaa cgggctgcgg gagcagggca tggagggtgt 480
 gtccattgag ggtatccacc ccaaggtcat ggagcgctc attgaattcg cctacacggc 540
 ctccatctcc atgggcgaga agtgtgtcct ccacgtcatg aacggcgctg tcatgtacca 600
 gatcgacagc gttgtccgtg cctgcagtga ctctctggtg cagcagctgg accccagcaa 660
 tgccatcggc atcgccaact tcgctgagca gattggtgt gtggagtgc accagcgtgc 720
 ccgggagtac atctacatgc attttggga ggtggccaag caagaggagt tcttcaacct 780
 gtccactgc caactggtga ccctcatcag ccgggacgac ctgaacgtgc gctgcgagtc 840
 cgagggtctc cagcctgca tcaactgggt caagtacgac tgcgaacagc gacggttcta 900
 cgtccaggcg ctgctgcggg ccgtgcgtg ccactcgtt acgccgaact tcctgcagat 960
 gcagctgcag aagtgcgaga tcctgcagtc cgactccgc tgcaaggact acctggtcaa 1020
 gatcttcgag gagctcacc tgacaaagc cagcagggtg atgccctgcc gggcgcccaa 1080
 ggtgggcgc ctgatctaca ccgcgggcgg ctacttcga cagtcgtca gctacctgga 1140
 ggcttacaac ccagtaacg gcacctggct ccggttggc gacctgcagg tgcgcggag 1200
 cggcctggcc ggtgcgttg tggcggggt gttgtacgcc gtggcgcca ggaacaactc 1260
 gcccgacggc aacaccgact ccagcgccct ggactgttac aaccccatga ccaatcagt 1320
 gtcgccctgc gcccctatga gcgtgcccc taaccgcatc ggggtgggg tcacgatgg 1380
 ccacatctat gccgtcggc gctcccacg ctgcatccac cacaacagt tggagaggta 1440
 tgagccagag cgggatgagt ggcacttgg ggcccaatg ctgacacgaa ggatcgggg 1500
 gggcggtgct gtcctcaatc gctgcttta tgcctgggg ggctttgac ggacaaaccg 1560
 ccttaattca gctgagtgt actaccaga gaggaacgag tggcgaatga tcacagcaat 1620
 gaacaccatc cgaagcggg caggcgtctg cgtcctgcac aactgtatct atgctgctgg 1680
 gggctatgat ggtcaggacc agctgaacag cgtggagcgc tacgatgtgg aaacagagac 1740
 gtggacttct gtagcccca tgaagcacc gcgaagtgc ctgggatca ctgtccacca 1800
 ggggagaatc tacgtcctt gaggtatga tggtcacag ttcctggaca gtgtggagt 1860
 ttacgaccca gatacagaca cctggagcga ggtgaccga atgacatcg gccggagtgg 1920
 ggtggcgctg gctgtacca tggagccctg ccggaagcag attgaccagc agaactgtac 1980
 ctgttgaggc acttttgtt cttgggcaaa aatacagtc aatggggagt atcattgtt 2040
 ttgtacaaa accgggacta aaagaaaaga cagcactgca aataacccat cttccgggaa 2100
 gggaggccag gatgcctcag tgttaaatg acatctcaa agaagtcaa agcgggaatc 2160
 atgtgcccct cagcggagcc ccgggagtgt ccaagacagc ctggctggga aaggggtgt 2220
 ggaaagagca ggcttcagg agagaggccc ccaaaccctc tggccgggta ataggcctgg 2280
 gtccactca ccatgccgg cagctgtcac catgtattt attcttgat acctgggagg 2340
 gggccaatg gggcctcagg gggaggcccc ctctggaat gtggttcca gggatggggc 2400
 tgtacataga agccaccgga tggcaattcc ccaccgatg gacagttatt ttgttgataa 2460

gtaaccctgt aattttccaa ggaaaataaa gaacagacta actagtgtct ttc 2513

<210> 4
<211> 2500
<212> DNA
<213> Homo sapiens

<400> 4
cccagcgcga gccaatggga agggctcggag gcatggcaca gccaatggga agggccgggg 60
caccaaagcc aatgggaagg gccgggagcg cgcggcgcgg gagatttaaa ggctgctgga 120
gtgaggggtc gccctgcac cctgtcccag ccgtcctgtc ctggctgtc gctctgcttc 180
gtgtgcctc cactatgtc tccctcgtg tcccgctcg gccatcacg gacccgcagc 240
agctgcagct ctgcgcgtg aaggggtca gcttggtcga caaggagaac acgccgccg 300
ccctgagcgg gacccgcgtc ctggccagca agaccgcgag gaggatcttc caggagccca 360
cggagccgaa aactaaagca gctgccccg gcgtggagga tgagccgctg ctgagagaaa 420
acccccgccg ctttgtcacc tccccatcg agtaccatga tatctggcag atgtataaga 480
aggcagaggc ttccttttgg accgccgagg aggttgacct ctccaaggac attcagcact 540
gggaatccct gaaaccgag gagagatatt ttatatccca tgttctggct tcttttgag 600
caagcgatgg catagtaaata gaaaacttgg tggagcgatt tagccaagaa gttagatta 660
cagaagcccg ctgtttctat ggcttccaaa ttgccatga aaacatacat tctgaaatgt 720
atagtcttct tattgacct tacataaaag atcccaaaga aagggaatct ctcttcaatg 780
ccattgaaac gatgccttgt gtcaagaaga aggcagactg ggccttgccg tggattggg 840
acaaagaggc tacctatggt gaacgtgtt tagcctttgc tgcagtggaa ggcattttct 900
tttccggttc ttttgcgtc atattctggc tcaagaaacg aggactgatg cctggcctca 960
cattttctaa tgaacttatt agcagagatg agggtttaca ctgtgatttt gcttgctga 1020
tgttcaaaca cctggtacac aaaccatcg aggagagagt aagagaaata attatcaatg 1080
ctgttcggat agaacaggag ttcctcactg aggccttgcc tgtgaagctc attgggatga 1140
attgcaactc aatgaagca tacattgagt ttgtggcaga cagacttatg ctggaactgg 1200
gttttagcaa ggttttcaga gtagagaacc catttgactt tatggagaat atttactgg 1260
aaggaaagac taacttctt gagaagagag taggcgagta tcagaggatg ggagtgatgt 1320
caagtccaac agagaattct tttaccttgg atgctgactt ctaaatgaac tgaagatgtg 1380
cccttacttg gctgattttt ttttccatc tcataagaaa aatcagctga agtgttacca 1440
actagccaca ccatgaattg tccgtaattg tcattaacag catctttaa actgtgtagc 1500
tacctcaca ccagtcctgt ctgtttatag tgctgtagt atcaccttt gccagaaggc 1560
ctggctggct gtgacttacc atagcagtga caatggcagt ctgggcttta aagtgagggg 1620
tgaccttta gtgagcttag cacagcggga ttaaacagtc cttaaccag cacagccagt 1680
taaaagatgc agcctcactg cttcaacgca gattttaatg ttacttaa taaaacctg 1740
gcactttaca acaataaaa cattgtttt tactcacggc ggcgataata gcttgattta 1800
tttggtttct acaccaata cattctcctg accactaatg ggagccaatt cacaattcac 1860
taagtacta aagtaagtta aacttgtgta gactaagcat gtaattttta agttttattt 1920
taatgaatta aaatatttgt taaccaactt taaagtcagt cctgtgtata cctagatatt 1980
agtcagtttg tgccagatag aagacaggtt gtgtttttat cctgtggctt gtgtagtgc 2040
ctgggattct ctgccccctc tgagtagagt gttgtgggat aaaggaatct ctcagggcaa 2100

```

ggagcttctt aagttaaatc actagaaatt taggggtgat ctgggccttc atatgtgtga 2160
gaagccggtt cattttatct ctcactgtat ttccctcaac gtctggttga tgagaaaaaa 2220
ttcttgaaga gttttcatat gtgggagcta aggtagtatt gtaaaatttc aagtcacctc 2280
taaacaaaat gatccaccta agatcttgcc cctgttaagt ggtgaaatca actagagggt 2340
gttctacaa gttgttcatt ctagtcttgt ttggtgtaag taggttgtgt gagttaattc 2400
atttatattt actatgtctg ttaaatcaga aattttttat tatctatgtt cttctagatt 2460
ttacctgtag ttcataaaaa aaaaaaaaaa aaaaaaaaaa 2500

```

```

<210> 5
<211> 991
<212> DNA
<213> Homo sapiens

```

```

<400> 5
gggatcagtc ttcccgcgtc cgccgattcc tcctccttgg tcgccgcgtc cttggctggc 60
gtcagaaaaa tggtacaaa cttcctagca catgagaaga tctggttcga caagttcaaa 120
tatgacgacg cagaaaggag attctacgag cagatgaacg ggcctgtgcg aggtgcctcc 180
cgccaggaga acggcgccac ggtgatcttc cgtgacattg cgagagccag agagaacatc 240
cagaaatccc tggtggaag ctcaggcccc ggggcctcca gcggcaccag cggagaccac 300
ggtgagctcg tcgtccgcat tgccagtctg gaagtggaga accagagtct gcgtggcgtg 360
gtacaggagc tgcagcaggc catctccaag ctggaggccc ggctgaacgt gctggagaag 420
agctcgctcg gccaccgggc caccgcccc cagaccagc acgtatctcc catgcgcaa 480
gtggagcccc cagccaagaa gccagccaca ccagcagagg atgacgagga tgatgacatt 540
gacctgtttg gcagtgacaa tgaggaggag gacaaggagg cggcacagct gcgggaggag 600
cggctacggc agtacgcgga gaagaaggcc aagaagcctg cactggtggc caagtcctcc 660
atcctgcttg atgtcaagcc ttgggatgat gagacggaca tgcccagct ggaggcctgt 720
gtgcgctcta tccagctgga cgggctggtc tggggggctt ccaagctggt gcccgtaggc 780
tacggtatcc ggaagctaca gattcagtgt gtggtggagg acgacaaggt ggggacagac 840
ttgctggagg aggagatcac caagtttgag gagcacgtgc agagtgtcga tatcgagct 900
ttcaacaaga tctgaagcct gagtgtgtgt acgtgcgcgc gtgcgtgagg gccctgccac 960
gattaaagac tgagaccggc aaaaaaaaaa a 991

```

```

<210> 6
<211> 824
<212> DNA
<213> Homo sapiens

```

```

<400> 6
cctcctgac agcagagggt gatctttgct gggaaacagc tggaagatgg acgcaccctg 60
tctgactaca acatccagaa agagtccacc ctgcacctg tgctccgtct tagaggtagg 120
atgcagatct tcgtgaagac cctgactggt aagaccatca ctctgaagt ggagccgagt 180
gacaccattg agaatgtcaa ggcaaagatc caagacaagg aaggcatccc tcctgaccag 240
cagagggtta tctttgctgg gaaacagctg gaagatggac gcaccctgtc tgactacaac 300
atccagaaag agtccaccct gcacctggtg ctccgtctta gaggtgggat gcagatcttc 360
gtgaagaccc tgactggtta gaccatcact ctggaagtgg agccgagtga caccattgag 420
aatgtcaagg caaagatcca agacaaggaa ggcacccctc ctgaccagca gaggttgatc 480
tttctgtaga aacagctgga agatggacgc accctgtctg actacaacat ccagaaagag 540

```

tccaccctgc acctggtgct ccgtctcaga ggtgggatgc agatcttcgt gaagaccctg 600
actggttaaga ccataccctc cgagggtggag ccagtgaca ccatacgagaa tgtcaaggca 660
aagatccaag ataaggaagg catccctcct gatcagcaga ggttgatctt tgctgggaaa 720
cagctggaag atggacgcac cctgtctgac tacaacatcc agaaagagtc cactctgcac 780
ttggtcctgc gcttgagggg ggggtgtctaa gtttccctt ttaa 824

<210> 7
<211> 3926
<212> DNA
<213> Homo sapiens

<400> 7
aattcttgga agaggagaac tggacgttgt gaacagagtt agctggtaaa tgcctcttta 60
aaagatccaa aaaatgagac ttctagcaaa gattatttgc cttatgttat gggctatttg 120
tgtagcagaa gattgcaatg aacttcctcc aagaagaaat acagaaattc tgacaggttc 180
ctggtctgac caaacatata cagaaggcac ccaggctatc tataaatgcc gccctggata 240
tagatctctt ggaatgtaa taatggtatg caggaagga gaatgggttg ctcttaatcc 300
attaaggaaa tgcagaaaaa ggccctgttg acatcctgga gatactcctt ttggtacttt 360
tacccttaca ggaggaaatg tgtttgaata tgggtgtaaa gctgtgtata catgtaatga 420
ggggtatcaa ttgctagggt agattaatta ccgtgaatgt gacacagatg gatggaccaa 480
tgatattcct atagtgaag ttgtgaagt tttaccagt acagaccag agaatggaaa 540
aattgtcagt agtgaatgg aaccagatcg ggaataccat tttggacaag cagtacggtt 600
tgtatgtaac tcaggctaca agattgaagg agatgaagaa atgcattgtt cagacgatgg 660
tttttgaggt aaagagaaac caaagtgtgt ggaatttca tgcaaatccc cagatgttat 720
aaatgatct cctatatctc agaagattat ttataaggag aatgaacgat ttcaatataa 780
atgtaacatg ggttatgaat acagtgaag aggagatgct gtatgcactg aatctggatg 840
gcgtccgttg ccttcctgtg aagaaaaatc atgtgataat ccttatattc caaatggtga 900
ctactcacct ttaaggatta aacacagaac tggagatgaa atcacgtacc agtgtagaaa 960
tggtttttat cctgcaaccc ggggaaatac agccaaatgc acaagtactg gctggatacc 1020
tgctccgaga tgtaccttga aaccttgtga ttatccagac attaaacatg gaggtctata 1080
tcatagaaat atgcgtagac catactttcc agtagctgta ggaataatatt actcctatta 1140
ctgtgatgaa cattttgaga ctccgtcagg aagtacttg gatcacattc attgcacaca 1200
agatggatgg tcgccagcag taccatgcct cagaaaatgt tattttcctt atttgaaaa 1260
tggatataat caaaatcatg gaagaaagtt tgtacagggt aaatctatag acgttgcttg 1320
ccatcctggc tacgtcttc caaaagcgca gaccacagtt acatgtatgg agaatggctg 1380
gtctctact ccagatgca tccgtgtcaa aacatgttc aaatcaagta tagatattga 1440
gaatgggttt atttctgaat ctcatgtatc atatgcctta aaagaaaaag cgaaatatca 1500
atgcaacta ggaatgtaa cagcagatgg tgaacatca ggatcaatta gatgtgggaa 1560
agatggatgg tcagctcaac ccacgtgcat taaatcttgt gatatcccag tatttatgaa 1620
tgccagaact aaaaatgact tcacatggtt taagctgaat gacacattgg actatgaatg 1680
ccatgatggt tatgaaagca atactggaag caccactggt tccatagtgt gtggttacia 1740
tggttggtct gatttaccga tatgttatga aagagaatgc gaacttccta aaatagatgt 1800
acacttagtt cctgatcgca agaaagacca gtataaagtt ggagaggtgt tgaaattctc 1860

```

ctgcaaacca ggatttacaa tagttggacc taattccgtt cagtgtctacc actttggatt 1920
gtctcctgac ctcccaatat gtaaagagca agtacaatca tgtgtgccac ctctgaact 1980
cctcaatggg aatgttaagg aaaaaacgaa agaagaatat ggacacagtg aagtgggtgga 2040
atattattgc aatcctagat ttctaataaa gggacctaataaaaattcaat gtgttgatgg 2100
agagtggaca actttaccag tgtgtattgt ggaggagagt acctgtggag atatacctga 2160
acttgaacat ggctgggccc agctttcttc ccctccttat tactatggag attcagtggg 2220
attcaattgc tcagaatcat ttacaatgat tggacacaga tcaattacgt gtattcatgg 2280
agtatggacc caacttcccc agtgtgtggc aatagataaa cttaagaagt gcaaatcatc 2340
aaatttaatt atacttgagg aacatttaaa aaacaagaag gaattcgatc ataattctaa 2400
cataaggtac agatgtagag gaaaagaagg atggatacac acagtctgca taaatggaag 2460
atgggatcca gaagtgaact gctcaatggc acaaatataa ttatgcccac ctccacctca 2520
gattcccaat tctcacaata tgacaaccac actgaattat cggtatggag aaaaagtatc 2580
tgttctttgc caagaaaatt atctaattca ggaaggagaa gaaattacat gcaaagatgg 2640
aagatggcag tcaataccac tctgtgttga aaaaattcca tggtcacaac cacctcagat 2700
agaacacgga accattaatt catccaggtc ttcacaagaa agttatgcac atgggactaa 2760
attgagttat acttgtgagg gtggtttcag gatattctgaa gaaaatgaaa caacatgcta 2820
catgggaaaa tggagttctc cacctcagtg tgaaggcctt ccttgtaaat ctccacctga 2880
gatttctcat ggtgtgttag ctcatatgac agacagttat cagtatggag aagaagttac 2940
gtacaaatgt tttgaagggt ttgaattga tgggcctgca attgcaaaat gcttaggaga 3000
aaaatggtct caccctccat catgcataaa aacagattgt ctcatgttac ctagctttga 3060
aatgccata cccatgggag agaagaagga tgtgtataag gcgggtgagc aagtgactta 3120
cacttgtgca acatattaca aaatggatgg agccagtaat gtaacatgca ttaatagcag 3180
atggacagga aggccaaatc gcagagacac ctctgtgtg aatccgcca cagtacaaaa 3240
tgcttatata gtgtcgagac agatgagtaa atatccatct ggtgagagag tacgttatca 3300
atgtaggagc ccttatgaaa tgtttgggga tgaagaagtg atgtgtttaa atggaaactg 3360
gacggaacca cctcaatgca aagattctac aggaaaatgt gggccccctc cacctattga 3420
caatggggac attacttcat tcccgttgc agtatatgct ccagcttcat cagttgagta 3480
ccaatgccag aacttgtatc aacttgagg taacaagcga ataacatgta gaaatggaca 3540
atggtcagaa ccacaaaaat gcttacatcc gtgtgtaata tcccgagaaa ttatggaaaa 3600
ttataacata gcattaaggt ggacagccaa acagaagctt tattcgagaa caggtgaatc 3660
agttgaattt gtgtgtaaac ggggatatcg tctttcatca cgttctcaca cattgcgaac 3720
aacatgttgg gatgggaaac tggagtatcc aacttgtgca aaaagataga atcaatcata 3780
aagtgcacac ctttattcag aactttagta ttaaatcagt tctcaatttc attttttatg 3840
tattgtttta ctctttttta ttcatatgta aaattttgga ttaattttg taaaatgtaat 3900
tataagctga gaccggtggc tctctt 3926

```

<210> 8
<211> 259
<212> DNA
<213> Homo sapiens

```

<400> 8
cagtcattct cataatcgcc caccgactta catcctcatt actattctgc ctagcaaaact 60

```

caaaactacga acgcactcac agtcgcatca taatcctctc tcaaggactt caaactctgc 120
 tcccactaat agctttttga tgacttctag caagcctcgc taacctcgcc ttacccccca 180
 ctattaacct actgggagaa ctctctgtgc tagtaaccac gttctcctga tcaaatagca 240
 ctctccagcc tctcaccgc 259

<210> 9
 <211> 4704
 <212> DNA
 <213> Homo sapiens

<400> 9
 ttattaatat cactatattt ttggaggag aggcacctt ctcactctt cttcctctcc 60
 gccaccctt actccctccc cctcatctac ctgtcaaagt cactgatctt ttgcatttcg 120
 gaagaggagc tcaacgggaa ggaattcccc ctctgggtgc gggctccgag agggggcgac 180
 ttgcaggagg cttcccccg gggcggaggc gaagggtgtt ggtgccagaa gaaaagaatg 240
 attgatggga aacagacacc gggctataga cactcatcct ttgcttcag atactgatat 300
 ctcagcctgc ttgagcatcc cttgtgagct gtgaacattg aggatcactc agggttatcg 360
 gatgtacaac gggagagcca tcgctttgct aaattattat ctgcaattgg acatctttta 420
 caaaaaccaa actagacctg agtctaatag atatgttcta agacaaagaa aaagctgcaa 480
 gttgttaacg cctaacacac aagtatgtta ggcttcacc aaagtcctca atatacctga 540
 atacgcacaa tatcttaact cttcatattt ggttttggga tctgctttga ggtccatct 600
 tcatttaaaa aaaaatacag agacctacct acccgtagc atacatacat atgtgtatat 660
 atatgtaaac tagacaaaga tcgcagatca taaagcaagc tctgctttag ttccaagaa 720
 gattacaaag aatttagaga tgtattgtc aagattcctg tcgattcatg ccctttgggt 780
 tacggtgtcc tcagtgatgc agccctaccc ttgggtttgg ggacattatg atttgtgtaa 840
 gactcagatt tacacggaag aagggaaggt ttgggattac atggcctgcc agccggaatc 900
 cacggacatg acaaaatata tgaaagtga actcgatcct ccggatatta cctgtggaga 960
 ccctcctgag acgttctgtg caatgggcaa tccctacatg tgcaataatg agtgtgatgc 1020
 gagtaccctt gagctggcac accccctga gctgatgttt gattttgaag gaagacatcc 1080
 ctccacattt tggcagtctg ccacttgga ggaagtatcc aagcctctcc aggttaacat 1140
 cactctgtct tggagcaaaa ccattgagct aacagacaac atagttatta cttttgaatc 1200
 tgggcgtcca gaccaaata tcttgagaa gtctctcgat tatggacgaa catggcagcc 1260
 ctatcagtat tatgccacag actgcttaga tgcttttcac atggatccta aatccgtgaa 1320
 ggatttatca cagcatcagg tcttagaaat catttgaca gaagagtact caacagggtg 1380
 tacaacaaat agcaaaataa tccactttga aatcaaagac aggttcgctg tttttgctgg 1440
 acctcgccta cgcaatatgg cttccctcta cggacagctg gatacaacca agaaactcag 1500
 agatttcttt acagtcacag acctgaggat aaggctgtta agaccagccg ttggggaaat 1560
 attttagat gagctacact tggcacgcta cttttacgag atctcagaca taaagggtcg 1620
 aggaagggtc aagtgtaatc tccatgccac tgtatgtgtg tatgacaaca gcaaattgac 1680
 atgcgaatgt gagcacaaca ctacaggtcc agactgtggg aaatgcaaga agaattatca 1740
 gggccgacct tggagtccag gctcctatct ccccatcccc aaaggcactg caaatacctg 1800
 tatccccagt atttccagta ttggtagtaa gtaaaaacaa aaacaaaaaa aacaccaaac 1860
 caagtctagg ctagctttgc tttgtgttgc acctcctcag atctattttc ccagtgtcca 1920

```

tttctgatgt aataggggtat tttctttgtg aattgcattt ttgtgttggg tttctgcaca 1980
gatctggtga gaacacagat aaagtgatta tttgtgcata actccatgaa catggcagtg 2040
ctatgacttt tctgactact ctaaccagt gagggtacc tagactcagg tgcaattcct 2100
tagataatca tcattcagga aaaatataag tagtcctatt tatccatact tagcaaccaa 2160
caaacaaatt gaactctctc ttagactgga tttggatgtc tgacataatt ttaaaaagca 2220
gaaaaagaaa gccaatgaat gccttgggta tatgcatcag aaccaagaa aaagtccatg 2280
ataccaaggg aagggaattt tgtaaatgca ttaaattcta tgttttgtga aggcctgaaa 2340
caggcaaat tgtgatcagt agtctctctg gagagataaa ggaaaaagag aatctgtaca 2400
ttcatttctc ctccctaaaa tacgatgatc tatgtcttct tgactactta gctttgagtt 2460
tgatatagaa agagtataaa aaatatgtgc agaatttggg agtgagagta ctgaaaattc 2520
ctttaataaa tctgttagta tgaatccaag caattgaaga gaaaccgctc ttcaaccatc 2580
tgtagaacac tccccggta tcaactacaa gaactttctt ccagctatca tgggagaacc 2640
aggtgtagct cccgcttcat gtgtaaaata atgatgcct catgccaagc ctgaaattca 2700
cattaagaaa atgccagta actttacaga gcaaaatttt aaattttttt tttatacatt 2760
gcacccttta tctctaattg ctaaaatctt tgaacaacta ctaagtaact gattacaaat 2820
aaattaccga gaaagcaaga ttacgcatgg taagcggaga gaattttcac tgtagtgta 2880
tcccctcaca ggcttgtgtc ataggtgctg tgccaggcag ggtgatcgca gtgtaaatag 2940
ccattgaatg attgcatc ccagcatcca tctaaaaagc aatactctga taatttggat 3000
aaagcaactt cctgcttctt ataaatgcgc agtcaggtgt ccaatttat aaatcaacc 3060
agtttacttg agcttgtgaa taggcctgga cactgatttg ttaagcgcta gatgtgtaa 3120
atgccatgaa aattggccac tttgtaaata gaagtagtgt tcacatccat ttagagatac 3180
cagcctaata ctacagcatc ctcttgtgta tcttgttgaa acagcatcag tgttaaaaac 3240
ttgcaaatga aaaccttcag ctctaatagt ctaatttttc tgctttagta tcccccttg 3300
catttgcta actgtatata taccaccaa tgtgctcctt tcaggccttg acaattgcat 3360
ttgcacgtgc attttagtc aacaggaag caagtagaag caagctgaca cagattattg 3420
aggctgctat agtgatctgg cctgtcagaa gtttcagaaa tggatggatg gaaaagtagt 3480
tctttggcgt tgggtgtctt ttctgtttg agtgtcagtt gtatgttgca tggcccctct 3540
aactgtactg ctactcgac atccattcg gccgcctcca ccacattccc catatctgag 3600
catcagcaga tgttgacctt ttacacatca aatcaggaaa tttctgtttt gttttgtttt 3660
gttttgtttt gaaatcagtg gtgacctgaa aggatgcttc gttgtgcctt tgaaaaaat 3720
atattaacct ttattatcga gaacctagga aaatttactc ctaataaaaa ccctctgact 3780
aaaagtgata ttttgactc tcccttcaat atgcctctgg ctgttccgct tagaatgcaa 3840
tgggtatttt ctgagatttc cagcaaacag gatgtaagag cttccagagg tcaccaaca 3900
tcacacatga ctgacttacc tgttctctgg ctttaaggt aaagagtac agtaaaacca 3960
tcaaacgtga ttgtatcttc taggtgctt taatggcatt cgaaagtcc ttctttgttg 4020
gcttataagt tgctttttgc gtgcactcgt ggattccttt cccctccaaa gggcaagaat 4080
tcacacgtag acgacactgc cgttccaga gggcacgga atgggtttt caaggtgcaa 4140
gccagagaaa aggaagctgt ttgatattt agctaagtta tgggtgtttg ccagtgtttt 4200
ttgcattacc ccaaagaagg aatcaatgac tataattcca ctaactatat agaaagatac 4260

```


cattatagca gatgtaacac ccctgagacc cggattatca cagcatagct caaggaaaat 4320
 aaatgatgta tattatcgat gtagattatt gatgtatata accatcagtt tacatacata 4380
 ttctgtatac acagtgatta aagggttttg agccctaata aatttcagta tagatctcaa 4440
 aatgccaacg cctgtattaa ggttcaaatg catggatagg gtggtcatcc tttccgatca 4500
 tctgctaaaa atgtttttga aacaaatttc ccattaaggt cattcgtacc tgcgtgtgtc 4560
 tatctattaa caaataggtt tcccataatc ctaaggatac ttgacttaga actcagtcac 4620
 tctgatctgc tttggccatg gctgaaaaaa tgctggtgat attgtcagca attaatgaat 4680
 cccaaaataa atctgtagcc ttg 4704

<210> 10
 <211> 10096
 <212> DNA
 <213> Homo sapiens

<400> 10
 ggagaagcgg gcgaattggg caccggtggc ggctgcgggc agtttgaatt agactctggg 60
 ctccagcccg ccgaagccgc gccagaactg tactctccga gaggtcgttt tcccgtcccc 120
 gagagcaagt ttatttaca atgttgagtg aataaagaag gcagaacaaa atgagctggg 180
 ctttggaaga atggaaagaa gggctgccta caagaactct tcagaaaatt caagagcttg 240
 aaggacagct tgacaaactg aagaaggaaa agcagcaaaag gcagtttcag cttgacagtc 300
 tcgaggctgc gccgcagaag caaacacaga aggttgaaaa tgaaaaaacc gaggttaca 360
 acctgaaaag ggagaatcaa agattgatgg aaatatgtga aagctctggag aaaactaagc 420
 agaagatttc tcatgaactt caagtcaagg agtcacaagt gaatttcag gaaggacaac 480
 tgaattcagg caaaaaacaa atagaaaaac tggaacagga acttaaaagg tgtaaatctg 540
 agcttgaaaag aagccaacaa gctgcgcagt ctgcagatgt ctctctgaat ccatgcaata 600
 caccacaaaa aattttttaca actccactaa caccaagtca atattatagt ggttccaagt 660
 atgaagatct aaaagaaaaa tataataaag aggttgaaaga acgaaaaaga ttagaggcag 720
 aggttaaaag cttgcaggct aaaaagcaa gccagactct tccacaagcc accatgaatc 780
 accgcgacat tgcccgcat caggcttcat catctgtgtt ctcatggcag caagagaaga 840
 cccaagtca tctttcatct aattctcaaa gaactccaat taggagagat ttctctgcat 900
 cttacttttc tggggaacta gaggtgactc caagtcgac aactttgcaa atagggaaaa 960
 gagatgctaa tagcagtttc tttggcaatt ctacagctcc tcacttttg gatcaattaa 1020
 aagcgcagaa tcaagagcta agaaacaaga ttaatgagtt ggaactacgc ctgcaaggac 1080
 atgaaaaaga aatgaaaggc caagtgaata agtttcaaga actccaactc caactggaga 1140
 aagcaaaagt ggaattaatt gaaaaagaga aagttttgaa caaatgtagg gatgaactag 1200
 tgagaacaac agcacaatac gaccaggcgt caaccaagta tactgcattg gaacaaaaac 1260
 tgaaaaaatt gacggaagat ttgagttgtc agcgacaaaa tgcagaaagt gccagatgtt 1320
 ctctggaaca gaaaattaag gaaaaagaaa aggagtttca agaggagctc tcccgtcaac 1380
 agcgtttctt ccaaacactg gaccaggagt gcacccagat gaaggccaga ctacccagg 1440
 agttacagca agccaagaat atgcacaacg tcctgcaggc tgaactggat aaactcacat 1500
 cagtaagca acagctagaa aacaatttgg aagagtttaa gcaaaagtgtg tgcagagctg 1560
 aacaggcgtt ccaggcgagt cagatcaagg agaattgagct gaggagaagc atggaggaaa 1620
 tgaagaagga aaacaacctc cttaagagtc actctgagca aaaggccaga gaagtctgcc 1680

```

acctggaggc agaactcaag aacatcaaac agtgtttaa tcagagccag aattttgcag 1740
aagaaatgaa agcgaagaat acctctcagg aaacatggt aagagatctt caagaaaaaa 1800
taaatacagca agaaaactcc ttgacttttag aaaaactgaa gcttgctgtg gctgatctgg 1860
aaaagcagcg agattgttct caagaccttt tgaagaaaag agaaccatcac attgaacaac 1920
ttaatgataa gttaagcaag acagagaaag agtccaaagc cttgctgagt gctttagagt 1980
taaaaaagaa agaataatgaa gaattgaaag aagagaaaac tctgttttct tgttgaaaaa 2040
gtgaaaacga aaaactttta actcagatgg aatcagaaaa ggaaaacttg cagagtaaaa 2100
ttaatcactt ggaaaacttg ctgaagacac agcaaataaa aagtcataaa tacaacgaga 2160
gagtaagaac gctggagatg gacagagaaa acctaagtgt cgagatcaga aaccttcaca 2220
acgtgttaga cagtaagtca gtggaggtag agaccagaa actagcttat atggagctac 2280
agcagaaagc tgagttctca gatcagaaac atcagaagga aatagaaaat atgtgtttga 2340
agacttctca gcttactggg caagttgaag atctagaaca caagcttcag ttactgtcaa 2400
atgaaataat ggacaagac cgtgtgtacc aagacttgca tgccgaatat gagagcctca 2460
gggatctgct aaaatccaaa gatgcttctc tggtgacaaa tgaagatcat cagagaagtc 2520
ttttggcttt tgatcagcag cctgccatgc atcattcctt tgcaaatata attggagaac 2580
aaggaagcat gccttcagag aggagtgaat gtcgtttaga agcagaccaa agtccgaaaa 2640
attctgccat cctacaaaat agagttgatt cacttgaatt ttcattagag tctcaaaaac 2700
agatgaactc agacctgcaa aagcagtggt aagagttggt gcaaatcaaa ggagaaatag 2760
aagaaaatct catgaaagca gaacagatgc atcaaagttt tgtggctgaa acaagtcagc 2820
gcattagtaa gttacaggaa gacacttctg ctcaccagaa tgtgttgct gaaaccttaa 2880
gtgcccttga gaacaaggaa aaagagctgc aactttttaa tgataaggta gaaactgagc 2940
aggcagagat tcaagaatta aaaaagagca accatctact tgaagactct ctaaaggagc 3000
tacaactttt atccgaaacc ctaagcttgg agaagaaaga aatgagttcc atcatttctt 3060
taaataaaag ggaattgaa gagctgaccc aagagaatgg gactcttaag gaaattaatg 3120
catccttaaa tcaagagaag atgaacttaa tccagaaaag tgagagtttt gcaactata 3180
tagatgaaag ggagaaaagc atttcagagt tatctgatca gtacaagcaa gaaaaactta 3240
ttttactaca aagatgtgaa gaaaccggaa atgcatatga ggatcttagt caaaaatata 3300
aagcagcaca ggaagaagaat tctaaattag aatgcttgct aaatgaatgc actagtcttt 3360
gtgaaaatag gaaaaatgag ttggaacagc taaaggaagc atttgcaaag gaacaccaag 3420
aattcttaac aaaattagca tttgctgaag aaagaaatca gaatctgatg ctagagttgg 3480
agcagtgca gcaagctctg agatctgaga tgacagataa ccaaaacaat tctaagagcg 3540
aggctggtgg tttaaagcaa gaaatcatga ctttaaagga agaacaaaac aaaatgcaaa 3600
aggaagttaa tgacttatta caagagaatg aacagctgat gaaggtaatg aagactaac 3660
atgaatgtca aaatctagaa tcagaaccaa ttaggaactc tgtgaaagaa agagagagtg 3720
agagaaatca atgtaatttt aaacctcaga tggatcttga agttaaagaa atttctctag 3780
atagttataa tgcgcagttg gtgcaattag aagctatgct aagaaataag gaattaaaac 3840
ttcaggaaag tgagaaggag aaggagtgcc tgcagcatga attacagaca attagaggag 3900
atcttgaaac cagcaatttg caagacatgc agtcacaaga aattagtggc cttaaagact 3960
gtgaaataga tgcggaagaa aagtatatct cagggcctca tgagttgtca acaagtcaaa 4020
acgacaatgc acaccttcag tgctctctgc aaacaacaat gaacaagctg aatgagctag 4080

```

```

agaaaatattg tgaataactg caggctgaaa agtatgaact cgtaactgag ctgaatgatt 4140
caaggtcaga atgtatcaca gcaactagga aaatggcaga agaggtaggg aaactactaa 4200
atgaagttaa aatattaaat gatgacagtg gtcttctcca tggtagtga gtggaagaca 4260
taccaggagg tgaatttggg gaacaaccaa atgaacagca ccctgtgtct ttggctccat 4320
tggacgagag taattcctac gagcacttga cattgtcaga caaagaagtt caaatgcact 4380
ttgccgaatt gcaagagaaa ttcttatctt tacaagtga acacaaaatt ttacatgac 4440
agcactgtca gatgagctct aaaatgtcag agctgcagac ctatgttgac tcattaaagg 4500
ccgaaaattt ggtcttgta acgaatctga gaaactttca aggtgacttg gtgaaggaga 4560
tgcagctggg cttggaggag gggctcgttc catccctgtc atcctcttgt gtgcctgaca 4620
gctctagtct tagcagtttg ggagactcct ccttttacag agctctttta gaacagacag 4680
gagatatgtc tcttttgagt aatttagaag gggctgtttc agcaaaccag tgcagtgtag 4740
atgaagtatt ttgcagcagt ctgcagacct atgttgactc attaaaggcc gaaaatttgg 4800
tcttgtcaac gaatctgaga aactttcaag gtgacttggg gaaggagatg cagctgggct 4860
tggaggaggg gctcgttcca tccctgtcat cctcttgtgt gcctgacagc tctagtctta 4920
gcagtttggg agactcctcc ttttacagag ctcttttaga acagacagga gatatgtctc 4980
ttttgagtaa tttagaaggg gttgtttcag caaaccagtg cagtgtagat gaagtatttt 5040
gcagcagctc gcaggaggag aatctgacca ggaagaaac cccttcggcc ccagcgaagg 5100
gtgttgaaga gcttgagtc ctctgtgagg tgtaccggca gtccctcag aagctagaag 5160
agaaaatgga aagtcaaggg attatgaaaa ataaggaaat tcaagagctc gagcagttat 5220
taagtcttga aaggcaagag cttgactgcc ttaggaagca gtatttgtca gaaaatgaac 5280
agtggcaaca gaagctgaca agcgtgactc tggagatgga gtccaagttg gcgacagaaa 5340
agaaacagac ggaacaactg tcaactgagc tggaaagtag acgactccag ctacaaggtc 5400
tggacttaag ttctcgtctc ttgcttgcca tcgacacaga agatgctatt caaggccgaa 5460
atgagagctg tgacatatca aaagaacata cttcagaaac tacagaaaaga acaccaaagc 5520
atgatgttca tcagatttgt gataaagatg ctgacagga cctcaatcta gacattgaga 5580
aaataactga gactggtgca gtgaaacca caggagagtg ctctggggaa cagtccccag 5640
ataccaatta tgagcctcca ggggaagata aaaccaggg ctcttcagaa tgcatttctg 5700
aattgtcatt ttctggtcct aatgctttgg tacctatgga tttcctggg aatcaggaag 5760
atatccataa tcttcaactg cgggtaaaag agacatcaaa tgagaatttg agattacttc 5820
atgtgataga ggaccgtgac agaaaagttg aaagtttgct aaatgaaatg aaagaattag 5880
actcaaaact ccatttacag gaggtacaac taatgaccaa aattgaagca tgcatagaat 5940
tggaaaaaat agttggggaa ctttaagaaag aaaactcaga ttttaagtga aaattggaat 6000
atttttcttg tgatcaccag gagttactcc agagagtaga aacttctgaa ggcctcaatt 6060
ctgattttaga aatgcatgca gataaatcat cacgtgaaga tattggagat aatgtggcca 6120
aggatgaatga cagctggaag gagagatttc ttgatgtgga aaatgagctg agtaggatca 6180
gatcgagaaa agctagcatt gagcatgaag ccctctacct ggaggctgac ttagaggtag 6240
ttcaaacaga gaagctatgt ttagaaaaag acaatgaaaa taagcagaag gttattgtct 6300
gccttgaaga agaactctca gtggtcacia gtgagagaaa ccagcttcgt ggagaattag 6360
atactatgtc aaaaaaacc acggcactgg atcagttgtc tgaaaaatg aaggagaaaa 6420

```

cacaagagct tgagtctcat caaagtgagt gtctccattg cattcaggtg gcagaggcag 6480
aggtgaagga aaagacggaa ctcccttcaga ctttgtcctc tgatgtgagt gagctgttaa 6540
aagacaaaac tcattctccag gaaaagctgc agagtttgga aaaggactca caggcactgt 6600
ctttgacaaa atgtgagctg gaaaaccaa ttgcacaact gaataaagag aaagaattgc 6660
ttgtcaagga atctgaaagc ctgcaggcca gactgagtga atcagattat gaaaagctga 6720
atgtctccaa ggccttgagg gccgcactgg tggagaaagg tgagttcgca ttgaggctga 6780
gctcaacaca ggaggaagtg catcagctga gaagaggcat cgagaaactg agagttcgca 6840
ttgaggccga tgaagaagag cagctgcaca tcgcagagaa actgaagaa cgcgagcggg 6900
agaatgattc acttaaggat aaagttgaga accttgaaag ggaattgcag atgtcagaag 6960
aaaaccagga gctagtgatt ctgtatgccg agaattccaa agcagaagta gagactctaa 7020
aaacacaaat agaagagatg gccagaagcc tgaagtttt tgaattagac cttgtcacgt 7080
taaggtctga aaaagaaaat ctgacaaaac aaatacaaga aaaacaaggt cagttgtcag 7140
aactagacaa gttactctct tcatttaaaa gtctgttaga agaaaaggag caagcagaga 7200
tacagatcaa agaagaatct aaaactgcag tggagatgct tcagaatcag ttaaaggagc 7260
taaattgaggc agtagcagcc ttgtgtggtg accaagaaat tatgaaggcc acagaacaga 7320
gtctagaccc accaatagag gaagagcatc agctgagaaa tagcattgaa aagctgagag 7380
cccgcctaga agctgatgaa aagaagcagc tctgtgtctt acaacaactg aaggaaagtg 7440
agcatcatgc agatttactt aagggtagag tggagaacct tgaagagag ctgagatag 7500
ccaggacaaa ccaagagcat gcagctcttg aggcagagaa ttccaaagga gaggtagaga 7560
ccctaaaagc aaaaatagaa gggatgaccc aaagtctgag aggtctggaa ttagatgttg 7620
ttactataag gtcagaaaaa gaagatctga caaatgaatt acaaaaagag caagagcgaa 7680
tatctgaatt agaaataata aattcatcat ttgaaaatat tttgcaagaa aaagagcaag 7740
agaaagtaca gatgaagaa aaatcaagca ctgccatgga gatgcttcaa acacaattaa 7800
aagagctcaa tgagagagtg gcagccctgc ataatgacca agaagcctgt aaggccaaag 7860
agcagaatct tagtagtcaa gtagagtgtc ttgaacttga gaaggctcag ttgctacaag 7920
gccttgatga ggccaaaaat aatttatattg ttttgcaatc ttcagtgaat ggcctcattc 7980
aagaagtga agatggcaag cagaaactgg agaagaagga tgaagaaatc agtagactga 8040
aaaatcaaat tcaagaccaa gagcagcttg tctctaaact gtcccaggtg gaaggagagc 8100
accaactttg gaaggagcaa aacttagaac tgagaaatct gacagtggaa ttggagcaga 8160
agatccaagt gctacaatcc aaaaatgcct ctttgagga cacattagaa gtgctgcaga 8220
gttcttacaa gaatctagag aatgagcttg aattgacaaa aatggacaaa atgtcctttg 8280
ttgaaaaagt aaacaaaatg actgcaaaag aaactgagct gcagagggaa atgcatgaga 8340
tggcacagaa aacagcagag ctgcaagaag aactcagtgg agagaaaaat aggctagctg 8400
gagagttgca gttactgttg gaagaaataa agagcagcaa agatcaattg aaggagctca 8460
cactagaaaa tagtgaattg aagaagagcc tagattgcat gcacaaagac cagggtgaaa 8520
aggaagggaa agtgagagag gaaatagctg aatatcagct acggcttcat gaagctgaaa 8580
agaacacca ggctttgtct ttggacacaa acaaacagta tgaagtagaa atccagacat 8640
accgagagaa attgacttct aaagaagaat gtctcagttc acagaagctg gagatagacc 8700
ttttaaagtc tagtaaagaa gagctcaata attcattgaa agctactact cagatttttg 8760
aagaattgaa gaaaaccaag atggacaatc taaaatatgt aaatcagttg aagaaggaaa 8820

```

atgaacgtgc ccaggggaaa atgaagtgtg tgatcaaadc ctgtaaagag ctggaagagg 8880
aaaaggagat actgcagaaa gaactctctc aacttcaagc tgcacaggag aagcagaaaa 8940
cagggtactgt tatggatacc aaggctgatg aattaacaac tgagatcaaa gaactgaaag 9000
aaactcttga agaaaaaacc aaggaggcag atgaataactt ggataagtac tgttccttgc 9060
ttataagcca tgaagagtta gagaaagcta aagagatggt agagacacaa gtggcccatc 9120
tgtgttcaca gcaatctaaa caagattccc gagggctctc tttgctaggt ccagttgttc 9180
caggaccatc tccaatccct tctgttactg aaaagagggt atcatctggc caaataaag 9240
cttcaggcaa gaggcaaga tccagtggaa tatgggagaa tggaggagga ccaacacctg 9300
ctaccccgaga gagcttttct aaaaaagca agaaagcagt catgagtggg attcacctg 9360
cagaagacac ggaagggtact gagtttgagc cagagggact tccagaagtt gtaaagaaag 9420
ggtttgctga catcccgaca ggaagacta gcccatatat cctgcgaaga acaaccatgg 9480
caactcggac cagccccgc ctggctgcac agaagttagc gctatccca ctgagtctcg 9540
gcaaagaaaa tcttcagag tctccaaac caacagctgg tggcagcaga tcacaaaagg 9600
tcaaagttgc tcagcggagc ccagtagatt caggcaccat cctccgagaa cccaccacga 9660
aatccgtccc agtcaataat ctctctgaga gaagtccgac tgacagcccc agagagggcc 9720
tgagggtcaa gcgaggccga cttgtccca gcccaaagc tggactggag tccaagggca 9780
gtgagaactg taagggtccag tgaaggcact ttgtgtgtca gtacccctgg gaggtgccag 9840
tcattgaata gataaggctg tgcctacagg acttctcttt agtcagggca tgctttatta 9900
gtgaggagaa aacaattcct tagaagtctt aaatatattg tactctttag atctcccatg 9960
tgtaggtatt gaaaaagttt ggaagcactg atcacctgtt agcattgccca tctcttact 10020
gcaatgtaaa tagtataaag ctatgtatat aaagcttttt ggtaatatgt tacaattaaa 10080
atgacaagca ctatat 10096

```

```

<210> 11
<211> 1532
<212> DNA
<213> Homo sapiens

```

```

<400> 11
gaattcgggc cgccgccagg tcgctgttgg tccacgccgc ccgtcgcgcc gcccgccgc 60
tcagcgtccg ccgccgcat gggagtgcag gtggaaacca tctcccagg agacgggcgc 120
accttcccca agcgggcca gacctgcgtg gtgcactaca ccgggatgct tgaagatgga 180
aagaaatttg attcctccc ggacagaaac aagccctta agtttatgct aggcaagcag 240
gagggtgatcc gaggtggga agaaggggtt gccagatga gtgtgggtca gagagccaaa 300
ctgactatat ctccagatta tgcctatggt gccactgggc acccaggcat catcccacca 360
catgccactc tcgtcttcca tgtggagctt ctaaaactgg aatgacagga atggcctcct 420
cccttagctc cctgttcttg gatctgccat ggagggatct ggtgcctcca gacatgtgca 480
catgagtcca tatggagctt ttcctgatgt tccactccac tttgtataga catctgccct 540
gactgaatgt gttctgtcac tcagctttgc ttccgacacc tctgtttcct ctccccctt 600
ctcctcgatg gtgtgtttac ctaaaactata tgccataaac ctcaagttat tcattttatt 660
ttgttttcat tttgggtga agattcagtt tcagtctttt ggatataggt ttccaattaa 720
gtacatgggc aagtattaac agcacaagtg gtaggttaac attagaatag gaattggtgt 780
tggggggggg gtttgcaaga atattttatt ttaatttttt ggatgaaatt tttatctatt 840

```

```

atatattaaa cattcttgct gctgctgctgc aaagccatag cagatttgag gcgctgttga 900
ggactgaatt actctccaag ttgagagatg tctttgggtt aaattaaaag ccctacctaa 960
aactgaggtg gggatgggga gagcctttgc ctccaccatt cccacccacc ctccccttaa 1020
accctctgcc ttgaaagta gatcatgttc actgcaatgc tggacactac aggtatctgt 1080
ccctggggca gcagggacct ctgaagcctt ctttgtggcc tttttttttt ttcacctgt 1140
ggtttttcta atggactttc aggaattttg taatctcata actttccaag ctccaccact 1200
tcctaaatct taagaacttt aattgacagt ttcaattgaa ggtgctgttt gtagacttaa 1260
caccagtgta aagccagcc atcatgacaa atccttgaat gttctcttaa gaaaatgatg 1320
ctggctcatcg cagcttcagc atctctgtt ttttgatgct tggctccctc tgetgatctc 1380
agtttcctgg cttttcctcc ctccagccct tctcaccct ttgctgtcct gtgtagtgat 1440
ttggtgagaa atcggtgctg cacccttccc ccagcaccat ttatgagtct caagttttat 1500
tattgcaata aaagtgcctt atgcccgaat tc 1532

```

```

<210> 12
<211> 969
<212> DNA
<213> Homo sapiens

```

```

<400> 12
ggatttcg gctccatggc aagatccctt ctctgcccc tgcagatcct actgctatcc 60
ttagccttg aaactgcagg agaagaagcc cagggtgaca agattattga tggcgcccca 120
tgtgcaagag gctcccaccc atggcaggtg gccctgctca gtggcaatca gctccactgc 180
ggaggcgctc tggtaaatga gcgctgggtg ctactgccg cccactgcaa gatgaatgag 240
tacaccgtgc acctgggcag tgatacgtg ggcgacagga gagctcagag gatcaaggcc 300
tcgaagtcac tccgccaccc cggctactcc acacagaccc atgttaatga cctcatgctc 360
gtgaagctca atagccaggc caggctgtca tccatggtga agaaagtcag gctgccctcc 420
cgctgcgaac cccctggaac cactgtact gtctccggtc ggggcactac cagcagccca 480
gatgtgacct ttccctctga cctcatgtgc gtggatgtca agctcatctc ccccaggac 540
tgcacgaagg ttacaagga ctactggaa aattccatgc tgtgcgctgg catcccgcac 600
tccaagaaaa acgctgcaa tggtgactca gggggaccgt tgggtgacag aggtaccctg 660
caaggctctg tgcctgggg aactttccct tgcggccaac ccaatgaccc aggagtctac 720
actcaagtgt gcaagttcac caagtggata aatgacacca tgaaaaagca tcgctaacgc 780
cacactgagt taattaactg tgtgcttcca acagaaaatg cacaggagtg aggacgccga 840
tgacctatga agtcaaat ttttaccct ttctcaaag atatatttaa acctcatgcc 900
ctgttgataa accaatcaaa ttggtaaaga cctaaaacca aaacaaataa agaaacacaa 960
aaccctcaa

```

```

<210> 13
<211> 1488
<212> DNA
<213> Homo sapiens

```

```

<400> 13
atggtaacgt ggctttacag atttttacc acttcaaata tggccgcca gctccgttct 60
cttttaccgc ctgatctacy gctacaattc tggcttcatg cccgcctcca aaagtgtctc 120
ctctcgaggg gttgtggttc ttactgcgca ggcgcaaaag caagtctct tccgggcaaa 180

```

atggcgatgg gactaatgtg cggacgccgg gagcttctgc gcttgctaca gtccggggtg 240
 cgggtccaca gcgtcgagg gccctcgcaa tggcttggga aaccgctgac cacacggctc 300
 ctattcccag tagccccgtg ctgctgtcgc ccacactacc tcttccttgc ggcttcgggc 360
 ccccgagcc tcagtacctc tgctatctct tttgcagaag tccaggttca ggccccctct 420
 gttgttgctg caactccctc acccacagca gtacctgagg tggcttctgg agagactgca 480
 gatgtagtcc aaactgctgc agagcagagc ttcgctgaac tggggctggg gtcatacacc 540
 ccagtgggac tgatccagaa tttactggaa tttatgcatg ttgatctggg cctaccttgg 600
 tggggggcca ttgctgcatg tacagtcttt gcccgctgcc tgatttttcc tctcatctg 660
 acggggccagc gagaggcagc caggatccac aatcaactgc cagagatcca gaagttttcc 720
 agtcaatca gagaggcaa gttagcagga gaccatattg agtattacaa ggcttcctcg 780
 gagatggcac ttaccagaa aaaacatggt attaaactct ataaacctct cattctccct 840
 gtgactcagg cccaatctt catctccttc ttcattgctt tgagagagat ggccaacctt 900
 cctgtgccc gccctgcagac aggtggctc tgggtgttcc aggatctcac ggtatccgat 960
 cccatctaca tattaccact ggcagtcact gctacaatgt gggctgttct tgagctaggt 1020
 gctgagacag gtgtgcaaag ttctgacctc cagtggatga gaaatgtcat cagaatgatg 1080
 cccctgataa ccttgcccat aaccatgcat ttccccacgg cagtgtttat gtactggctc 1140
 tctccaatt tgttttcctt ggtccaagta tctgtctcc ggattccagc agtacgcact 1200
 gtacttaaaa tccccagcg tgtgtacat gacctggaca aattacctcc acgggaaggc 1260
 ttctagaga gcttcaaaaa aggttggaat aatgctgaaa tgacgcgtca gctgcgagag 1320
 cgtgaacaac gcattgcgaa tcagttggag ctacgagcca ggggtccttt acgacagacc 1380
 ttaccacaca accctctcct acaacctgga aaggataacc ctcccaatat ccctagcagc 1440
 agcagcaaac caaagtcaaa gtatccctgg cagcacacac ttggctga 1488

<210> 14
 <211> 2945
 <212> DNA
 <213> Homo sapiens

<400> 14
 ccagccccc ttcccttccc tgacctctc ttgccatgc cccagacatg gggaacgcgg 60
 cgaccgcaa gaaaggcagc gaggtggaga gcgtgaaaga gtttctagcc aaagccaaag 120
 aagacttttt gaaaaaatgg gagaatccaa ctccagaataa tgccggactt gaagattttg 180
 aaaggaaaaa aaccttggga acaggttcat ttggaagagt catgttggtg aaacacaaag 240
 ccactgaaca gtattatgcc atgaagatct tagataagca gaaggttggt aaactgaagc 300
 aaatagagca tactttgaat gaaaaagaa tattacaggc agtgaatttt cctttccttg 360
 ttcgactgga gtatgctttt aaggataatt ctaatttata catggttatg gaatatgtcc 420
 ctgggggtga aatgttttca catctaagaa gaattggaag gttcagttag ccccatgcac 480
 ggttctatgc agctcagata gtgctaacat tcgagtacct ccattcacta gacctcatct 540
 acagagatct aaaacctgaa aatctcttaa ttgacctca aggtatatc caggctcagc 600
 actttgggtt tgccaaaaga gttaaaggca gaacttgac attatgtgga actccagagt 660
 atttggctcc agaaataatt ctccagcaagg gctacaataa ggcaagtggat tgggtggcat 720
 taggagtgtc aatctatgaa atggcagctg gctatcccc attctttgca gaccaaccaa 780
 ttcagattta tgaaaagatt gttcttgga aggtccgatt cccatccac ttcagttcag 840

```

atctcaagga ccttctacgg aacctgctgc aggtggattt gaccaagaga ttggaaatc 900
taaagaatgg tgtcagtgat ataaaaactc acaagtgggt tggcacgaca gattggattg 960
ctattttacca gaggaagggt gaagctccat tcatacaaaa gtttagaggc tctggagata 1020
ccagcaactt tgatgactat gaagaagaag atatccgtgt cctcataaca gaaaaatgtg 1080
caaaagaatt tggatgaattt taaagaggaa caagatgaca tctgagctca cactcagtgt 1140
ttgcactctg ttgagagata aggtagagct gagaccgtcc ttgttgaagc agttacctag 1200
ttccttcatt ccaacgactg agtgaggctt ttattgccat catccgtgtg cgcactctgc 1260
atccacctat gtaacaaggc accgctaagc aagcattgtc tgtgccataa cacagtacta 1320
gaccactttc ttaacttctct ttgggttgc tttctctct cctacateca tttcttcctt 1380
ttcaatttca ttgggtttct ctaaacagtg ctccatttta tttgttgggt gtttcagatg 1440
ggcagtgtta tggctacgtg atatttgaag ggaaggataa gtgttgcttt cagtagttat 1500
tgccaatatt gttgttggc aatggcttga agataaactt tctaataatt attatttctt 1560
tgagttagctc agacttggtt ttgcaaaaac tcttggtaat ttttgaagat agactgtctt 1620
atcaccaagg aaatttatac aaattaagac taactttctt ggaattcact attctggcaa 1680
taaatttttg tagactaata cagtacagct agaccagaa atttgaagg ctgtagatca 1740
gaggttctag ttccctttcc ctctttttat atcctctct ccttgagtaa tgaagtgacc 1800
agcctgtgta gtgtgacaaa cgtgtctcat tcagcaggaa aaactaatga tatggatcat 1860
caccagatt ctctcacttg gtaccagcat ttctgtaggt attagagaag agttctaagt 1920
tttctaaacc ttaactgttc cttaaggatt ttagccagta ttttaataga acatgattaa 1980
tgaaagtac aaattttaa tttctctaa tagtcctcat cataaacttt ttaaaggaaa 2040
ataagcaaac taaaaagaac attggttttag ataaatactt atactttgca aagtcaaaaa 2100
tggcttgatt tttgaaaca atatagaggt attcatattt aaatgagggt ttacatttgt 2160
tttgttttgt aaccgttaa aagaagttgt ttccagctaa ttattgtggt gtactatatt 2220
tgtgagccta gggtaggggc actgctgcaa cttctgcttt catcccatgc ctcacatag 2280
aggaaaggga acaaatgtga taaaacctgc cacaattgta ttttaatttt gaggtatgat 2340
attttcagat atttcataat ttctaacctc tgttctctca gtaaacagaa tgtctgatcg 2400
atcatgcaga tacaatgttg gtatttgaga ggtagtttt tttctacac tttttttg 2460
caactgactt aacaacattg ctgtcagggt gaaatttcaa gcacttttgc acatttagtt 2520
cagtgtttgt tgagaatcca tggttaacc cacttgtttt gctatttttt tctttgcttt 2580
taattttccc catctgattt tatctctgcy ttccagtgc ctaccttaa acaacacacg 2640
agaagagtta aactgggttc attttaatga tcaatttacc tgcataataa atttattttt 2700
aatcaagctg atcttaatgt atataatcat tctatttgct ttattatcgg tgcaggtagg 2760
tcattaacac cacttctttt catctgtacc acaccctggt gaaacctttg aagacataaa 2820
aaaaacctgt ctgagatgtt ctttctacca atctatatgt ctttcgggta tcaagtgttt 2880
ctgcatggta atgtcatgta aatgctgata ttgatttcac tggccatct atatttaaaa 2940
cgtgc 2945

```

```

<210> 15
<211> 1622
<212> DNA
<213> Homo sapiens
<400> 15

```



```

ggcaagatgg cgccgggtggg ggtggagaag aagctgctgc taggtcccaa cgggcccgcg      60
gtggcgggccg ccggcgacct gaccagttag gaggaggaag gccagagcct atggtcctcc     120
attctgagcg aagtgtccac ccgcgccagg tccaagctgc cgtccggcaa gaacatcctg     180
gtcttcggtg aagatggttc tggtaaaaca accctcatga ctaaaactaca aggagctgag     240
catggcaaaa aaggaagagg cctagaatat ctctacctca gtgtccatga tgaggaccga     300
gatgatcaca cgcgctgcaa cgtgtggatt ctggatggag acttgtacca caaaggcctg     360
ctgaaatttg cagtttctgc tgaatccttg ccagagaccc tcgtcatttt tgttcagac     420
atgtctagac ctggactgt gatggaatct ctgcagaaat gggctagtgt ttacgtgag     480
cacattgata aaatgaaaat tccaccagaa aaaatgaggg agctggaacg gaagtttgtg     540
aaagattttc aagactatat ggaacctgaa gaaggttgtc aaggttcccc acagagaaga     600
ggccctctga cctcaggctc cgatgaagaa aatgttgccc tgcctctggg tgacaatgtg     660
ctgactcata acctggggat cccggtgttg gtggtgtgca caaagtgtga tgcggtgagt     720
gtcctggaga aggagcacga ttacagggat gagcatttg actttatcca gtcacacctg     780
cggaggttct gccttcagta tggagctgcc ttgatttaca catcagtga agaagagaaa     840
aacctcgact tgttgtataa gtatattgtt cataaaacat acggtttcca cttcaccaca     900
cctgccttag ttgtgaaaaa ggatgccgtt tttatacctg caggctggga caatgaaaag     960
aaaatagcta tttacatga aaattttaca accgtgaagc cgaagatgc atatgaagac    1020
tttattgtga aacctcccg gagaaagctg gtccacgaca aagagttggc agcagaagat    1080
gagcaggtgt tcctaataa gcaacagtca ctcttgcca agcaaccagc cactcccacg    1140
agagcttctg aatctcctgc aagaggaccc tctggctctc caaggaccca gggtcgggga    1200
gggccagcca gtgtgcctag ctctcccca ggcacgtcag taaaaaagcc ggacccaaac    1260
atcaaaaata atgcagcaag tgaaggggtg ttggccagct tctcaacag tctgttgagt    1320
aaaaagacag gctctcctgg aagtcctggt gctggtggg tgacagagcac agccaagaag    1380
tcaggacaaa agactgtgtt gtcaaatgtt caggaagaac tggatagaat gactcgaag    1440
ccagactcta tggtaacaaa ctctcaaca gaaaatgaag cctgaacctc cttaaaaagt    1500
gcatatgtcg aatgacaaa taactatgta tattgatctg ctaagaccag gatttttctg    1560
atatggcaca tgctatcagt tttttggggc aggggagatg aactttaaaa aaaaaaaaaa    1620
aa                                                                    1622

```

<210> 16
<211> 7694
<212> DNA
<213> Homo sapiens

```

<400> 16
gcaacgaagg taccatggcc gttgtcgtcg ccgccgcggc tcccggggct ggatgggggg      60
ccgaggccag ccagtggcac ccggaagaaa gagacgcggc ggcggcgacg ccgacaccct     120
caggacgagt gtccggactt gccacagacc tcaaggagga gacggcgagg cccggccccc     180
gctgtccctg gtgtaagaa gtcgccgtag ccgtcgcggc cgggactccc cgggctctcg     240
cccttcagggt ttcgttgaca ctcaggaccg tacgtacgct gcgccatgtt caagaaactg     300
aagcaaaaag tcagcgagga gcagcagcag ctccagcagg cgctggctcc tgctcaggcg     360
tcctccaatt cttcaacacc aacaagaatg aggagcagga catcttcatt tacagagcaa     420
cttgatgaag gtacacccaa tagagagtca ggtgacacac agtcttttgc acagaagctc     480

```

cagctccggg tgccctccgt ggagtctttg tttcgaaglc cyataaagga atccctatcc 540
 cggctcttctt ctaaagagtc tttggtacga acatcttcca gagaatccct gaatcgactt 600
 gacctggaca gttctactgc cagttttgat ccacctcttg atatggatag cgaggctgaa 660
 gacttggtag ggaattcaga cagtctcaac aaagaacagt tgattcagcg gttgcgaaga 720
 atggaacgaa gcttaagtag ctacagggga aaatattctg agcttggtac agcttatcag 780
 atgcttcaga gagagaagaa aaagctacaa ggtatattaa gtcagagtca ggataaatca 840
 cttcggagaa tagcagaatt aagagaggag ctccaaatgg accagcaggc aaagaaacat 900
 ctgcaaggag agtttgatgc atcttttagag gagaaagatc agtatatcag tgttctccaa 960
 actcaggttt ctctactgaa acaacgatta cgaaatggcc cgatgaatgt tgatgtactg 1020
 aaaccacttc ctacagctgga accacaggct gaagtcttca ctaaagaaga gaatccagaa 1080
 agtgatggag agccagtagt ggaagatgga acttctgtaa aaacactgga aacactccag 1140
 caaagagtga agcgtcaaga gaacctactt aagcgttgta aggaacaat tcagtcacat 1200
 aaggaacaat gtacactatt aactagtga aaagaagctc tgcaagaaca actggatgaa 1260
 agacttcaag aactagaaaa gataaaggac cttcatatgg ccgagaagac taaacttacc 1320
 actcagttgc gtgatgcaaa gaacttaatt gaacagcttg aacaagataa gggaatggta 1380
 atcgagaga caaaacgtca gatgcatgaa accctggaaa tgaaagaaga agaaattgct 1440
 caactccgta gtcgcatcaa acagatgact acccaggag aggaattacg ggaacagaaa 1500
 gaaaagtcg aaagagctgc ttttgaggaa cttgaaaaag ctttgagtac agcccaaaaa 1560
 acagaggaag cacggagaaa actgaaggca gaaatggatg aacaaataaa aactatcgaa 1620
 aaaacaagt agggaggaacg catcagctt caacaggaat taagtcgggt gaaacaggag 1680
 gttgttgatg taatgaaaa atcctcagaa gaacaaattg ctaagctaca gaagcttcat 1740
 gaaaaggagc tggccagaaa agagcaggaa ctgaccaaga agcttcagac ccgagaaagg 1800
 gaatttcagg aacaaatgaa agtagctctt gaaaagagtc aatcagaata tttgaagatc 1860
 agccaagaaa aagaacagca agaactcttg gccctagaag agttagagtt gcagaaaaaa 1920
 gcaatcctca cagaaagtga aaataaactt cgggaccttc agcaagaagc agagacttac 1980
 agaactagaa ttcttgaaat ggaaagtctt ttggaaaaaa gcttacaaga aaacaaaaat 2040
 cagtcaaaag atttggctgt tcactcgaa gctgaaaaaa ataagcaca taaggagatt 2100
 acagtcagtg ttgaaaaaca caagacagaa ttggaaagcc ttaagcatca gcaggatgcc 2160
 ctttgactg aaaaactcca agtcttaag caacaatc agactgaaat ggaaaaactt 2220
 agggaaaagt gtgaacaaga aaaagaaaca ttgttgaaag acaagagat tatcttcag 2280
 gccacatag aagaaatgaa tgaaaagact ttgaaaagc ttgatgtgaa gcaaacagaa 2340
 ctagaatcat tatcttctga actgtcagaa gtattaaaag cccgtcaca actagaagag 2400
 gaactttctg ttctgaaaga tcaaacagat aaatgaagc aggaattaga ggccaagatg 2460
 gatgaacaga aaatcatca ccagcagcaa gttgacagta tcattaaaga acacgaggta 2520
 tctatccaga ggactgagaa ggcattaaaa gatcaaatca atcaactga gcttctcttg 2580
 aaggaaaagg acaagcattt gaaagagcat caggctcatg tagaaaattt agaggcagat 2640
 attaaaagg ctgaagggga actccagcag gcactctgta agctggacgt ttttcagtct 2700
 taccagagtg ccacacatga gcagacaaaa gcataatgagg aacagttggc ccaattgcag 2760
 cagaagtgtg tggatttgg aacagaaaga attcttctta ccaaacaggt tgctgaagtt 2820
 gaagcacaaa agaaagatgt ttgtactgag ttgatgctc aaaaaatcca ggtgcaggac 2880

ttaatgcagc aacttgaaaa acaaaatagt gaaatggagc aaaaagttaa atctttaacc 2940
 caagtctatg agtccaaact tgaagatggt aacaaagaac aggaacagac aaagcaaatc 3000
 ttggtggaaa aggaaaaatat gattttacaa atgagagaag gacagaagaa agaaattgag 3060
 atactcacac agaaattgtc agccaaggag gacagtattc atattttgaa tgaggaatat 3120
 gaaaccaa ataaaaacca agaaaaaag atggaaaaag ttaagcagaa agcaaaggag 3180
 atgcaagaaa cgttaaagaa aaaattactg gatcaggaag ccaaacttaa gaaagagctt 3240
 gaaaatactg ctctagagct tagtcagaaa gaaaaacagt ttaatgcca aatgctggaa 3300
 atggcacagg ctaactcagc tggaatcagt gatgcagtgt caagactgga acaaaaccaa 3360
 aaagaacaaa tagaaagtct tactgaggtt catcgacgag aactcaatga tgtcatatca 3420
 atctgggaaa agaaacttaa tcagcaagct gaagaacttc aggaatata tgaatccaa 3480
 ttacagga aagaacaaga ggtagcagaa ctgaaacaaa agatcctcct atttgggtgt 3540
 gaaaaagaag agatgaacaa ggaataaca tggctgaagg aagaaggtgt taagcaggat 3600
 acaacattaa atgaattaca ggaacagtta aagcagaagt ctgccatgt gaattctctt 3660
 gcacaagatg aaactaaact gaaagctcat cttgaaaagc tagaggttga cttgaataag 3720
 tctctgaagg aaaatacttt tctcaagag cagctagtgt aactgaagat gctggcagaa 3780
 gaagataagc ggaaggttct tgagttgact agcaagtga aaaccacaga tgaagaattc 3840
 cagagtttga aatcttcaca tgaaaaaagt acaaaaagcc tagaggacaa gagcttgaa 3900
 tttaaaaaac tgtctgagga actagcgatt cagctagata ttgctgtaa gaaaaccgaa 3960
 gccttattag aagctaaaac aaatgagcta atcaacatta gtagtagtaa aactaatgcc 4020
 attctttcta ggatttctca ttgtcagcac cgtacaacta aagttaagga ggcactgtta 4080
 attaaaactt gcacagtttc tgaattagaa gcacaactta gacagttgac agaggagcaa 4140
 aatacactaa atatttcttt tcaacaggct actcatcagt tagaagaaaa agaaaatcaa 4200
 attaagagca tgaaggctga tattgaaagt cttgtaacag aaaaagaagc cttacagaag 4260
 gaaggaggca atcagcaaca ggctgcttct gaaaaggagt cttgtataac acagttgaag 4320
 aaagagttat ctgaaaacat caatgctgtc acattgatga aagaagagct taaagaaaaa 4380
 aaagttgaga ttagcagtct tagtaacaa ctaactgatt tgaatgttca gcttcaaaat 4440
 agcatcagcc tatccgaaaa agaagcagcc atttcacac taagaaagca gtatgatgaa 4500
 gaaaaatgtg aattgctgga tcaggtgcaa gatttatctt ttaaagtga cactctgagt 4560
 aaagagaaaa tttctgctct tgagcaggta gatgactggt ccaataaatt ctcagaatgg 4620
 aagaagaaag cacagtcaag atttacacag catcaaaaca ctgttaaaga attgcagatc 4680
 cagcttgagt taaaatcaaa ggaagcttat gaaaaggatg agcagataaa tttattgaag 4740
 gaagagcttg atcagcaaaa taaaagattt gattgtttaa aggggtgaaat ggaagacgac 4800
 aagagcaaga tggagaaaaa ggagtcta attagaacag agttaagtc tcaaacagca 4860
 agaattatgg aattagagga ccatattacc cagaaaacta ttgaaataga gtccttaaat 4920
 gaagtcttta aaaattacaa tcaacaaaag gatattgaac acaagaatt ggttcagaaa 4980
 cttcaacatt ttcaagagtt aggagaagaa aaggacaaca gggtaaaga agctgaagaa 5040
 aaaatcttaa cacttgaaaa ccaagtttat tccatgaaag ctgaactga aactaagaag 5100
 aaagaattag aacatgtgaa ttttaagtgtg aaaagcaaag aggaggagtt aaaggcattg 5160
 gaagataggc ttgagtcaga aagtgtctga aaattagcag agttgaagag aaaagctgaa 5220

caaaaaattg ctgccattaa gaagcagttg ttatctcaaa tggaagagaa agaagaacag 5280
tataaaaaag gtacagaaag ccatttgagt gagctaaata caaaattgca ggaagagaa 5340
agggaagttc acatcttgga agaaaaactt aagtcagtg aaagttcaca gtcagaaaca 5400
ttaattgtac ccagatcagc aaaaaatgtg gcagcatata ctgaacaaga agaagcagat 5460
tccaaggct gtgtgcagaa gacatatgaa gaaaaaatca gtgttttaca aagaaactta 5520
actgaaaaag aaaagctatt gcagagggta gggcaggaaa aagaagagac agtttcttct 5580
cattttgaaa tgcgatgcca ataccaggag cgcttaataa agctagaaca tgctgaggca 5640
aagcaacatg aagatcaaag tatgataggt catcttcaag aggagcttga agaaaaaac 5700
aagaaatatt cttgatagt agcccagcat gtggaaaaag aaggaggtaa aaataacata 5760
caggcaaacg aaaaactgga aaatgtgttt gacgacgtcc agaaaaccct ccaggagaag 5820
gaactaacct gtcagatttt ggagcaaaaag ataaaagagc tggattcctg cttagtaaga 5880
cagaaagaag tacatagagt tgaaatggaa gatttgacct caaatatga aaaattacag 5940
gctttacaac agatggatgg aagaaataaa cccacagaac ttttggaaag aaacactgaa 6000
gaaaagtcca aatcacattt ggtccaaccc aaattgctta gtaacatgga agcccagcac 6060
aatgatctgg agtttaaatt agccggggca gaacgggaga aacagaaact gggcaaggag 6120
attgttagat tgcagaaaga ccttcgaatg ttgagaaagg agcatcagca agaattggaa 6180
atactaaaga aagaatatga tcaagaaagg gaagagaaaa tcaaacagga gcaggaagat 6240
cttgaaactga agcacaattc cacattaaaa cagctgatga gggagttaa tacacagctg 6300
gcacaaaagg aacaagagct ggaatgacc ataaaagaaa ctatcaataa ggcccaggag 6360
gtggaggctg aactttttaga aagccatcaa gaagagacaa atcagttact taaaaaatt 6420
gctgagaaag atgatgatct aaaacgaaca gccaaaagat atgaagaaat cttgatgct 6480
cgtgaagaag aaatgactgc aaaagtaagg gacctgcaga ctcaactga ggagctgcag 6540
aagaaatacc agcaaaagct agagcaggag gagaaccctg gcaatgataa tgtaacaatt 6600
atggagctac agacacagct agcacagaag acgactttaa tcagtattc gaaattgaaa 6660
gagcaagagt tcagagaaca gattcacaat ttagaagacc gtttgaagaa atatgaaaag 6720
aatgtatatg caacaactgt ggggacacct tacaagggtg gcaatttgta ccatacggat 6780
gtctcactct ttggagaacc taccgaattt gattatttgc gaaaagtgt ttttgagtat 6840
atgatgggtc gtgagactaa gaccatggca aaagttataa ccaccgtact gaagttccct 6900
gatgatcaga ctcaaaaaat tttgaaaga gaagatgctc ggctgatgtt tacttcacct 6960
cgcagtggta tcttctgagt aaaccatcag tctgtgctta gtaacatgt gtcatggctc 7020
cgatcttcat cttgaagaag agtgacattg ggtgactgct gcttgaaaa ctgtccacac 7080
ttgctactct ttgagaatga agttgtcatt cagggccct catgtagcca aaagaccaag 7140
aaaaatctg cccacagata agttgcagac tgcctttaaa atagatttta tcagtggaga 7200
aatggtgata gtttttctt cagtttctc ttgggaagga gttttatgtt gtttaaaaga 7260
tattttgata acttaacctg ctttatggc ttacataata ttccttcat ccattctttt 7320
taaagaacgg cttaccttct ctatttattt ttagggatgat ttttaaaaa gacttgtgca 7380
atacattttg aggtgaaact tagtgattt tttctgataa attagagcat ttaattgact 7440
attttattca ggttgatctg ttgaatatgt gctaaagacc agttctttaa gcttaagacat 7500
gtaaaaaatc ccaaatggca gtacctcatt gtttacttag ctttgtact tataattttc 7560
agaggaaaaa acactactgt aaattgtgaa tagccaatac ataactgtat tgtatgcaaa 7620

tctgtgattg ttggcagtgt catctctgag aaacagataa ataaagttaa ttactataa 7680
aaaaaaaaaaaa 7694

<210> 17
<211> 3080
<212> DNA
<213> Homo sapiens

<400> 17
gaaataatgg aggaattgctg tagcctggac ccacgacggc aggaattatt agaggccagg 60
tttactggag taggtgttag taagggacca cttaatagtg agtcttccaa ccagagcttg 120
tgcagcgtcg gatccttgag tgataaagaa gtagagactc ccgagaaaaa gcagaatgac 180
cagcgaaatc ggaaaagaaa agctgaacca tatgaaacta gccaaaggaa aggcactcct 240
aggggacata aaattagtga ttactttgag cgacgagtag aacagcccct ctatggttta 300
gatggcagtg ctgcaaagga ggcaacggag gagcagctcg ctctgccaac cctcatgtca 360
gtgatgctag ctaaacctcg gcttgaccca gagcagctgg cgcaaagggg agctggcctc 420
tgcttcactt ttgtttcagc tcagcaaaac agtccctcat ctacgggac tggaacaca 480
gagcattcct gcagctccca aaaacagatc tccatccagc acagacagac ccagtccgac 540
ctcacaatag aaaaaatc tgactagaa aacagtaaga attctgactt agagaagaag 600
gaggaagaa tagatgattt attaagagcc aactgtgatt tgagacggca gattgatgaa 660
cagcaaaaga tgctagagaa atacaaggaa cgattaaata gatgtgtgac aatgagcaag 720
aaactcctta tagaaaagtc aaaacaagag aagatggcgt gtagagataa gagcatgcaa 780
gaccgctga gactgggcca ctttactact gtccgacacg gagcctcatt tactgaacag 840
tggacagatg gttatgcttt tcagaatctt atcaagcaac aggaaggat aaattcacag 900
aggaagaga tagaaagaca acggaatatg ttagcaaagc ggaacactcc tgccatgggt 960
caggccctc ctgcaaccaa tgagcagaaa cagcggaaaa gcaagaccaa tggagctgaa 1020
aatgaaacgt taacgttagc agaataccat gaacaagaag aaatcttcaa actcagatta 1080
ggctacttta aaaaggagga agcagagatc caggcagagc tggagagact agaaaagggt 1140
agaaatctac atacaggga actaaaaagg atacataatg aagataattc acaatttaaa 1200
gatcatccaa cgctaaatga cagatatttg ttgttacatc ttttgggtag aggaggtttc 1260
agtgaagttt acaaggcatt tgatctaaca gagcaaagat acgtagctgt gaaaattcac 1320
cagttaaata aaaactggag agatgagaaa aaggagaatt accacaagca tgcattgtagg 1380
gaataccgga ttcataaaga gctggatcat ccagaaatag ttaagctgta tgattacttt 1440
tacttgata ctgactcgtt ttgtacagta ttagaatact gtgagggaaa tgatctggac 1500
ttctacctga aacagcacia attaatctcg gagaaagagg cccggtccat tatcatgcag 1560
attgtgaatg ctttaaagta cttaaatgaa ataaacctc ccatacata ctatgacctc 1620
aaaccaggta atattctttt agtaaatggt acagcgtgtg gagagataaa aattacagat 1680
tttggctttt cgaagatcat ggatgatgat agctacaatt cagtggatgg catggagcta 1740
acatcacaaag gtgctgttac ttattggtat ttaccaccag agtgtttgtt ggttgggaaa 1800
gaaccaccaa agatctcaaa taaagtgtat gtgtggtcgg tgggtgtgat cttctatcag 1860
tgtctttatg gaagggaagc ttttggccat aaccagtctc agcaagacat cctacaagag 1920
aatacgattc ttaaagctac tgaagtgcag ttcccgccea agccagtagt aacacctgaa 1980
gcaaaggcgt ttattcgacg atgcttgacc taccgaaagg aggaccgat tgatgtccag 2040

cagctggcct gtgatcccta cttgttgccct cacatccgaa agtcagtcct tacaagtagc 2100
 cctgctggag ctgctattgc atcaacctct ggggcgtcca ataacagttc ttctaattga 2160
 gactgactcc aaggccacaa actgttcaac acacacaaag tggacaaatg gcgttcagca 2220
 gcggttttgg aacatagcga atccgaatgg atctgatgaa acctgtacca ggtgctttta 2280
 ttttcttgct tttttcccat ccatagagca tgacagcatc gattctcatt gaggagaaac 2340
 cttgggcagc tccggccagg cctttagga aaaggccccc cccgaggttc cagcgtcaac 2400
 ggccactgtg tgtggctgct ctgagtgagg aaaaaattaa aaagaaaaac tggttccatg 2460
 tactgtgaac ttgaaaactt gcagactcag ggggttcctt gatgcagtgc ttcagatgaa 2520
 gaatgtggac ttgaaaatac agactgggct agtccagtgt ctatatataa acttgttctt 2580
 ttcttttaac aaagtttagg taacatctcc tgaaaagctt gtagcacaaa ggctcagctg 2640
 gggatggtgt ttgacttcgg aggaaaaaag ttgctattgc ccgttaaagg cactagagtt 2700
 agtgttttat ccctaataa tttcaatttt taaaacatg cagcttcctt ctcccctttt 2760
 ttatttttga aagaatacat ttggtcataa agtgaaacct gtattagcaa gtacgtggca 2820
 atgttcattc caatcagatg cagctttctc ctccgtctgg tctcctgttt gcaattgctt 2880
 ccctcatctc agtagggaaa aaattgagtg ggagtactga gatgtgtggg tttttgccat 2940
 tggacaaaga atgaggttag aagactgcag cttggagtct ctctaggttt tcaactattt 3000
 cttcacaatt tgaacacttg acggttgctc cttttaattt atttgaagtg ctattttttt 3060
 aaataaaggt tcactgttcc 3080

<210> 18
 <211> 7596
 <212> DNA
 <213> Homo sapiens

<400> 18
 gtggctgcgg ctggggacgt gcgcccgcgc caccatcttc ggctgaagag gcaattgctt 60
 ttggatcggt ccatttaca tggcgagag aactggactc gaggatccag agaggatctt 120
 ctttgtggac agggctgtca tctacaacct tgccactcaa gctgattgga cagctaaaaa 180
 gctagtgtgg attccatcag aacgccatgg ttttgaggca gctagtatca aagaagaacg 240
 gggagatgaa gttatggtgg agttggcaga gaatggaaag aaagcaatgg tcaacaaaga 300
 tgatattcag aagatgaacc cacctaagtt ttccaagtg gaggatatgg cagaattgac 360
 atgcttgaat gaagcttccg ttttacataa tctgaaggat cgctactatt caggactaat 420
 ctatacttat tctggactct tctgtgtagt tataaacctt tacaagaatc ttccaattta 480
 ctctgagaat attattgaaa tgtacagagg gaagaagcgt catgagatgc ctccacacat 540
 ctatgctata tctgaatctg cttacagatg catgcttcaa gatcgtgagg accagtcaat 600
 tctttgcacg ggtgagtcag gtgctgggaa gacagaaaat acaaagaaag ttattcagta 660
 ccttgcccat gttgcttctt cacataaagg aagaaggac cataatatc ctggggaact 720
 tgaacggcag cttttgcaag caaatccaat tctcgaatca tttggaaatg cgaagactgt 780
 gaaaaatgat aactcatctc gttttggcaa atttattcgg atcaactttg atgtaactgg 840
 ctatatcggt ggggccaaca ttgaacata ccttctggaa aagtctcgtg ctgttcgtca 900
 agcaaaagat gaacgtactt ttcatatctt ttaccagttg ttatctggag caggagaaca 960
 cctaaagtct gatttgcttc ttgaaggatt taataactac aggtttctct ccaatggcta 1020
 tattcctatt ccgggacagc aagacaaaga taatttcag gagaccatgg aagcaatgca 1080

cataatgggc ttctcccatg aagagattct gtcaatgctt aaagtagtat cttcagtgc 1140
acagtttggg aatatttctt tcaaaaagga gagaaatact gatcaagctt ccatgccaga 1200
aaatacagtt gcgcagaagc tctgccatct tcttgggatg aatgtgatgg agtttactcg 1260
ggccatcctg actccccgga tcaaggtcgg ccgagactat gtgcaaaaag cccagaccaa 1320
agaacaggca gattttgcag tagaagcatt ggcaaaagct acctatgagc ggctctttcg 1380
ctggctcggt catcgcatca ataaagctct ggataggacc aaacgtcagg gagcatcttt 1440
cattggaatc ctggatattg ctggatttga aatttttgag ctgaactcct ttgaacaact 1500
ttgcatcaac tacaccaatg agaagctgca gcagctgttc aaccacacca tgtttatcct 1560
agaacaagag gaataccagc gcgaaggcat cgagtggaaac ttcacgatt tcgggctgga 1620
tctgcagcca tgcacgacc taatagagag acctgcgaac cctcctggtg tactggccct 1680
tttggatgaa gaatgctggt tcctaaagc cacagataaa acctttgttg aaaaactggt 1740
tcaagagcaa ggttcccact ccaagtttca gaaacctcga caattaaaag acaagctga 1800
tttttgcatc atacattatg cagggaaagt ggactataag gcagatgagt ggctgatgaa 1860
gaatatggac ccctgaatg acaacgtggc cacccttttg caccagtcac cagacagatt 1920
tgtggcagag ctttggaag atgtggaccg tatcgtgggt ctggatcaag tcaactggtat 1980
gactgagaca gcttttggt ccgcatataa aaccaagaag ggcatgttgc gtaccgttgg 2040
gcaactctac aaagaatctc tcaccaagct gatggcaact ctccgaaaca ccaaccctaa 2100
ctttgttcgt tgtatcattc caaatcacga gaagagggt ggaaaattgg atccacacct 2160
agtccatgat cagcttcgct gtaatggtgt cctggaagg atccgaatct gtcgccaggg 2220
ctccctaac cgaatagttt tccaggaatt cagacagaga tatgagatcc taactccaaa 2280
tgctattcct aaaggtttta tggatggtaa acaggcctgt gaacgaatga tccgggcttt 2340
agaattggac ccaaacttgt acagaattgg acagagcaag atatttttca gagctggagt 2400
tctggcacac ttagaggaag aaagagattt aaaaatcacc gatatcatta tcttcttcca 2460
ggcggtttgc agagggttgc tggccagaaa ggcctttgac aagaagcagc agcaactaag 2520
tgccttaaag gtcttcgacg ggaactgtgc cgcgtacctg aaattacggc actggcagtg 2580
gtggcgagtc ttcacaaagg tgaagccgct tctacaagt actcgccagg aggaagaact 2640
tcaggccaaa gatgaagagc tgttgaagg gaaggagaag cagacaaaag tgaaggaga 2700
gctggaggag atggagcgga agcaccagca gcttttagaa gagaagaata tccttgca 2760
acaactacaa gcagagactg agctcttgc tgaagcagaa gagatgagg caagacttgc 2820
tgctaaaaag caggaattag aagagattct acatgacttg gactctaggg ttgaagaaga 2880
agaagaaaga aacaaatcc tccaaatga aaagaaaaa atgcaagcac atattcagga 2940
cctggaagaa cagctagacg aggaggaagg ggctcgcaa aagctgcagc tggaaaagg 3000
gacagcagag gccaatgca agaagatgga agaggagatt ctgcttctcg aggacaaaa 3060
ttccaagttc atcaagaaa agaaactcat ggaagatcgc attgctgagt gttccttca 3120
gctggctgaa gaggaagaaa aggcgaaaaa cttggccaaa atcaggaata agcaagaagt 3180
gatgatctca gatttagaag aacgcttaaa gaaggagaa aagactcgtc aggaactgga 3240
aaaggccaaa agaaaactcg acggggagac gaccgacctg caggaccaga tcgcagagct 3300
gcaggcgagc attgatgagc tcaagctgca gctggccaag aaggaggagg agctgcaggg 3360
cgcactggcc agaggtagt atgaacact ccataagaac aatgccctta aagttgtgcg 3420

agagctacaa gcccaaattg ctgaacttca ggaayaclll yaalccyaya ayycllccag 3480
 gaacaaggcc gaaaagcaga aaagggactt gaggaggaa ctggaagctc tgaaaacaga 3540
 gctggaggac acgctggaca ccacggcagc ccagcaggaa ctacgtacaa aacgtgaaca 3600
 agaagtggca gagctgaaga aagctcttga ggaggaaact aagaacctg aagctcaaat 3660
 ccaggacatg agacaaagac acgcaacagc cctggaggag ctctcagagc agctggaaca 3720
 ggccaagcgg ttcaaagcaa atctagagaa gaacaagcag ggcctggaga cagataacaa 3780
 ggagctggcg tgtgaggtga aggtcctgca gcaggtaag gctgagctcg agcacaagag 3840
 gaagaagctc gacgcgcagg tccaggagct ccatgccaaag gtctctgaag gcgacaggct 3900
 caggggtggag ctggcggaga aagcaagtaa gctgcagaat gagctagata atgtctccac 3960
 ccttctggaa gaagcagaga agaagggtat taaatttgct aaggatgcag ctagtcttga 4020
 gtctcaacta caggatacac aggagcttct tcaggaggag acacgccaga aactaaacct 4080
 gagcagtcgg atccggcagc tgaagagga gaagaacagt cttcaggagc agcaggagga 4140
 ggaggaggag gccaggaaga acctggagaa gcaagtgcg gccctgcagt cccagttggc 4200
 tgataccaag aagaaagtag atgacgacct gggaacaatt gaaagtctgg aagaagccaa 4260
 gaagaagctt ctgaaggacg cgagggccct gagccagcgc ctggaggaga aggcaactggc 4320
 gtatgacaaa ctggagaaga ccaagaaccg cctgcagcag gagctggacg acctcacggt 4380
 ggacctggac caccagcgcc aggtcgcctc caacttgag aagaagcaga agaagtttga 4440
 ccagctgtta gcagaagaga agagcatctc tgctcgctat gccgaagagc gggaccgggc 4500
 cgaagccgag gccagagaga aagaaccacaa agccctgtca ctggcccggg ccctcgagga 4560
 agccctggag gccaaaggag agtttgagag gcagaacaag cagctccgag cagacatgga 4620
 agacctcatg agctccaaag atgatgtggg aaaaaacgtt cacgaacttg aaaaatccaa 4680
 acgggcccta gagcagcagg tggaggaaat gaggaccag ctggaggagc tggagacga 4740
 actccaggcc acggaagatg ccaagcttcg tctggaggtc aacatgcagg ccatgaaggc 4800
 gcagttcgag agagacctgc aaaccaggga tgagcagaat gaagagaaga agcggctgct 4860
 gatcaaacag gtgcgggagc tcgaggcgga gctggaggat gagaggaaac agcgggcgct 4920
 tgctgtagct tcgaagaaaa agatggagat agacctgaag gacctgaag cccaaatcga 4980
 ggctgcgaac aaagctcggg atgaggtgat taagcagctc cgcaagctcc aggctcagat 5040
 gaaggattac caactgtaat tagaagaagc tcgtgcatcc agagatgaga tttttgctca 5100
 atccaaagag agtgaaaaga aattgaagag tctggaagca gaaatccttc aattgcagga 5160
 ggaacttgcc tcactctgagc gagcccgcg acacgccgag caggagagag atgagctggc 5220
 ggacgagatc accaacagcg cctctggcaa gtccgcgctg ctggatgaga agcggcgctc 5280
 ggaagctcgg atcgacagc tggaggagga gctggaagag gagcagagca acatggagct 5340
 gctcaacgac cgcttccgca agaccactct acaggtggac aactgaacg ccgagctagc 5400
 agccgagcgc agcggcgccc agaagagtga caatgcagc cagcaactgg agcggcagaa 5460
 caaggagctg aaggccaagc tgcaggaaact cgagggtgct gtcaagtcta agttcaaggc 5520
 caccatctca gccctggagg ccaagattgg gcagctggag gagcagcttg agcagggaagc 5580
 caaggaacga gcagccgcca acaaatagtg ccgtcgact gagaagaagc tgaagaaat 5640
 cttcatgcag gttgaggatg agcgtcgaca cgcgaccag tataaagagc agatggagaa 5700
 ggccaacgct cggtgaagc agcttaaagc ccagctggag gaagcagaag aagaagcgac 5760
 gcgtgccaac gcactctggc gtaaaactcca gcgggaactg gatgatgcca ccgaggccaa 5820

cgagggcctg agccgcgagg tcagcacccct gaagaaccgg ctgaggcggg gtggccccc 5880
 cagcttctct tccagccgat ctggccggcg ccagctgcac cttgaaggag cttccctgga 5940
 gctctccgac gatgacacag aaagtaagac cagtgatgtc aacgagacgc agccacccca 6000
 gtcagagtaa agttgcagga agccagagga ggcaatacag tgggacagtt aggaatgcac 6060
 ccggggcctc ctgcagatct cggaattgg caagctacgg gattccttcc tgaagatca 6120
 actgtgtctt aaggctctcc agcctatgca tactgtatcc tgcttcagac ttaggtacaa 6180
 ttgctccctt tttatatac agacacacac aggacacata tattaacag attgtttcat 6240
 cattgcatct attttccata tagtcatcaa gagaccattt tataaacat ggtaagaccc 6300
 tttttaaaac aaactccagg cccttggttg cgggtcgctg ggttattggg gcagcgccgt 6360
 ggtcgctact cagtcgtctt gcatgctctc tgcatacag acaggtaacc tagttctgtg 6420
 ttcacgtggc ccccgactcc tcagccacat caagtctcct agaccactgt ggactctaaa 6480
 ctgcacttgt ctctctcatt tccttcaaat aatgatcaat gctatttcag tgagcaaaact 6540
 gtgaaagggg ctttgaaag agtaggaggg gtgggctgga tcggaagcaa caccatttg 6600
 gggttaccat gtccatcccc caaggggggc cctcccctc gagtcgatgg tgtcccgcat 6660
 ctactcatgt gaactggcct tggcgagggc tggctctgtc atagaaggga tagtgccac 6720
 actgcagctg agggccaggc tggcagccat ggatcatgta gacttccaga tggctcccg 6780
 aaccgcctgg ctctgccggc gccctcctca cgtcaggagc aagcagccgt ggaccctaa 6840
 gccgagctgg tggaaagccc ctccccctcg ccagccgggc cctcatgctg accttgcaaa 6900
 ttcagccgct gctttgagcc caaaatggga atattggttt tgtgtccgag gcttgttcca 6960
 agtttgtaa tgaggtttat ggagcctcca gaacagatgc catcttcttg aatgttgaca 7020
 tgccagtggg tgtgactcct tcatttttcc ttctcccttc cctttggaca gtgttacagt 7080
 gaacacttag catectgttt ttggttgga gtaagcaaa ctgacattac ggaaagtgcc 7140
 ttagacacta cagtactaag acaatgttga atatatcatt cgcctctata acaattta 7200
 gtattcagtt ttgactgtgc ttcatatcat gtacctctct agtcaaagtg gtattacaga 7260
 cattcagtga caatgaatca gtgttaattc taaatccttg atcctctgca atgtgcttga 7320
 aaacacaaac cttttgggtt aaaagcttta acatctatta ggaagaattt gtcctgtggg 7380
 tttggaatct tggattttcc ccctttatga actgtactgg ctgttgacca ccagacacct 7440
 gaccgcaaat atcttttctt gtattcccat atttctagac aatgattttt gtaagacaat 7500
 aaatttatct attatagata ttgcgccctg ctctgtttac ttgaagaaaa aagcacccgt 7560
 ggagaataaa gagacctcaa taaacaaaaa aaaaaa 7596

<210> 19
 <211> 3528
 <212> DNA
 <213> Homo sapiens

<400> 19
 tatgcatgga gtggacctgt aggcgacttg catcgtcttc aacatgaaga tagccacagt 60
 gtcagtgtt ctgcccttgg ctctttgcct catacaagat gctgccagta agaatagaaga 120
 tcaggaaatg tgccatgaat ttcaggcatt tatgaaaaat ggaaaactgt tctgtcccca 180
 ggataagaaa ttttttcaaa gtcttgatgg aataatgttc atcaataaat gtgccacgtg 240
 caaaatgata ctggaaaaag aagcaaaatc acagaagagg gccaggcatt tagcaagagc 300
 tcccaaggct actgccccaa cagagctgaa ttgtgatgat tttaaaaaag gagaaagaga 360

tggggatttt atctgtcctg attattatga agctgtttgt ggcacagatg ggaaaacata	420
tgacaacaga tgtgactgt gtgctgagaa tgcgaaaacc gggcccaaa ttggtgtaaa	480
aagtgaaggg gaatgtaaga gcagtaatcc agagcaggat gtatgcagtg cttttcgcc	540
ctttgttaga gatggaagac ttggatgcac aagggaat gatcctgttc ttggtcctga	600
tgggaagacg catggcaata agtgtgcaat gtgtgctgag ctgtttttaa aagaagctga	660
aatgccaa cgagaggggtg aaactagaat tcgacgaaat gctgaaaagg atttttgcaa	720
ggaatatgaa aaacaagtga gaaatggaag gctttttgt acacgggaga gtgatccagt	780
ccgtggccct gacggcagga tgcattgcaa caaatgtgcc ctgtgtgctg aaattttcaa	840
gcggcgtttt tcagagggaaa acagtaaaac agatcaaaat ttgggaaaag ctgaagaaaa	900
aactaaagtt aaaagagaaa ttgtgaaact ctgcagtcaa tatcaaaatc aggcagaaga	960
tggaatactt ttctgtacca gagaaaatga ccctattcgt ggtccagatg ggaaaatgca	1020
tggcaacttg tgttccatgt gtcaagtcta cttccaagca gaaaatgaag aaaagaaaaa	1080
ggctgaagca cgagctagaa acaaaaagaga atctggaaaa gcaacctcat atgcagagct	1140
ttgcaatgaa tatcgaaagc ttgtgaggaa cggaaaactt gcttgacca gagagaacga	1200
tcctatccag ggcccagatg ggaagtgc cggcaacacc tgctccatgt gtgaggtctt	1260
cttccaagca gaagaagaag aaaagaaaaa gaaggaaaggc gaatcaagaa acaaaagaca	1320
atctaagagt acagcttcct ttgaggagtt gtgtagtga taccgcaa atccaggaaaa	1380
cggacggcct ttttgacca gagagaatga ccccatccag ggcccagatg ggaaaatgca	1440
tggcaacacc tgctccatgt gtgaggtctt ctttcaaca gaagaaagag caagagcaaa	1500
ggctaaaaga gaagctgcaa aggaaatctg cagtgaattt cgggaccaag tgaggaaagg	1560
aacacttata tgcaccagg agcataatcc tgtccgtgga ccagatggca aaatgcatgg	1620
aaacaagtgt gccatgtgt ccagtgtgtt caaactgaa gaagaagaga agaaaaatga	1680
taaagaaga aaagggaaag ttgaggctga aaaagttaag agagaagcag ttcaggagct	1740
gtgcagtga tatcgtcatt atgtgaggaa tggacgactc ccctgtacca gagagaatga	1800
tcctattgag ggtctagatg ggaaaatcca cggcaacacc tgctccatgt gtgaagcctt	1860
cttccagcaa gaagcaaaag aaaaagaaag agctgaacc agagcaaaag tcaaaagaga	1920
agctgaaaag gagacatgc atgaatttcg gagacttttg caaaatggaa aacttttctg	1980
cacaagagaa aatgatcctg tgcgtggccc agatggcaag acccatggca acaagtgtgc	2040
catgtgtaag gcagctcttc agaagaaaaa tgaggaaaga aagaggaaag aagaggaga	2100
tcagagaaat gctgcaggac atggttccag tgggtgtgga ggaggaaaca ctgaggacga	2160
atgtgctgag tatcaggaa aaatgaaaaa tggaaagactc agctgtactc gggagagtga	2220
tcctgtacgt gatgctgatg gcaaatcgta caacaatcag tgtaccatgt gtaaagcaaa	2280
attggaaga gaagcagaga gaaaaaatga gtattctcgc tccagatcaa atgggactgg	2340
atcagaatca ggaagagata catgtgatga gtttagaagc caaatgaaaa atggaaaact	2400
tatctgcact cgagaaagt accctgtccg ggtccagat ggaagacac atggtaataa	2460
gtgtactatg tgtaaggaaa aactggaaag ggaagcagct gaaaaaaaaa agaaagagga	2520
tgaagacagg agcaatacag gagaaaggag caatacagga gaaaggagca atgacaaaga	2580
ggatctgtgt cgtgaatttc gaagcatgca gagaaatgga aagcttatct gcaccagaga	2640
aaataaccct gttcgaggcc catatggcaa gatgcacatc aataaatgtg ctatgtgtca	2700

```

gagcatcttt gatcgagaag ctaatgaaag aaaaaayaaa yalyaayaya aalcaaytag 2760
caagccctca aataatgcaa aggatgagtg cagtgaattt cgaaactata taaggaacaa 2820
tgaactcatc tgccctagag agaattgacct agtgcacggt gctgatggaa agttctatac 2880
aaacaagtgc tacatgtgca gagctgtctt tctaacagaa gctttggaaa gggcaaagct 2940
tcaagaaaag ccatcccatg ttagagcttc tcaagaggaa gacagcccag actctttcag 3000
ttctctggat tctgagatgt gcaaagacta ccgagtattg cccaggatag gctatctttg 3060
tccaaaggat ttaaagcctg tctgtggtga cgatggccaa acctacaaca atccttgcat 3120
gctctgtcat gaaaacctga tacgccaaac aaatacacac atccgcagta cagggaagtg 3180
tgaggagagc agcaccaccg gaaccaccgc agccagcatg cccccgtctg acgaatgaca 3240
ggaagattgt tgaagccat gagggaaaaa ataaaccca gttctgaatc acctaccttc 3300
acctctgtga tatacaaga attctctgga gcttgtctta tttgctatag aaaacaatac 3360
agagcttttg ggaatggaat cactgatttt cagtcttttc catttctttc ctcttagaat 3420
ctgtgatctg agggataaaa gacatttcca ccaagtttga gccctcaaaa tgtctctgatt 3480
acaatgctgt ctgtccaact gcctgttcaa taaaagtaaa ctcagcag 3528

```

<210> 20
 <211> 647
 <212> DNA
 <213> Homo sapiens

```

<400> 20
gctcactgag caccgtccca gcatccggac accacagcgg cccttcgctc cacgcagaaa 60
accacacttc tcataccttc actcaacact tccttcccca aagccagaag atgcacaagg 120
aggaacatga ggtggctgtg ctgggggcac ccccagcac catccttcca aggtccaccg 180
tgattaacat ccacagcgag acctccgtgc ccgaccatgt cgtctggtcc ctgttcaaca 240
ccctcttctt gaactggtgc tgtctgggct tcatagcatt cgctactcc gtaaagtcta 300
gggacaggaa gatggttggc gacgtgaccg gggcccaggc ctatgcctcc accgccaagt 360
gcctgaacat ctgggccctg attctgggca tcctcatgac cattggattc atcctgttac 420
tggtattcgg ctctgtaaca gtctaccata ttatgttaca gataatacag gaaaaacggg 480
gttactagta gccgccata gcctgcaacc ttgactctcc actgtgcaat gctggccctg 540
cacgctgggg ctgttgcccc tgcccccttg gtcctgcccc tagatacagc agtttatacc 600
cacacacctg tctacagtgt cattcaataa agtgcacgtg cttgtga 647

```

<210> 21
 <211> 1590
 <212> DNA
 <213> Homo sapiens

```

<400> 21
gaggcagttc tggtgccact ctctctcctg tcaatgatgg atctcagaaa taccacagcc 60
aaatctctgg acaagttcat tgaagactat ctcttgccag acacgtgttt ccgcatgcaa 120
atcgaccatg ccattgacat catctgtggg ttcttgaagg aaaggtgctt ccgaggtagc 180
tcctaccctg tgtgtgtgtc caaggtggtg aaggggtggt cctcaggcaa gggcaccacc 240
ctcagaggcc gatctgacgc tgacctggtt gtcttctca gtcctctcac cacttttcag 300
gatcagttaa atcgccgggg agagttcatc caggaaatta ggagacagct ggaagcctgt 360
caaagagaga gagcactttc cgtgaagttt gaggtccagg ctccacgctg gggcaacccc 420
cgtgcgctca gcttcgtact gagttcgctc cagctcgggg aggggggtga gttcgatgtg 480

```

```

ctgcctgcct ttgatgccct gggtcagttg actggcagct ataacctaa ccccaaatac 540
tatgtcaagc tcatcgagga gtgcaccgac ctgcagaaag agggcgagtt ctccacctgc 600
ttcacagaac tacagagaga cttcctgaag cagcgcccca ccaagctcaa gagcctcatc 660
cgcctagtca agcactggta ccaaaattgt aagaagaagc ttgggaagct gccacctcag 720
tatgccctgg agctctgac ggtctatgct tgggagcgag ggagcatgaa aacacatttc 780
aacacagccc aaggatttcg gacggctctg gaattagtca taaactacca gcaactctgc 840
atctactgga caaagtatta tgactttaaa aacccatta ttgaaaagta cctgagaagg 900
cagctcacga aacccaggcc tgtgatcctg gacccggcgg accctacagg aaacttgggt 960
ggtggagacc caaagggttg gaggcagctg gcacaagagg ctgaggcctg gctgaattac 1020
ccatgcttta agaattggga tgggtcccca gtgagctcct ggattctgct ggctgaaagc 1080
aacagtacag acgatgagac cgacgatccc aggacgtatc agaaatatgg ttacattgga 1140
acacatgagt accctcatct ctctcataga ccagcagcgc tccaggcagc atccaccca 1200
caggcagaag aggactggac ctgcaccatc ctctgaatgc cagtgcattc tgggggaaag 1260
ggctccagtg ttatctggac cagttccttc attttcaggt gggactcttg atccagagaa 1320
gacaaagctc ctcatgagc tgggtgataa tccaagacag aacccaagtc tcctgactcc 1380
tggccttcta tgcctctat cctatcatag ataacttct ccacagcctc acttcattcc 1440
acctattctc tgaatatatt ccctgagaga gaacagagag atttagataa gagaatgaaa 1500
ttccagcctt gactttcttc tgtgcacctg atgggagggt aatgtctaata gtattatcaa 1560
taacaataaa aataaagcaa ataccaaaaa 1590

```

```

<210> 22
<211> 1113
<212> DNA
<213> Homo sapiens

```

```

<400> 22
atggagaatc aggtgttgac gccgcattgt tactgggctc agcgacaccg cgagctatat 60
ctgcgcgtgg agctgagtga cgtacagaac cctgccatca gcatcactga aaacgtgctg 120
catttcaaag ctcaaggaca tggtgccaaa ggagacaatg tctatgaatt tcacctggag 180
ttcttagacc ttgtgaaacc agagcctggt taaaaactga cccagaggca ggtaaacatt 240
acagtacaga agaaagttag tcagtgttgg gagagactca caaagcagga aaagcgacca 300
ctgttttttg ctctgactt tgatcgttgg ctggatgaat ctgatgcgga aatggagctc 360
agagctaagg aagaagagcg cctaaataaa ctccgactgg aaagcgaagg ctctcctgaa 420
actcttacia acttaaggaa aggatacctg tttatgtata atcttgtgca attcttggga 480
ttctcctgga tctttgtcaa cctgactgtg cgattctgta tcttgggaaa agagtccttt 540
tatgacacat tccatactgt ggctgacatg atgtatttct gccagatgct ggcagttgtg 600
gaaactatca atgcagcaat tggagtcact acgtcaccgg tgctgccttc tctgatccag 660
cttcttggaa gaaattttat tttgtttatc atctttggca ccatggaaga aatgcagaac 720
aaagctgttg tttctttgt gttttatttg tggagtgcaa ttgaaatctt caggtactct 780
ttctacatgc tgacgtgcat tgacatggat tggaggtgc tcacatggct tcgttacact 840
ctgtggatc ccttatatcc actgggatgt ttggcggaag ctgtctcagt gattcagctc 900
attccaatat tcaatgagac cggacgatc agtttcacat tgccatatcc agtgaaaaac 960
aaagtttagat tttccttttt tcttcagatt tatcttataa tgatattttt aggtttatac 1020

```

ataaatatttc gtcaccttta taaacagcgc agactgaaaa tgagggcagg cgcagtggt 1080
catgcctgtg atcccagcgc tttgggaggc tga 1113

<210> 23
<211> 2385
<212> DNA
<213> Homo sapiens

<400> 23
aaaccctc cacttacta ccagacaacc ttagccaaac catttaccba aataaagtat 60
aggcgataga aattgaaacc tggcgcaata gatatagtag cgcaaggga agatgaaaaa 120
ttataaccaa gcataatata gcaaggacta acccctatac cttctgcata atgaattaac 180
tagaaataac tttgcaagga gagtcaaagc taaggccccc gaaaccaggc gagctaccta 240
agaacagcta aaagagcaca cccgtctatg tagcaaaata gtgggaagat ttataggtag 300
aggcgacaaa cctaccgagc ctggtgatag ctggttgccc aagatagaat cttagtccaa 360
ctttaaattt gccacagaa cctctaaat ccccttgtaa atttaactgt tagtccaaag 420
aggaacagct ctttgacac taggaaaaaa cttgttagag agagtgtcag cccaattcca 480
cacttttcca catgttggtt ggccttgagg tggtagccat aagcattttt ggaattcaac 540
taaaaactga aggatccttg aggacggcag tacctggcat acctacacag tcagcgttca 600
acaagtgttt gcaaaggtag attggggcac tgggggcacg agtgatctgt gacaatatcc 660
ctggtttggt gagccggcag cggcagctgt gccagcgtta cccagacatc atgcgttcag 720
tgggcgaggg tgcccagaa tggatccgag agtgtagca ccaattccgc caccaccgt 780
ggaactgtac caccctggac cgggaccaca ccgtctttg ccgtgtcatg ctcagaagta 840
gccgagaggg agcttttcta tatgccatct catcagcagg ggtgatccac gctattactc 900
gcgcctgtag ccagggtgaa ctgagtgtgt gcagctgtga cccctacacc cgtggccgac 960
accatgacca gcgtgggact tttgactggg gtggctgcag tgacaacatc cactacggtg 1020
tccgttttgc caaggccttc gtggatgcca aggagaagag gcttaaggat gcccgggccc 1080
tcataaactt acataataac cgctgtggtc gcacggctgt gcggcggttt gtcaagctgg 1140
agtgtaaagt ccatggcgtg agtggttcct gtactctgcg cacctgctgg cgtgcactct 1200
cagatttccg ccgcacaggt gattacctgc ggcgacgcta tgatggggct gtgcaggtga 1260
tggccaccca agatggtgcc aacttcaccg cagcccgcca aggctatcgc cgtgccaccc 1320
ggagtgtact tgtctacttt gacaactctc cagattactg tgtcttgagc aaggctgcag 1380
gttccctagg cactgcaggc cgtgtctgca gcaagacatc aaaaggaaca gacggttggtg 1440
aatcatgtg ctgtggccga gggtagcaca caactcgagt caccctgtgt acccagtggtg 1500
agtgcaaat ccactggtgc tgtgctgtac ggtgcaagga atgcagaaat actgtggacg 1560
tccatacttg caaagcccc aagaaggcag agtggctgga ccagacctga acacacagat 1620
acctactca tccctccaat tcaagcctct caactcaaaa gcacaagatc cttgcatgca 1680
caccttctc caccctccac cctgggctgc taccgcttct atttaaggat gtagagagta 1740
atccataggg accatggtgt cctggctggt tccttagccc tgggaaggag ttgtcagggg 1800
atataagaaa ctgtgcaagc tcctgattt cccgctctgg agatttgaag ggagagtaga 1860
agagataggg ggtctttaga gtgaaatgag ttgcactaaa gtacgtagtt gaggtcctt 1920
ttttcttcc tttgcaccag cttcccgaca cttcttggtg tgcaagagga agggtagctg 1980
tagagagctt ctttttgttt ctacctggcc aaagttagat gggacaaaga tgaatggcat 2040

gtcccttctc tgaagtcctg ttgagcagaa ctacctggtg ccccgaaaga aaaatcttag 2100
 gctaccacat tctattattg agagcctgag atgttagcca tagtggacaa ggttcattc 2160
 acatgctcat atgtttataa actgtgtttt gtagaagaaa aagaatcata acaatacaaa 2220
 cacacattca ttctctcttt ttctctctac cattctcaac ctgtattgga cagcactgcc 2280
 tcttttgctt acttgtctgc tgttcaaact gaggtggaat gcagtgggtc ccatgcttaa 2340
 cagatcatta aaacacccta gaacactcct aggatagatt aatgt 2385

<210> 24
 <211> 814
 <212> DNA
 <213> Homo sapiens

<400> 24
 cagctctgag cattcagcag attcaagatg aagctgaaca tctccttccc agccactggc 60
 tgccagaaac tcattgaagt ggacgatgaa cgcacacttc gtactttcta tgagaagcgt 120
 atggccacag aagttgtctg tgacgctctg ggtgaagaat ggaaggggta tgtggtccga 180
 atcagtgggtg ggaacgacaa acaagggttc cccatgaagc aggggtgtctt gacccatggc 240
 cgtgtccgcc tgctactgag taaggggcat tctgtttaca gaccaaggag aactggagaa 300
 agaaagagaa aatcagttcg tgggtgcatt gtggatgcaa atctgagcgt tctcaacttg 360
 gttattgtaa aaaaggaga gaaggatatt cctggactga ctgatactac agtgcctcgc 420
 cgctgtggcc ccaaaagagc tagcagaatc cgcaaagctt tcaatctctc taaagaagat 480
 gatgtccgcc agtatgttgt aagaaagccc ttaaataaag aaggaagaa acctaggacc 540
 aaagcaccga agattcagcg tcttgttact ccacgtgtcc tgcagacaa acggcggcgt 600
 attgctctga agcaacagcg taccaagaaa aataaagaag aggctgcaga atatgctaaa 660
 cttttggcca agagaatgaa ggaggctaag gagaagcgc aggaacaaat tgcgaagaga 720
 cgcagacttt cctctctcgc agcttctact tctaagctg aatccagtca gaaatagatt 780
 ttttgagtaa gaaataaata agatcagact ctga 814

<210> 25
 <211> 1434
 <212> DNA
 <213> Homo sapiens

<400> 25
 atgaagagtc ttccaatcct actgttgctg tgcgtggcag tttgctcagc ctatccattg 60
 gatggagctg caaggggtga ggacaccagc atgaaccttg ttcagaaata tctagaaaac 120
 tactacgacc tcgaaaaaga tgtgaaacag tttgttagga gaaaggacag tggtcctggt 180
 gttaaaaaaa tccgagaaat gcagaagttc cttggattgg aggtgacggg gaagctggac 240
 tccgacactc tggaggtgat gcgcaagccc aggtgtggag ttcctgacgt tggtcacttc 300
 agaacctttc ctggcatccc gaagtggagg aaaaccaccc ttacatacag gattgtgaat 360
 tatacaccag atttgccaaa agatgctgtt gattctgctg ttgagaaagc tctgaaagtc 420
 tgggaagagg tgactccact cacattctcc aggtgtgatg aaggagaggc tgatataatg 480
 atctcttttg cagttagaga acatggagac ttttaccctt ttgatggacc tggaaatgtt 540
 ttggccatg cctatgcccc tgggccaggg attaatggag atgccactt tgatgatgat 600
 gaacaatgga caaaggatc aacagggacc aatttatttc tcgttgctgc tcatgaaatt 660
 ggccactccc tgggtctctt tcaactcagc aacactgaag ctttgatgta cccactctat 720

cactcactca cagacctgac tcggttccgc ctgcttcaag atgataaaaa tggcattcag 780
 tccctctatg gacctcccc tgactccct gagaccccc tggtaaccac ggaacctgtc 840
 cctccagaac ctgggagcc agccaactgt gatcctgctt tgcctttga tgcgtcagc 900
 actctgaggg gagaaatcct gatctttaa gacaggcact ttggcgcaa atccctcagg 960
 aagcttgaac ctgaattgca ttgatctct tcattttggc catctcttcc ttcaggcgtg 1020
 gatgccgat atgaagtac tagcaaggac ctggttttca ttttaaagg aaatcaattc 1080
 tgggccatca gaggaatga ggtacgagct ggataccaa gaggcacca caccctaggt 1140
 tccccccaa ccgtgaggaa aatcgatgca gccatttctg ataaggaaaa gaacaaaaca 1200
 tatttctttg tagaggacaa atactggaga ttgatgaga agagaaattc catggagcca 1260
 ggctttccca agcaaatagc tgaagacttt ccagggattg actcaaagat tgatgctgtt 1320
 ttgaagaat ttgggttctt ttatttctt actggatctt cacagttgga gtttgacca 1380
 aatgcaaaga aagtgcaca cactttgaag agtaacagct ggcttaattg ttga 1434

<210> 26
 <211> 540
 <212> DNA
 <213> Homo sapiens

<400> 26
 cttttcgatc cgccatctgc ggtggagccg caaccaaatt gcagattttc gtgaaaaccc 60
 ttacggggaa gaccatcacc ctgaggttg aacctcga tacgatagaa aatgtaaagg 120
 ccaagatcca ggataaggaa ggaattctc ctgatcagca gagactgac tttgctggca 180
 agcagctaga agatggacgt actttgtctg actacaatat tcaaaaggag tctactctt 240
 atcttgtgtt gagacttctg ggtggtgcta agaaaaggaa gaagaagtct tacaccactc 300
 ccaagaagaa taagcacaag agaaagaagg ttaagctggc tgcctgaaa tattataagg 360
 tggatgagaa tggcaaaatt agtcgccttc gtcgagagt cccttctgat gaatgtggtg 420
 ctgggtgtt tatggcaagt cactttgaca gacattattg tggcaaatgt tgcctgactt 480
 actgtttcaa caaacagaa gacaagtaac tgtatgagtt aataaaagac atgaactaac 540

<210> 27
 <211> 2400
 <212> DNA
 <213> Homo sapiens

<400> 27
 taggatggaa aggcagatgt aaagtccctc atggcgaaat ataacacggg gggcaacccg 60
 acagaggatg tctcagtaa tagccgaccc ttcagagtca cagggccaaa ctcatcttca 120
 ggaatacaag caagaaagaa cttattcaac aaccaaggaa atgccagccc tcctgcagga 180
 cccagcaatg tacctaagtt tgggtccca aagccactg tggcagtcaa accttcttct 240
 gaggaaaagc ctgacaagga acccaagccc ccgtttctaa agccactgg agcaggccaa 300
 agattcgaa caccagccag cttgaccacc agagacccc aggcgaaagt gggatttctg 360
 aaacctgtag gcccgaagcc catcaacttg ccaaaagaag attccaaacc tacatttccc 420
 tggcctcctg gaaacaagcc atctcttcac agtgtaaacc aagaccatga cttaaagcca 480
 ctaggcccg aatctgggcc tactcctcca acctcagaaa atgaacagaa gcaagcgttt 540
 cccaaattga ctgggttaa agggaaattt atgtcagcat cacaagatct tgaaccaag 600
 cccctcttcc ccaaacccgc ctttgccag aagccgccc taagtaccga gaactcccat 660
 gaagacgaaa gccccatgaa gaatgtgtct tcataaaaag ggtcccagc tccctggga 720

gtcagggtcca aaagcgggccc tttaaaacca gcaaggggaag actcagaaaa taaagaccat 780
 gcagggggaga tttcaagttt gccctttcct ggagtgggtt tgaaacctgc tgcgagcagg 840
 ggaggcctag gtctctccaa aaatggtgaa gaaaaaaagg aagataggaa gatagatgct 900
 gctaagaaca ccttcagag caaaataaat caggaagagt tggcctcagg gactcctcct 960
 gccagggtcc ctaaggcccc ttctaagctg acagtggggg ggccatgggg ccaaagtcag 1020
 gaaaaggaaa agggagacaa gaattcagcc accccgaac agaagccatt gcctcccttg 1080
 tttacctggt gtccacctcc accaaaacc aacagaccac caaatgtga cctgacgaaa 1140
 ttccacaaaa cctcttctg aaacagtact agcaaaggcc agacgtctta ctcaacaact 1200
 tccctgccac cacctccacc atcccatccg gccagccaac caccattgcc agcatctcac 1260
 ccatcacaac caccagtccc aagcctacct ccagaaaca ttaacctcc gtttgacct 1320
 aaaagccctg tcaatgaaga caatcaagat ggtgtcacgc actctgatgg tgctggaaat 1380
 ctatagtagg aacaagacag tgaaggagaa acatatgaag acatagaagc atccaaagaa 1440
 agagagaaga aaagggaaaa ggaagaaaag aagaggttag agctggagaa aaaggaacag 1500
 aaagagaaag aaaagaaaga acaagaaata aagaagaaat ttaactaac aggccctatt 1560
 caagtcatcc atcttgcaaa agcttgttgt gatgtcaag gaggaagaa tgaactgagc 1620
 ttcaagcaag gagagcaaat tgaatcatc cgcatacag acaaccaga aggaaaatgg 1680
 ttgggcagaa cagcaagggg tcatatggc tatattaaa caactgctgt agagattgac 1740
 tatgattctt tgaactgaa aaaagactct cttggtgccc cttcaagacc tattgaagat 1800
 gaccaagaag tatatgatga tgttcagag caggatgata ttagcagcca cagtcagagt 1860
 ggaagtggag ggatattccc tccaccacca gatgatgaca tttatgatgg gattgaagag 1920
 gaagatgctg atgatgggtt cctgctcct cctaaacaat tggacatggg agatgaagtt 1980
 tacgatgatg tggatacctc tgatttcctt gtttcatcag cagagatgag tcaaggaact 2040
 aattttgaa aagctaagac agaagaaaag gaccttaaga agctaaaaaa gcaggaaaaa 2100
 gaagaaaaag acttcaggaa aaaatttaa tatgatggtg aaattagagt cctatattca 2160
 actaaagtta caacttccat aacttctaaa aagtggggaa ccagagatct acaggtaaaa 2220
 cctggtgaat ctctagaagt tatacaaacc acagatgaca caaaagtct ctgcagaaat 2280
 gaagaaggga aatatggtta tgtccttcgg agttacctag cggacaatga tggagagatc 2340
 tatgatgata ttgctgatg ctgcatctat gacaatgact agcactcaac tttggtcatt 2400

<210> 28
 <211> 794
 <212> DNA
 <213> Homo sapiens

<400> 28
 tagcggcagc ggctccggca gggctctgcgc gacggatgga agcggatagt gtctccgact 60
 ctctcagcct ctgcctccgc gtccgggcag cacgctcaag gccgggatgg cggcggcggc 120
 ggcggcagga agcgggacgc cccgagagga ggaggtacct gctggggagg cagcggcctc 180
 gcagccccag gcccacaaga gtgtgcctgg ggctcgtctc tcgaggttgc ctctggcgcg 240
 agtgaaggcc ttggtgaagg cagatccga cgtgacgcta gcgggacagg aagccatctt 300
 cattctggca cgagccgcgg aactgtttgt ggagaccatt gcaaaagatg cctactgttg 360
 cgctcagcag ggaaaaagga aaacccttca gaggagagac ttggataatg caatagaagc 420
 tgtggatgaa tttgcttttc tggaggtac tttagattga ttgccgagcg gggcagtttt 480

gtgagccttc atctgaagcc ttcagttcac ccctctgcac aggcctcagc tttgaagaac 540
 ggagtctttg cacttacaca cactcttcct gttctgcctt cacctatgcc gggataagca 600
 gagatctcat caattagctc ttctctgcaa ggtcttcac tatttctgtc tgtcttccat 660
 atcaagcctg gatgcagctg ctgctgctta gagcagagat gaagaaagtg ttctgcataa 720
 gtggcttcct gaatgatgag gaccagaata aagggttttg atcaacctca aaaaaaaaaa 780
 aaaaaaaaaa aaaa 794

<210> 29
 <211> 826
 <212> DNA
 <213> Homo sapiens

<400> 29
 cgggaaagat ggcagtgcac atatccaaga ggaggaagtt tgcgtctgat ggcattctca 60
 aagctgaact gaatgagttt ctactcggg agctggctga agatggctac tctggagttg 120
 aggtgcgagt tacaccaacc aggacagaaa tcattatctt agccaccaga acacagaatg 180
 ttcttgggtga gaagggcccg cggtatcggg aactgactgc tgtagttcag aagaggtttg 240
 gctttccaga gggcagtgtg gagctttatg ctgaaaaggt ggcactaga ggtctgtgtg 300
 ccattgccca ggcagagtct ctgcgttaca aactcctagg agggcttgct gtgcggaggg 360
 cctgctatgg tgtgctgcgg ttcattcatg agagtggggc caaagctgc gaggttctgg 420
 tgtctgggaa actccgagga cagagggcta aatccatgaa gtttctggat ggcctgatga 480
 tccacagcgg agacctgtt aactactacg ttgacctgc tgtgcgccac gtgttctca 540
 gacagggtgt gctgggcatc aaggtgaaga tcatgctgcc ctgggaccca actggaaga 600
 ttggccctaa gaagccctg cctgaccag tgagcattgt ggaacccaaa gatgagatac 660
 tgcccaccac ccccatctca gaacagaagg gtgggaagcc agagccgcct gccatgcccc 720
 agccagtccc cacagcataa caggtctctc ttggcagctg tattctggag tctggatgtt 780
 gctctctaaa gacctttaat aaaattttgt acaaggcgg gaattc 826

<210> 30
 <211> 721
 <212> DNA
 <213> Homo sapiens

<400> 30
 tcgagccagc gtcgccgca tgggtgtgtt ggagagcgag cagttcctga cggagctgac 60
 cagacttttc cagaagtgcc ggacgtcggg cagcgtctat atcaccttga agaagtatga 120
 cggctgaacc aaaccattc caaagaaagg tactgtggag ggctttgagc ccgcagacaa 180
 caagtgtctg ttaagagcta ccgatgggaa gaagaagatc agcactgttg tgagctccaa 240
 ggaagtgaat aagtttcaga tggcttattc aaacctcctt agagctaaca tggatgggtt 300
 gaagaagaga gacaaaaaga acaaaactaa gaagaccaa gcagcagcag cagcagcagc 360
 agcagcacct gccgcagcag caacagcagc aacaacagca gcaacaacag cagcaacagc 420
 agcacagtaa agggcataca ttctctgctt tcaccaatta accactgaat tgctattttt 480
 tccttttggc cagatagcta ggtttctggt tccccacag taggtgtttt cacataagat 540
 tagggctcct ttggaaagaa tagttgcagt gtttatagga tagttgtgtt aagaatctag 600
 ttatttttgc atttgctaa ttggtctgtg ctgcatggtt atatactcct ggattataga 660
 ttaaaagtct ctgtagacat ctctgtgaag agcaagctat cattaacat gtctgtttat 720

c

721

<210> 31
 <211> 2905
 <212> DNA
 <213> Homo sapiens

<400> 31
 tagcgattcc ctgcttgtct cgccgacccc ctgcgcctt ctgcagactc cgtggctggc 60
 gctcggcgcg tgaggaagca cggcggcccg agttcgcggg gaaggccgca gtcgcggagg 120
 cagcggcgcg gtccggggca cgggctgggg gagaggccgc tccgctgggc gaatgtgaca 180
 agccccacc cccaccgcct tcctcccag agcgcgagga gcgcgggcca ccccggggcc 240
 ccgccaggcc acagaccccg ccagcggcc agcaccggc gcaggcccg cagccgagct 300
 gcgcggcgcc accatgcagg tcaccctgaa gacctccag cagcagacct tcaagataga 360
 cattgacccc gaggagacgg tgaagcact gaaagagaag attgaatctg aaaaggggaa 420
 agatgccttt ccagtagcag gtcaaaaatt aatttatgca ggcaaatcc tcaatgatga 480
 tactgctctc aaagaatata aaattgatga gaaaaacttt gtggtggtta tggtagcaaa 540
 acccaaagca gtgtccacac cagcaccagc tacaactcag cagtcagctc ctgccagcac 600
 tacagcagtt acttctcca ccaccacaac tgtggctcag gtcacaacc ctgtccctgc 660
 cttggccccc acttccacac ctgcatccat cactccagca tcagcgacag catcttctga 720
 acctgcacct gctagtgcag ctaacaaga gaagcctgca gaaaagccag cagagacacc 780
 agtggctact agcccaacag caactgacag tacatcgggt gattcttctc ggtcaaacct 840
 ttttgaagat gcaacgagtg cacttgtagc gggtcagtct tacgagaata tggtaactga 900
 gatcatgtca atgggctatg aacgagagca agtaattgca gccctgagag ccagtttcaa 960
 caaccctgac agagcagtg agtatctttt aatgggaatc cctggagata gagaaagtca 1020
 ggcgtggtt gacccccctc aagcagctag tactggggct cctcagctct cagcagtgcc 1080
 tgcagctgca gcaactacga cagcaacaac tacaacaaca agttctggag gacatccct 1140
 tgaattttta cggaatcagc ctgagtttca acagatgaga caaattattc agcagaatcc 1200
 ttcttctgct ccagcgttac tacagcagat aggtcgagag aatcctcaat tacttcagca 1260
 aattagccaa caccaggagc attttattca gatgttaaat gaaccagttc aagaagctgg 1320
 tggtaagga ggaggagggt gaggtggcag tggagggaatt gcagaagctg gaagtggcca 1380
 tatgaactac attcaagtaa cacctcagga aaaagaagct atagaaaggt taaaggcatt 1440
 aggatttctt gaaggacttg tgatacaagc gtattttgct tgtgagaaga atgagaattt 1500
 ggctgccaat tttcttctac agcagaactt tgatgaagat tgaaggggac ttttttatat 1560
 ctcacacttc acaccagtgc attacactaa cttgttcact ggattgtctg ggatgacttg 1620
 ggctcatatc cacaataactt ggtataaggt agtagattgt tgggggtggg gagggaggga 1680
 tctaggatac agggcagggg taaatacagt gcatgtctgc ttcaattagc agatgccgca 1740
 actccacaca gtgtgtaaaa tatatacaac caaaaatcag cttttgcagg tctttatttc 1800
 ttctgtaaaa cagtaggtaa cttttcctag gtttctctt ttttagtgta ctgatccag 1860
 aaacttagtg taatgccctg ctttatatat ctttgactta acattggttt cagaaagaat 1920
 cttagctacc tagaatttac agtctctgtt tcatggcaac actggataat ggctttgtga 1980
 aatttaaaaa attttttag cgactgtaaa cagaaatgcc aaattgatgg ttaattgttg 2040
 ctgcttcaaa aataagtata aaattaatat gtaagggaagc ccattctttc atgttaata 2100

ctgggggtgg gaggggagaa aggggaacctt ttctctaaat gaaataaatt actgctattt 2160
 taaaatttct tgatcattga atgtgagacc ctctaacat gatttgagaa gctgtacaag 2220
 tataggcaga gttattttcc tgtttacatt tttttttgt ttgggggaaa aaattggtag 2280
 gtgtctaatt actgtttact tcattgttat attgcagtaa aagttttaaa acaaccattg 2340
 catgtttgct ttgtatgtat ccctttgtga aattagcact ttgggggcca atggagaaat 2400
 gcagcattca ctctccctgt cttttcccct tccctcagca gaaacgtgtt tatcagcaag 2460
 tcgtgagtca aactgctgcc ttttaaaaaa cccacaaaat gctgattcag ttcaaaatta 2520
 atgcaaatgt ttcaaaactg ggtttctgat atttgtaa atgtttcttt attagataag 2580
 agtgatttac cattaaagtc attagtataa tattgctttc aaaaagaaat ggtagacaaa 2640
 actataatcc agcatctttt attgcattgg aaagactggc aaagtctttt ggatgggttg 2700
 ggagatgtgg ctggaaagta ctttggaata tatacaatca agatatctca tggcatatta 2760
 aaagaaaaat cttaaatagca gtgttggtt ttatttggat tttttcatct cagttttttc 2820
 tgtggaatct ccttcattgg cattgttatt taatcataaa cggggcagat gtctacttgt 2880
 tcagtttttc aaatctgttt tcctg 2905

<210> 32
 <211> 3774
 <212> DNA
 <213> Homo sapiens

<400> 32
 ccgcccgtccc tgcgtccttc ggtctctgct cccgggaccc gggctccgcc gcagccagcc 60
 agcatgtcgg ggatcaagaa gcaaaagacg gagaaccagc agaaatccac caatgtagtc 120
 tatcaggccc accatgtgag caggaataag agagggaag tggttggaac aaggggtggg 180
 ttccgaggat gtaccgtgtg gctaacaggt ctctctggtg ctggaaaaac aacgataagt 240
 ttgcccctgg aggagtacct tgcctcccat gccatccctt gttactccct ggatggggac 300
 aatgtccgtc atggccttaa cagaaatctc ggattctctc ctggggacag agaggaaaat 360
 atccgcccga ttgctgaggt ggctaagctg ttgctgatg ctggctctgt ctgcattacc 420
 agctttatct ctccattcgc aaaggatcgt gagaatgccc gcaaaatata tgaatcagca 480
 gggctgccat tctttgaaat attttagat gcacctctaa atatttgtga aagcagagac 540
 gtaaaaggcc tctataaaaa ggccagagct ggggagatta aaggatttac aggtattgat 600
 tctgattatg agaaacctga aactcctgag cgtgtgctta aaaccaatct gtccacagtg 660
 agtgactgtg tccaccaggt agtggaaact ctgcaagagc agaacattgt accctatact 720
 ataatacaag atatccacga actctttgtg ccggaaaaca aacttgacca cgtccgagct 780
 gaggtgaaa ctctcccttc attatcaatt actaagctgg atctccagtg ggtccaggtt 840
 ttgagcgaag gctgggccac tcccctcaaa ggtttcatgc gggagaagga gtacttacag 900
 gttatgcact ttgacaccct gctagatgat ggcgtgatca acatgagcat ccccatgtga 960
 ctgcccgtct ctgcagagga taagacacgg ctggaagggt gcagcaagtt tgcctggca 1020
 catggtggac ggagggtagc tatcttacga gacgctgaat tctatgaaca cagaaaagag 1080
 gaacgtgtt cccgtgtttg ggggacaaca tgtacaaaac acccccatat caaatggtg 1140
 atggaaagtg gggactggct ggttgggtga gaccttcagg tgcaggagaa aataagatgg 1200
 aatgatgggc tggaccaata ccgtctgaca cctctggagc tcaaacagaa atgtaaagaa 1260
 atgaatgctg atgcggtgtt tgcattccag ttgcgcaatc ctgtccacaa tggccatgcc 1320

ctgttgatgc aggacactcg ccgcaggctc ctggggggg gctacggcg cccggcctc 1380
ctactacacc ctctggggcg ctggaccaag gatgacgatg tgcctctaga ctggcggatg 1440
aagcagcacg cggctgtgct cgaggaaggg gtcctggatc ccaagtcaac cattgttgcc 1500
atctttccgt ctccccgtt atatgctggc cccacagagg tccagtggca ctgcaggctc 1560
cggatgattg cgggtgcaa tttctacatt gtggggaggg accctgcagg aatgccccat 1620
cctgaaacca agaagatct gtatgaacc actcatggg gcaaggtctt gagcatggc 1680
cctggcctca cctctgtga aatcattcca tccgagtgg ctgcctacaa caaagccaaa 1740
aaagccatgg acttctatga tctagcaagg cacaatgagt ttgacttcat ctcaggaact 1800
cgaatgagga agctcgccc ggaaggagag aatccccag atggcttcat ggccccaaa 1860
gcattggaag tcctgacaga ttattacagg tccctggaga agaactaagc ctttggctcc 1920
agagtttctt tctgaagtgc tctttgatta cttttctat ttttatgatt agatgctttg 1980
tattaaattg ctctctcaat gatgcatttt aacttttata atgaagtaa agttgtgtct 2040
ataattaa aaaatatat atatatacac acacacatat acatacaaag tcaaactgaa 2100
gaccaaatct tagcaggtaa aagcaatatt cttatacatt tcataataaa attagctcta 2160
tgtattttct actgcacctg agcaggcagg tccagattt cttaaggctt tgtttgacca 2220
tgtgtctagt tacttgctga aaagtgaata tttttccag catgtcttga caacctgtac 2280
tcttccaatg tcatttatca gttgtaaaat atatcagatt gtgtcctctt ctgtacaatt 2340
gacaaaaaaa aatttttttt tctcactcta aaagaggtgt ggctcacatc aagattcttc 2400
ctgatatttt acctcatgct gtacaagcct taatgtgtaa tcatatctta cgtgttgaag 2460
acctgactgg agaacaataa tgtgcaataa cgtgaatttt atcttagaga tctgtgcagc 2520
ctagatttta cctcatgctg tacaagcct taatgttga atcatatctt acgtgttgag 2580
acctgactgg agaacaataa tgtgcaataa cgtgaatttt atcttagaga tctgtgcagc 2640
ctattttctg tcacaaaagt tatattgtct aataagagaa gtcttaatgg cctctgtgaa 2700
taatgtaact cagttacacg gtgactttta atagcataca gtgattgat gaaaggacgt 2760
caaacaatgt ggcgatgtcg tggaaagtta tctttccgc tctttgctgt ggtcattgtg 2820
tcttgcagaa aggatggccc tgatgcagca gcagcgccag ctgtaataaa aaataattca 2880
cactatcaga ctagcaaggc actagaactg gaaaagacca cagaaaacaa agaatccaac 2940
cctttcatct tacagggtga caaactgtga tgatgcacat gtatgtgttt tgaagctgt 3000
gagcaccgta acaaatgta aatttgccat tattaggaaa gtgctggtgg cagtgaagaa 3060
gcaccaggc cacttgactc ccagtctggt gcctgtcta caccagacaa cacaggagct 3120
gggtcagatt cccctcagct gcttaacaaa gttcctcga cagaaagtgc ttacaaagct 3180
gccttctcgg atactgaaag gtcgagtttt ctgaactgca ctgattttat tgcagttgaa 3240
aaacccaaag ctattccaaa gatttcaagc tgttctgaga catcttctga tggctttact 3300
tcttgagagg caatgttttt actttatgca taattcattg ttgccaagga ataaagtga 3360
gaaacagcac ctttttaata tataggctc tctggaagag acctaaattt agaaagagaa 3420
aactgtgaca atttcatat tctcattctt aaaaaacact aatcttaact aacaaaagtt 3480
cttttgagaa taagtacac acaatggcca cagcagttt tctttaatag tatagtgcct 3540
atactcatgt aatcggttac tcaactactg ctttaaaaaa aaccagcata tttattgaaa 3600
acatgagaca ggattatagt gccttaaccg atatattttg tgacttaaaa aatacattta 3660
aaactgctct tctgctctag taccatgctt agtgcaaatg attatttcta tgtacaactg 3720

atgcttgttc ttattttaat aaatttatca gagtgaaaaa aaaaaaaaaa aaaa 3774

<210> 33
 <211> 3614
 <212> DNA
 <213> Homo sapiens

<400> 33
 gtccgccaaa acctgcgcgg ataggggaaga acagcacccc ggcgccgatt gccgtaccaa 60
 acaagcctaa cgtccgctgg gccccggacg ccgcgcggaa aagatgaatt tacaaccaat 120
 tttctggatt ggactgatca gttcagtttg ctgtgtgttt gctcaaacag atgaaaatag 180
 atgtttaaaa gcaaatgcc aatcatgtgg agaattgata caagcagggc caaattgtgg 240
 gtggtgcaca aattcaacat ttttacagga aggaatgcct acttctgcac gatgtgatga 300
 tttagaagcc ttaaaaaaga aggggtgccc tccagatgac atagaaaatc ccagaggctc 360
 caaagatata aagaaaaata aaaatgtaac caaccgtagc aaaggaacag cagagaagct 420
 caagccagag gatattcatc agatccaacc acagcagttg gttttgcgat taagatcagg 480
 ggagccacag acatttcat taaaattcaa gagagctgaa gactatccca ttgacctcta 540
 ctaccttatg gacctgtctt attcaatgaa agacgatttg gagaatgtaa aaagtcttgg 600
 aacagatctg atgaatgaaa tgaggaggat tacttcggac ttcagaattg gatttggtctc 660
 atttgtggaa aagactgtga tgccttcat tagcacaaca ccagctaagc tcaggaaccc 720
 ttgcacaagt gaacagaact gcaccacccc atttagctac aaaaatgtgc tcagctttac 780
 taataaagga gaagtattta atgaacttgt tggaaaacag cgcatatctg gaaatttgga 840
 ttctccagaa ggtggtttcg atgccatcat gcaagttgca gtttgtggat cactgattgg 900
 ctggaggaa gttacacggc tgctgggtgt ttccacagat gccgggttct actttgctgg 960
 agatgggaaa cttggtggca ttgttttacc aaatgatgga caatgtcacc tggaaaataa 1020
 tatgtacaca atgagccatt attatgatta tccttctatt gctcaccttg tccagaaact 1080
 gagtgaanaa aatattcaga caatttttgc agttactgaa gaatttcagc ctgtttacaa 1140
 ggagctgaaa aacttgatcc ctaagtcagc agtaggaaca ttatctgcaa attctagcaa 1200
 tgtaattcag ttgatcattg atgcatacaa tccctttcc tcagaagtca ttttgaaaaa 1260
 cggcaaatg tcagaaggag taacaataag ttacaaatct tactgcaaga acgggggtgaa 1320
 tggacagagg gaaaatggaa gaaaatgttc caatatttcc attggagatg aggttcaatt 1380
 tgaaattagc ataacttcaa ataagtgccc aaaaaggat tctgacagct ttaaaattag 1440
 gcctctgggc tttacggagg aagtagaggt tattcttcag tacatctgtg aatgtgaatg 1500
 ccaaagcgaa ggcattccctg aaagtcctaa gtgtcatgaa ggaatggga catttgatg 1560
 tggcgcgtgc aggtgcaatg aagggcgtgt tggtagacat tgtgaatgca gcacagatga 1620
 agttaacagt gaagacatgg atgcttactg caggaaagaa aacagttcag aaatctgcag 1680
 taacaatgga gagtgcgtct gcggacagtg tgtttgtagg aagagggata atacaaatga 1740
 aatttattct ggcaatttct gcgagtgtga taatttcaac tgtgatagat ccaatggctt 1800
 aatttggtga ggaatgggtg tttgcaatg tcgtgtgtgt gagtgaacc ccaactacac 1860
 tggcagtga tgtactgtt ctttggtatc tagtacttgt gaagccagca acggacagat 1920
 ctgcaatggc cggggcatct gcgagtgtgg tgtctgtaag tgtacagatc cgaagtttca 1980
 agggcaaacg tgtgagatgt gtcagacctg ccttggtgtc tgtgctgagc ataaagaatg 2040
 tgttcagtgc agagccttca ataaaggaga aaagaaagac acatgcacac aggaatgttc 2100

```

ctattttaac attaccaagg tagaaagtcg ggacaaatta cccagccgg tccaacctga 2160
tcctgtgtcc cattgtaagg agaaggatgt tgacgactgt tggttctatt ttacgtattc 2220
agtgaatggg aacaacgagg tcatggttca tgtgtggag aatccagagt gtcccactgg 2280
tccagacatc attccaattg tagctggtgt ggttgctgga attgttctta ttggccttgc 2340
attactgctg atatggaagc ttttaatgat aattcatgac agaagggagt ttgctaaatt 2400
tgaaaaggag aaaatgaatg ccaaatggga cacgggtgaa aatcctatct ataagagtgc 2460
cgtaacaact gtggtcaatc cgaagtatga gggaaaatga gtactgccg tgcaaatccc 2520
acaacactga atgcaaagta gcaatttcca tagtcacagt taggtagctt tagggcaata 2580
ttgccatggt ttactcatg tgcaggtttt gaaaatgtac aatatgtata atttttaaaa 2640
tgttttatta ttttgaat aatgtttaa ttcattccag ggactgacaa aagacttgag 2700
acaggatggt tattcttctg agctaaggtc acattgtgcc ttttgacct tttcttctg 2760
gactattgaa atcaagctta ttgattaag tgatatttct atagcgattg aaagggcaat 2820
agttaaagta atgagcatga tgagagtctt tgtaaatcat gtattaaaac tgatttttag 2880
ctttacatat gtcagtttgc agttatgcag aatccaaagt aatgtcctg ctactagtt 2940
aaggattggt ttaaatctgt tattttgcta tttgcctgtt agacatgact gatgacatat 3000
ctgaaagaca agtatgtga gagttgctg tgtaaaatac gttgaaata gttgatctac 3060
aaaggccatg ggaataatc agagagttag gaaggaaaaa ccaatagctt taaaacctgt 3120
gtgccatttt aagagttact taatgtttg taacttttat gccttcactt tacaattca 3180
agccttagat aaaagaaccg agcaatttct tgctaaaag tccttgattt agcactattt 3240
acatacagcg cactcttacc aaagtatttg ctgaatggg accttttgag ttgaatttat 3300
tttattattt ttattttgtt taatgtctg tgctttctat cacctcttct aatcttttaa 3360
tgtattgtt tgcaatttg gggtaagact ttttatgag tacttttct ttgaagtttt 3420
agcgggtcaat ttgcctttt aatgaacatg tgaagttata ctgtggctat gcaacagctc 3480
tcacctacgc gagtcttact ttgagttagt gccataacag accactgtat gtttacttct 3540
caccatttga gttgccatc ttgtttcaca ctactcacat tcttgtttta agtgccctta 3600
gttttaacag ttca 3614

```

```

<210> 34
<211> 2701
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)..(2701)
<223> n=A,T,C, or G

```

```

<400> 34
actggcggtg gcctacggtg agcggcctgg ccggagcgcg agagtggag gtggtggcgt 60
tcgtctctcc taggggctgt cgggagctca gcgnggaccg agcctgggag gccggcgggt 120
gccagcacct ttcggcttct gagacggcgg cacagcggca ttcaggttct aaatggcttc 180
taagaagttg ggtgcagatt ttcattggac tttcagttac cttgatgatg tccatttaa 240
gacaggagac aaattcaaaa caccagctaa agttggctta cctattggct tctccttgcc 300
tgattgtttg caggttgta gagaagtaca gtatgacttc tctttggaaa agaaaacat 360
tgagtgggct gaagagatta agaaaatcga agaagccgag cggaagcag agtgcaaaat 420

```

```

tgcggaagca gaagctaaag tgaattctaa gagtggccca gagggcgata gcaaaatgag 480
cttctccaag actcacagta cagccacaat gccacctcct attaacccca tcctcgccag 540
cttgacgac aacagcatcc tcacaccaac tcgggtcagc agtagtgcca cgaaacagaa 600
agttctcagc ccacctcaca taaaggcgga tttcaatctt gctgactttg agtgtgaaga 660
agaccattt gataatctgg agttaaaac tattgatgag aaggaagagc tgagaaatat 720
tctggtagga accactggac ccattatggc tcagttattg gacaataact tgcccagggg 780
aggctctggg tctgtgttac aggatgagga ggtcctggca tccttggaac gggcaaccct 840
agatttcaag cctcttcata aaccctaatg ctttataacc ttaccacagt tgggcaactg 900
tgaaaagatg tcaactgtctt ccaaagtgtc cctccccctt atacctgcag taagcaatat 960
caaatccctg tctttccca aacttgactc tgatgacagc aatcagaaga cagccaagct 1020
ggcgagcact ttccatagca catcctgcct ccgcaatggc acgttcaga attccctaaa 1080
gccttcacc caaagcagtg ccagtgaagt caatgggcat cacactcttg ggctttcagc 1140
tttgaacttg gacagtggca cagagatgcc agcctgaca tcctccaga tgccttcctt 1200
ctctgttttg tctgtgtgca cagaggaatc atcacctcca aatactggc ccacggtcac 1260
ccctcctaat ttctcagtg cacaagtgcc caacatgcc agctgtccc aggcctattc 1320
tgaactgcag atgctgtccc ccagcgagcg gcagtgtgtg gagacggtgg tcaacatggg 1380
ctactcgtac gagtgtgtcc tcagagccat gaagaagaaa ggagagaata ttgagcagat 1440
tctcgactat ctctttgcac atggacagct ttgtgagaag ggcttcgacc ctcttttagt 1500
ggaagaggct ctggaatgc accagtgttc agaagaaaag atgatggagt ttcttcagtt 1560
aatgagcaaa tttaaggaga tgggctttga gctgaaagac attaggaag ttttgctatt 1620
acacaacaat gaccaggaca atgctttgga agacctcatg gctcgggcag gagccagctg 1680
agaccaggcc ctgcctaggc cctgccgag aaccaccatc cctgggaggc cctgcagagc 1740
ccacctgtgg ggaagagaa ggggcagctt ccggattttc ttttgggggt tagaaggta 1800
ggtgtggaga ctgctcgcca gtctctgtga gcctaggccc tgagctggg aggtggggaa 1860
gattcgggca tgtgagtgcc ccagaaactg tcctggctcc ttcctgatta aacgcatttg 1920
cattttgaga agtgtccttc ccacttcagc cctccggaga gactacccta gtctttcttg 1980
ggtgtttatg tcctcagctg aagcctggcc tagttgtga gaggggctgg ggagatggg 2040
cgggagggcc agactcagtg ctgctgtgga gctagggtgt tcccccttc cctgagactg 2100
gttgactgaa ctccagtaaa gttgagttca agtgaaagat tcttcaggg ttttattttt 2160
tccccctcta acaaagtctc atagtgttaa cactggttct gcaatatctc tgagggtcaa 2220
agaatgcact tttccctatg gggcccagag tttgccttt ctgccaggca gtcaccacgc 2280
ttccctaccc cagcctgttt cttttggctt ggtttggacc acagtcctct gctaccagg 2340
gttttagagc ccctgtctta ggaacagtt taagaaatca ttggccctt cccagcacat 2400
tgaatgggta agcagacagg ccatgattta gttggccagc actaactcca cctctgttct 2460
ccttgaacag ctccccctcc agcccactgc tttaggatga cacaatgaat aacacctagt 2520
catagaaatc agtctctctg gtttgtttt tattatgttg tacatcatta aagatctaaa 2580
tacaaaggat atacagtctt gaatctaaaa taatttgcta actattttga ttcttcagag 2640
agaactacta ataaaaatct aaaaggtaaa aaaaaaaaa aaaaaaaaaa 2700
a 2701

```

<210> 35
 <211> 2318
 <212> DNA
 <213> Homo sapiens

<400> 35
 gccacgaagg ccacagacgc cttccccctt ggactctcat tcccttttcc acggagcccc 60
 gcgctttcgt gagccccctc gaggaacctg gtctccgcat ccagttacca cctcctgcct 120
 cagaggccat ctgagccctt cgcacctcgc ccctcagtc ccccttgccc ccccgcgag 180
 atcgctcgc tccctccgc cccccatca tcccttcct cgcagttccc ctgtcctgag 240
 gggagccccg ccacggcagc gacagcgggc aggaggaga aagtgaaggt tgggcgacac 300
 ttggcctcac tcccggtag gcgcacccac ggggaggaga ggaggagccg agagagctga 360
 gcagcgcgga agtagctgct gctggtggtg acaatgtcaa ataacggcct agacattcaa 420
 gacaaacccc cagcccctcc gatgagaaat accagcacta tgattggagt cggcagcaaa 480
 gatgctgaa ccctaaacca tggttctaaa cctctgcctc caaacccaga ggagaagaaa 540
 aagaaggacc gattttaccg atccatttta cctggagata aaacaaataa aaagaaagag 600
 aaagagcggc cagagatttc tctcccttca gattttgaac acacaattca tgtcggtttt 660
 gatgctgtca caggggagtt tacgggaatg ccagagcagt gggcccgctt gcttcagaca 720
 tcaaatatca ctaagtcgga gcagaagaaa aaccgcagg ctgttctgga tgtgttgag 780
 ttttacaact cgaagaagac atccaacagc cagaaatata tgagctttac agataagtca 840
 gctgaggatt acaattcttc taatgccttg aatgtgaagg ctgtgtctga gactcctgca 900
 gtgccaccag tttcagaaga tgaggatgat gatgatgat atgctacccc accaccagt 960
 attgctccac gccagagca caaaaatct gtatacacac ggtctgtgat tgaaccactt 1020
 cctgtcactc caactcggga cgtggctaca tctccattt cacctactga aaataacacc 1080
 actccaccag atgctttgac ccggaatact gagaagcaga agaagaagcc taaaaatgtct 1140
 gatgaggaga tcttgagaa attacgaagc atagttagtg tggcgcatcc taagaagaaa 1200
 tatacacggt ttgagaagat tggacaagggt gcttcaggca ccgtgtacac agcaatggat 1260
 gtggccacag gacaggaggt ggccattaag cagatgaatc ttcagcagca gcccaagaaa 1320
 gagctgatta ttaatgagat cctggctatg agggaaaaca agaaccctaa cattgtgaat 1380
 tacttgaca gttacctcgt gggagatgag ctgtgggttg ttatggaata cttggctgga 1440
 ggctccttga cagatgtggt gacagaaact tgcattgag aaggccaaat tgcagctgtg 1500
 tgccgtgagt gtctgcaggc tctggagttc ttgcattcga accaggtcat tcacagagac 1560
 atcaagagt acaatattct gttgggaatg gatggctctg tcaagctaac tgactttgga 1620
 ttctgtgcac agataacccc agagcagagc aaacggagca ccatggtagg aaccctatc 1680
 tggatggcac cagaggttgt gacacgaaag gcctatgggc ccaaggttga catctggtcc 1740
 ctgggcatca tggccatcga aatgattgaa ggggagcctc catacctcaa tgaaaacct 1800
 ctgagagcct tgtacctcat tgccaccaat gggaccccag aacttcagaa cccagagaag 1860
 ctgtcagcta tcttcggga ctttctgaac cgctgtctcg atatggatgt ggagaagaga 1920
 ggttcagcta aagagctgct acagcatcaa ttcctgaaga ttgccaagcc cctctccagc 1980
 ctactccac tgattgtgc agctaaggag gcaacaaaga acaatcacta aaaccacact 2040
 caccacagcc tcattgtgcc aagctctgtg agataaatgc acatttcaga aattccaact 2100
 cctgatgccc tcttctcctt gccttgcttc tccatttcc tgatctagca ctctcaaga 2160

ctttgatcct tggaaaccgt gtgtccagca ttgaaagaaa cctgaaacaa atgaaacatc 2220
 agatgatggc catttctaaa taaggaattt cctcccaatt catggatatg aggggtggtt 2280
 atgattaagg gtttatataa ataaatgttt ctagtcctt 2318

<210> 36
 <211> 4264
 <212> DNA
 <213> Homo sapiens

<400> 36
 atttcccgcc agcaggagcc gcgcggtaga tgcggtgctt ttaggagctc cgtccgacag 60
 aacggttggg ccttgccggc tgtcggtagt tcgcgacaga gcaccctgta cagcttcttc 120
 cccaagtctc cggcgctgag tgatgccaac aaggcctcgg ccagggcctc acgcgaaggc 180
 ggccgtgccg ccgctgcccc cggggcctct cctccccag gcggggatgc ggccctggagc 240
 gaggtgggc ctgggcccag gcccttgccg cgatccgctt caccgcccac ggcaagaac 300
 ctcaacggag ggctgcggag atcggtagcg cctgctgccc ccaccagtgt tgacttctca 360
 ccaggagatt tggtttggc caagatggag ggttaccctt ggtggccttg tctggtttac 420
 aaccaccctt ttgatggaac attcatccgc gagaaggga aatcagtcctg tgttcagtga 480
 cagttttttg atgacagccc aacaaggggc tgggttagca aaaggctttt aaagccatat 540
 acaggttcaa aatcaaagga agcccagaag ggaggtcatt ttacagtgc aaagcctgaa 600
 atactgagag caatgcaacg tgcagatgaa gccttaata aagacaagat taagaggctt 660
 gaattggcag tttgtgatga gccctcagag ccagaagagg aagaagagat ggaggtaggc 720
 acaacttacg taacagataa gagtgaagaa gataatgaaa ttgagagtga agaggaagta 780
 cagcctaaga cacaaggatc taggcgaagt agccgcaaaa taaaaaacg aagggtcata 840
 tcagattctg agagtacat tgggtgctct gatgtggaat ttaagccaga cactaaggag 900
 gaaggaagca gtgatgaaat aagcagtgga gtgggggata gtgagagtga aggcctgaac 960
 agccctgtca aagttgctcg aaagcggag agaatgtga ctggaaatgg ctctcttaaa 1020
 aggaaaagct ctaggaaagga aacgccctca gccaccaaac aagcaactag catttcatca 1080
 gaaaccaaga atactttgag agctttctct gccctcaaaa attctgaatc ccaagcccac 1140
 gttagtggag gtggtgatga cagtgtgcgc cctactgttt ggtatcatga aactttagaa 1200
 tggcttaagg aggaaaagag aagagatgag cacaggagga ggccctgatca ccccgatttt 1260
 gatgcactca cactctatgt gcctgaggat ttctcaatt cttgtactcc tgggatgagg 1320
 aagtgggtgc agattaagtc tcagaacttt gatctgtca tctgttaca ggtggggaaa 1380
 ttttatgagc tgtaccacat ggatgctctt attggagtca gtgaactggg gctgggtattc 1440
 atgaaaggca actgggcccac ttctggcttt cctgaaattg catttgcccg ttattcagat 1500
 tccctgtgac agaagggcta taaagtagca cgagtggaac agactgagac tccagaaatg 1560
 atggaggcac gatgtagaaa gatggcacat atatccaagt atgatataggt ggtgaggagg 1620
 gagatctgta ggatcattac caagggtaca cagacttaca gtgtgctgga aggtgatccc 1680
 tctgagaact acagtaagta tcttcttagc ctcaaagaaa aagaggaaga ttcttctggc 1740
 catactcgtg catatggtgt gtgctttgtt gatacttcac tgggaaagtt tttcataggt 1800
 cagttttcag atgatcgcca ttgttcgaga tttaggactc tagtggcaca ctatccccc 1860
 gtacaagttt tatttgaaaa aggaaatctc tcaaaggaaa ctaaaacaat tctaaagagt 1920
 tcattgtcct gttctcttca ggaaggctcg ataccggct cccagttttg ggatgcatcc 1980

```

aaaactttga gaactctcct tgaggaagaa tatctctggg 2040
ggggtgatgt taccacaggt gcttaaaggt atgacttcag agtctgattc cattgggttg 2100
acaccaggag agaaaagtga attggccctc tctgctctag gtggttggtg cttctacctc 2160
aaaaaatgcc ttattgatca ggagctttta tcaatggcta attttgaaga atatattccc 2220
ttggattctg acacagtcag cactacaaga tctggtgcta tcttcaccaa agcctatcaa 2280
cgaatggtgc tagatgcagt gacattaaac aacttggaaga tttttctgaa tggaacaaat 2340
ggttctactg aaggaaccct actagagagg gttgatactt gccatactcc ttttggttaag 2400
cggctcctaa agcaatggct ttgtgcccc aactgtaacc attatgctat taatgatcgt 2460
ctagatgcca tagaagacct catggttggt cctgacaaaa tctccgaagt ttagagctt 2520
ctaaagaagc ttccagatct tgagaggcta ctcaagtaaa ttcataatgt tgggtctccc 2580
ctgaagagtc agaaccaccc agacagcagg gctataatgt atgaagaaac tacatacagc 2640
aagaagaaga ttattgattt tctttctgct ctggaaggat tcaaagtaat gtgtaaaatt 2700
atagggatca tggaagaagt tgctgatggt ttaagtcta aaatccttaa gcaggtcac 2760
tctctgcaga caaaaaatcc tgaaggtcgt tttcctgatt tgactgtaga attgaaccga 2820
tgggatacag cctttgacca tgaagaggtc cgaagactg gacttattac tcccaaagca 2880
ggctttgact ctgattatga ccaagctctt gctgacataa gagaaatga acagagcctc 2940
ctggaatacc tagagaaca gcgcaacaga attggctgta ggaccatagt ctattggggg 3000
attggttaga accgttacca gctggaatt cctgagaatt tcaccactcg caatttgcca 3060
gaagaatacg agttgaaatc taccaagaag ggctgtaaac gatactggac caaaactatt 3120
gaaaagaagt tggctaactc cataaatgct gaagaacgga gggatgtatc attgaaggac 3180
tgcatcgccg gactgttcta taactttgat aaaaattaca aggactggca gctctgctga 3240
gagtgtatcg cagtgttga tgttttactg tgcctggcta actatagtcg agggggtgat 3300
ggtcctatgt gtcgccagc aattctgttg ccggaagata cccccccctt cttagagctt 3360
aaaggatcac gccatccttg cattacgaag actttttttg gagatgattt tattcctaatt 3420
gacattctaa taggctgtga ggaagaggag caggaaaatg gcaaagccta ttgtgtgctt 3480
gttactggac caaatatggg gggcaagtct acgcttatga gacaggctgg cttattagct 3540
gtaatggccc agatgggttg ttacgtccct gctgaagtgt gcaggctcac accaattgat 3600
agagtgttta ctgacttggt tgcctcagac agaataatgt cagggtgaaag tacatttttt 3660
gttgaattaa gtgaaactgc cagcatactc atgcatgcaa cagcacattc tctggtgctt 3720
gtggatgaat taggaagagg tactgcaaca tttgatggga cggcaatagc aaatgcagtt 3780
gttaaagaac ttgctgagac tataaatgt cgtacattat ttcaactca ctaccattca 3840
ttagtagaag attattctca aaatgttgct gtgcgcctag gacatatggc atgcatggta 3900
gaaaatgaat gtgaagacc cagccaggag actattacgt tcctctataa attcattaag 3960
ggagcttgtc ctaaaagcta tggctttaat gcagcaaggc ttgctaactc cccagaggaa 4020
gttattcaaa agggacatag aaaagcaaga gaatttgaga agatgaatca gtcactacga 4080
ttatttcggg aagtttgctt ggctagtga aggtcaactg tagatgctga agctgtccat 4140
aaattgctga ctttgattaa ggaattatag actgactaca ttggaagctt tgagttgact 4200
tctgaccaa ggtggttaaat tcagacaaca ttatgatcta ataaacttta ttttttaaaa 4260
atga 4264

```

<210> 37
 <211> 2106
 <212> DNA
 <213> Homo sapiens

<400> 37
 gtatacgaaa tcataaaatc tcatagatgt atcctgagta gggcggggcc cgtgaaaccc 60
 tctgaatctg cggccaccac ccggttaaggc taaatactaa tcagacaccg atagtgaact 120
 agtaccgtga gggaaagggtg aaaagaaccc gagaggggag tgaatagat tctgaaacca 180
 ttactttaca agtgggtccat ttactttaca gtgtcagagc acgttaaagt gtgatggcgt 240
 acatcttgca gtatgggccc gcgagttatg ttaatatgca aggttaagca gaaaaagcg 300
 gagccgtagg gaaaccgagt ctgaataggc cgactttagt atattggcat ataccgaaa 360
 tcagggtatc tatccatgag caggttgaag cttaggtaaa actaagtga ggaccgaacc 420
 gtagtacgt aaaaagtgcc cggatggact tgtggatagt ggtgaaattc caatcgaacc 480
 tggagatagc tggttctctt cgaaatagct ttagggctag cgtatagtat tgtttaatgg 540
 gggtagagca ctgaatgtgg aatggcggca tctagctgta ctgactataa tcaaaactccg 600
 aataccatta aaattaagct atgcagtcgg aacgtggtat caccattgat atctccttgt 660
 ggaaatttga gaccagcaag tactatgtga ctatcattga tgccccagga cacagagact 720
 ttatccaaaa catgattaca gggacctctc aggctgactg tgcgtcctg attgttctg 780
 ctggtgttgg tgaatttgaa gctggtatct ccaagaatgg gcagaccgga gagcatgcc 840
 ttctggctta cacactgggt gtgaaacaac taattgtcgg tgttaacaaa atggattcca 900
 ctgagccacc ctacagccag aagagatatg aggaaattgt taaggaagtc agcacttaca 960
 ttaagaaaat tggctacaac cccgacacag tagcatttgt gccaatcttct ggttggaaatg 1020
 gtgacaacat gctggagcca agtgctaaca tgccttggtt caagggatgg aaagtcaccc 1080
 gtaaggatgg caatgccagt ggaaccacgc tgcttgaggc tctggactgc atcctaccac 1140
 caactcgtcc aactgacaag cccttggggc tgcctctcca ggtgtctac aaaattggtg 1200
 gtattgttac tgttcctgtt ggccgagtg agactggtgt tctcaaacc ggatgtgtg 1260
 tcaccttttg tccagtcaac gttacaacgg aagtaaaatc tgcgaaatg caccatgaag 1320
 ctttgggtga agctcttctt ggggacaatg tgggttcaa tgtcaagaat gtgtctgtca 1380
 aggatgttcg tctgggaac gttgctggtg acagcaaaaa tgaccacca atggaagcag 1440
 ctggcttccc tgcctcagtg attatcctga accatccagg ccaataaagc gccggctatg 1500
 cccctgtatt ggattgccac acggctcaca ttgcatgcaa gtttctgag ctgaaggaaa 1560
 agattgatcg ccgttctggt aaaaagctgg aagatggccc taaattcttg aagtctggtg 1620
 atgctgccat tgttgatag gtctctggca agcccatgtg tgttgagagc ttctcagact 1680
 atccaccttt gggctgcttt gctgttcgtg atatgagaca gacagttgag gtgggtgtca 1740
 tcaaagcagt ggacaagaag gctgctggag ctggcaaggc caccaagtct gccagaaaag 1800
 ctcaagaaggc taaatgaata ttatccctaa tctcccacc ccactcttaa tcagtgtgtg 1860
 aagaccggtc tcagaactgt ttgtttcaat tgccatttaa gtttagtagt aaaagactgg 1920
 ttaatgataa caatgcatcg taaaaccttt cagaaggaaa ggagaatgtt ttgtggacac 1980
 gttggttttc ttttttgcgt gtggcagttt tagttattag tttttaaaat cagtactttt 2040
 taatggaaac aacttgaccc ccaaatgtgt cacagaattt tgggacccat taaaaggtta 2100
 actggg 2106

<210> 38
 <211> 1272
 <212> DNA
 <213> Homo sapiens

<400> 38
 gccggaggag acgcacgcag ctgactttgt cttctccgca cgactgttac agaggtctcc 60
 agagccttct ctctctgtg caaaatggca actcttaagg aaaaactcat tgcaccagtt 120
 gcggaagaag aggcaacagt tccaaacaat aagatcactg tagtgggtgt tggacaagtt 180
 ggtatggcgt gtgctatcag cattctggga aagtctctgg ctgatgaact tgctcttggtg 240
 gatgttttgg aagataagct taaaggagaa atgatggatc tgcagcatgg gagcttattt 300
 cttcagacac ctaaaattgt ggcagataaa gattattctg tgaccgcaa ttctaagatt 360
 gtagtggtta ctgcaggagt ccgtcagcaa gaaggggaga gtcggctcaa tctggtgcag 420
 agaaatgtta atgtcttcaa attcattatt cctcagatcg tcaagtacag tcctgattgc 480
 atcataattg tggtttccaa ccagtggtac attcttacgt atgttacctg gaaactaagt 540
 ggattaccca aacaccgcgt gattggaagt ggatgtaatc tggattctgc tagatttcgc 600
 taccttatgg ctgaaaaact tggcattcat ccagcagct gccatggatg gatthttggg 660
 gaacatggcg actcaagtgt ggctgtgtgg agtgggtgta atgtggcagg tgtttctctc 720
 caggaattga atccagaaat gggaaactgac aatgatagtg aaaattggaa ggaagtgcac 780
 aagatgggtg ttgaaagtgc ctatgaagtc atcaagctaa aaggatatac caactgggct 840
 attggattaa gtgtggctga tcttattgaa tccatgtga aaaatctatc caggattcat 900
 cccgtgtcaa caatggtaaa ggggatgtat ggcatgaga atgaagtctt cctgagcctt 960
 ccatgtatcc tcaatgcccg gggattaacc agcgttatca accagaagct aaaggatgat 1020
 gaggttgctc agctcaagaa aagtcagat accctgtggg acatccagaa ggacctaaaa 1080
 gacctgtgac tagtgagctc taggctgtag aaatttaaaa actacaatgt gattaactcg 1140
 agcctttagt tttcatccat gtacatggat cacagtttgc tttgatcttc ttcaatatgt 1200
 gaatttgggc tcacagaatc aaagcctatg cttggtagct cttgaacaaa taaaattaac 1260
 tattgtagtg tg 1272

<210> 39
 <211> 4704
 <212> DNA
 <213> Homo sapiens

<400> 39
 ttattaatat cactatattt ttggaggag aggcaccttt ctcatctct cttctctctc 60
 gccaccctt actccctccc cctcatctac ctgtcaaagt cactgatctt ttgcatttcg 120
 gaagaggacg tcaacgggaa ggaattcccc ctctgggtgc gggctccgag agggggcgac 180
 ttgcaggagg ctcccccccg gggcggaggc gaaggggtgt ggtgccagaa gaaaagaatg 240
 attgatggga aacagacacc gggctataga cactcatcct ttgcttcag atactgatat 300
 ctcagcctgc ttgagcatcc cttgtgagct gtgaacattg aggatcactc agggttatcg 360
 gatgtacaac gggagagcca tcgctttgct aaattattat ctgcaattgg acatctttta 420
 caaaaaccaa actagacctg agtctaatag atatgttcta agacaaagaa aaagctgcaa 480
 gttgttaacg cctaacacac aagtatgtta ggcttcacc aaagtcctca atatactga 540
 atacgcacaa tatcttaact cttcatattt ggthttggga tctgctttga ggtcccatct 600
 tcatttaaaa aaaaatacag agacctacct acccgtagc atacatacat atgtgtatat 660

atatgtaaac tagacaaaga tcgcagatca taagagagc tctgctcttg tctccaaaga 720
 gattacaaag aatttagaga tgtatttgtc aagattcctg tcgattcatg ccctttgggt 780
 tacggtgtcc tcagtgatgc agccctaccc ttgggtttgg ggacattatg atttgtgtaa 840
 gactcagatt tacacggaag aagggaagt ttgggattac atggcctgcc agccggaatc 900
 cacggacatg acaaaatatt tgaagtgaa actcgatcct ccggatatta cctgtggaga 960
 ccctcctgag acgttctgtg caatgggcaa tccctacatg tgcaataatg agtgtgatgc 1020
 gagtaccctt gagctggcac acccccttga gctgatgttt gattttgaag gaagacatcc 1080
 ctccacattt tggcagctg ccacttgga ggagtatccc aagcctctcc aggttaacat 1140
 cactctgtct tggagcaaaa ccattgagct aacagacaac atagttatta cctttgaatc 1200
 tggggtcca gacaaatga tctgggaga gtctctcgat tatggacgaa catggcagcc 1260
 ctatcagtat tatgccacag actgcttaga tgcttttcac atggatccta aatccgtgaa 1320
 ggatttatca cagcatcagg tcttagaat catttgaca gaagagtact caacagggta 1380
 tacaacaaat agcaaaataa tccactttga aatcaaagac aggttcgctg tttttgctgg 1440
 acctcgcta cgcaatatgg ctccctcta cggacagctg gatacaacca agaaactcag 1500
 agatttcttt acagtcacag acctgaggat aaggctgtta agaccagccg ttggggaaat 1560
 attttagat gagctacact tggcacgcta cttttacgag atctcagaca taaaggtgag 1620
 aggaaggtgc aagtgtaatc tccatgccac tgtatgtgtg tatgacaaca gcaaattgac 1680
 atgcgaatgt gagcacaaca ctacaggtcc agactgtggg aaatgcaaga agaattatca 1740
 gggccgacct tggagtccag gctcctatct ccccatcccc aaaggcactg caaatacctg 1800
 tatccccagt atttccagta ttggtagtaa gtaaaaacaa aaacaaaaaa aacaccaaac 1860
 caagtctagg ctagctttgc ttgtttgttc acctcctcag atctattttc ccagtgtcca 1920
 tttctgatgt aataggttat tttctttgtg aattgcattt ttgtgttggg tttctgcaca 1980
 gatctggtga gaacacagat aaagtgatta ttgtgcata actccatgaa catggcagtg 2040
 ctatgacttt tctgactact ctaaccagt gagggctacc tagactcagg tgcaattcct 2100
 tagataatca tcattcagga aaaatataag tagtctatt tatccatact tagcaaccaa 2160
 caaacaatt gaactctctc ttagactgga ttggatgtc tgacataatt ttaaaaagca 2220
 gaaaatgaaa gcaatgaat gccttgggta tatgcatcag aaccaagaa aaagtccatg 2280
 ataccaaggg aagggaattt tgtaaatgca ttaaatctta tgttttgta aggcctgaaa 2340
 caggcaaat tgtgatcagt agtctctctg gagagataaa gaaaaagag aatctgtaca 2400
 ttcatctctc ctctctaaaa tacgatgatc tatgtctctt tgactactta gctttgagtt 2460
 tgatatagaa agagtataaa aaatatgtgc agaatttggg agtgagagta ctagaaattc 2520
 ctttaataaa tctgttagta tgaatccaag caattgaaga gaaaccgctc tcaaccatc 2580
 tgtagaacac tccccggta tcaactacaa gaactttctt ccagctatca tgggagaacc 2640
 aggtgtagct cccgcttcat gtgtaaaata atgatgccct catgccaagc ctgaaattca 2700
 cattaagaaa atgccagta actttacaga gcaaaatttt aaattttttt tttatacatt 2760
 gcacccttta tctctaattg ctaaaatctt tgaacaacta ctaagtaact gattacaaat 2820
 aaattaccga gaaagcaaga ttacgcatgg taagcggaga gaattttcac tgtagtgtca 2880
 tcccctcaca ggcttgtgct ataggtgctg tgccaggcag ggtgatcgca gtgtaaatag 2940
 ccattgaatg attgcgattc ccagcatcca tctaaaaagc aatactctga taatttggat 3000
 aaagcaactt cctgcttctt ataaatgcgc agtcaggtgt cccaatttat aaatcaacct 3060

```

agtttacttg agcttgtgaa taggcctgga cactgatttg ttaagcgcta gatgtggtaa 3120
atgccatgaa aattggccac ttgttaaata gaagtagtgt tcacatccat ttagagatac 3180
cagcctaata ctacagcatc ctctttgtga tcttgttgaa acagcatcag tgttaaaaac 3240
ttgcaaatga aaaccttcag ctctaatagt ctaatttttc tgcttttagta tcccccttg 3300
catttgcccta actgtatata taccaccaca tgtgctcctt tcaggccttg acaattgcat 3360
ttgcacgtgc attttagtgc aacagggag caagtagaag caagctgaca cagattattg 3420
aggctgctat agtgatctgg cctgtcagaa gtttcagaaa tggatggatg gaaaagtagt 3480
tctttggcgt tgggtgtct tctgttttg agtgtcagtt gtatgttgca tggccctct 3540
aactgtactg ctactcgac atccattcg gccgcctcca ccattccc catatctgag 3600
catcagcaga tgttgacctt ttacacatca aatcaggaaa tttctgtttt gttttgtttt 3660
gtttgtttt gaaatcagtg gtgacctgaa aggatgcttc gttgtgcctt tgaaaaaat 3720
atattaacct ttattatcga gaacctagga aaatttactc ctaataaaaa ccctctgact 3780
aaaagtgata ttttgactc tcccttcaat atgcctctgg ctgttccgct tagaatgcaa 3840
tgggtatttt ctgatttc cagcaaacag gatgtaagag cttccagagg tcaccaaca 3900
tcacacatga ctgacttacc tgttctctgg cttttaaggt aaagagtac agtaaaacca 3960
tcaaacgtga ttgtatcttc taggctgctt taatggcatt cgaagttcc tctttgttg 4020
gcttataagt tgctttttgc gtgactcgt ggattcctt cccctccaa ggcagaagt 4080
tcacacgtag acgactgc cgttccaga ggcacggga atgggtttt caaggtgcaa 4140
gccagagaaa aggaagctgt ttgatattt agctaagta tgggtgttg ccagtgctt 4200
ttgcattacc ccaagaagg aatcaatgac tataattcca ctaactatat agaaagatac 4260
cattatagca gatgtaacac ccctgagacc ccgattatca cagcatagct caaggaaaat 4320
aatgatgta tattatcgat gtagattatt gatgtatata accatcagtt tacatacata 4380
ttctgtatac acagtgatta aaggttttg agccctaata aatttcagta tagatctcaa 4440
aatgccaacg cctgtattaa ggttcaaatg catggatagg gtggtcatcc tttccgatca 4500
tctgctaaaa atgtttttga aacaaattc ccattaaggt cattcgtacc tgctgtgtc 4560
tatctattaa caaataggt tcccataatc ctaaggatac ttgacttaga actcagtcac 4620
tctgatctgc tttggccatg gctgaaaaa tgctggtgat attgtcagca attaatgaat 4680
cccaaaataa atctgtagcc ttg 4704

```

```

<210> 40
<211> 573
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)..(573)
<223> n=A,T,C, and G

```

```

<400> 40
cgaaggggct ggctagctga ccaccagggc ccctgctggc tctgaccgcc ctccatccc 60
aagtaattat ttacatgttt cgcgttcgct tatgtattat gtgtaatcat ggcacagtat 120
cctgaagccg tcggagtctg tgtgctggg caaggtctgg gacaaattta agaagagaga 180
gctctccttc ctccactaag agcggaaaat gaacaaatcc caggaacaag tgtcattcaa 240
ggatgtatgt gtggacttca ctcaggaaga gtggtatctg ctggaccctg ctcagaagat 300

```

tctatacaga gatgtgatcc tggaaaatta tagcaatctt gtctcagtag ggtattgcat 360
 tactanacca gaagtgatct ttaagatcgg agcaaggagg aagagccctg ggatattnga 420
 aaaagggtatt cccaagccc agtggccanc ccagaaaagg aaatggaaag ttggatgaac 480
 gtggttagag agcagcccag gaaaatgaag atgncccatt tttggggagc ctcctattcc 540
 cacaaccaac aaaacagtaa gtggttgaa aat 573

<210> 41
 <211> 3306
 <212> DNA
 <213> Homo sapiens

<400> 41
 gcagcgcctc cgcacctggt aggtgctcag ttaacgtggg agaaatgaag agtgaagggtg 60
 ccgcacatct tggatattct ccaggacatg gtggcggggt gctatgagtt ttcctgttct 120
 gcagaatgaa gaggtgctg ctcaggaata tgaacaaccc ggccaagacc acaaaacaag 180
 gaagcaccgg cagggccggg attcaggtct gggtttgtct gactccagag cccagtgcct 240
 tgttctccat ggctgctggt tgctacctct ttgatgaaca tctagatttg tgccttctc 300
 tgagggtgcc ccagatttca gcagttcgag gccagctcag cttttcctt caccaatggc 360
 ctagaagagg ccaacaagg agctttgagg ctgccccaaa gtggagagtg gcagtgaac 420
 attggacgcc agagtggagg ccacagcgca gtggcctata tgggtttaga gcgtgaggcc 480
 tccacgtgga cttgaatgca gaccccaggc ctgccgtgt tgacctggg caagtgactt 540
 aacctctctg agcctccatt gccccacctg taaaatgagg ggtttatagt acctgcttca 600
 taaagttgct atggagatga cagcagaagc cataggaccc cgggtgccatt tggaggaccc 660
 gtcgtggggg gcacttttcc caggccaggc accccttca tcccggagcc cctcagtggc 720
 ttggaactcc tccgtctcag acccagcttc aacagagtgg cccagggtg ggtccgtaac 780
 ctcccagagt ccgaggagct gtagccctag cctgaatctt cagttcccca gtctcggggg 840
 cctggttaaca tccggagcca agacttgtgg acagcacttc acagttgaag aagggccttc 900
 acacacaaaa cctgattgca aatggcttca gaggtcacca agttcagtcg tcccaaaaca 960
 tgggtgtgtt tcaaaattac ctggggatgt tgttccaaat ccagacaact ggactgtccc 1020
 agacttgag catcagagtc tcctgagtcg aggaatctgt attattaata gcaaccaggg 1080
 ccgggtgtcg tggctcacgc ctgtcatccc agcactttgg gaggccgagg caggaggatc 1140
 acctgaggtc aggagtttga gaccagtctg gccaaaatag tggaaccccg tcgctactaa 1200
 aaatacaaaa atgagtcgga catggtggtg catgcctgta atcccagcta ctggggaggc 1260
 tgagacagga gaatcacttg aactacgagg cagagggttg agtgagccga gattgcgcca 1320
 ctgcacccca gcttgacaa cagagtgaaga ctccttctca aaagtaaata aataaatagc 1380
 aaccagtact ccaggtgatt ccagcataac ttatccatgg tttgtgtcat taggagtcca 1440
 catcacacc tctgtctttt cctgttctct tagtgtacac tccccgggtg acagggtgct 1500
 cactggcacc ccattcttct gtgaataact caaataatta gaaaatgttc cttttactga 1560
 gatgcagttg gtcttcatct attcatgtc taaacagttc ctaagcgctg actgtgcgct 1620
 agacactgcc agggccgggc ctgaggagg aaaagacagt agggagaca ttatagagca 1680
 tgaagtcacc ataattttcc ctaaagcatg cttattgaca attgaggaac aaagtgttgt 1740
 ggagcagaag aaggagtccc tcaccctagg tgtgagatgg gattctggaa gcttcctgaa 1800
 ggatttgagt gggaccttgt gggaggcgtg agagtccatg aagggggtgt gagggggagg 1860

gtatttcttg aaagtggacc agcatgtgca aaaatatgga actgagcacg ggtgcagggt 1920
 gttctgcaga agggagaagg ctgtgctaga ggagccagtg agggccagca tggggtgggc 1980
 ttcactaagg aaatgggaa ggttttagtg atgggtcttg ctgggtgctg tgtgggagcg 2040
 atattggaga agggtaatgc cagaagccag gaagcctgca agggatgagg ccatgggaat 2100
 ggagagaagg ggcacccac tgggcaccta acaggacagg tgcaaagtgg ggtgcttatt 2160
 aagattcctt ctttccactc cttttgagc aggcctgctta aagtgggtgt gatgatgatg 2220
 atgatgatgg cagctttata tcgagtcct cagtgccttg gctggtagta gtttctctac 2280
 atatcttatt tctaattctc agaacaaccc tgagagaaag atattgttgt cccacttta 2340
 cagatgtgga tatttaggcc aaaaggagga agtgacttgt ccaggggcag acaccaaag 2400
 ggaatctgat tccagtggat gtctcttttc agtgacttg gtggtcaatg cccactcgct 2460
 ctgaaatcat ctgactgtga tgccctgcct tggagttag aagttgagt caggcttggg 2520
 agtcagactg gatgggtag gttctaactc tgccactgct agccgatga acttgagcaa 2580
 gtcatttcac atctccgagc ctctgtttct ccaagtgtaa gatgaggaca agtataaaac 2640
 ctcccttatg ggtttgttgt gaacacagt cagggcacat ttataataag agctcagtca 2700
 atggtaggtt tcatgcaact gctgctctag gctggaaaag ttgttcttg actggatgca 2760
 gcatgagaag ctggctgcta agatgtcact ggggtcact aaagctgaag cctgaaggaa 2820
 agcctctcat tgctgtagag ctctccctgc ctctctctt gggggcgatg ggaaggtca 2880
 ggagtccagc ccattcccag ggtgtgtggg atagcgattg cttttcctt ttgctctgga 2940
 gtttactcc cttctgggt cccaagggcc caatggcctg acttttagaa ttgcttgcaa 3000
 ttggtgttt ctctgaatt tggggctgc catttaaac caggtttcca tgagctgaag 3060
 accagccatt caagaatctg aaaagtagac aagaggactc cagttgcctc aggttggttc 3120
 tgctgtgctc tggaagtaa ctgcagccac caggtatgaa aaggagcctg gtgggagac 3180
 cactgcaccc aaacaaatc ctttcttct ctgagaatgt gacttttct ggtgtgttaa 3240
 aaaagaaaa aaaaagaatg ctcatgttaa aaataaaaa ataataataa aaaaaaaaa 3300
 aaaaaa 3306

<210> 42
 <211> 1613
 <212> DNA
 <213> Homo sapiens

<400> 42
 gccacggcgc ggacgccatg cacacggacc ctgactactc ggctgcctat gtcgtcatag 60
 aaactgatgc agaagatgga atcaaggggt gtggaattac cttcactctg gaaaaggca 120
 ctgaagtgtg tgtctgtgct gtgaatgccc tgcacacca tgtgtcaac aaggacctca 180
 aggacattgt tggtgacttc agaggcttct ataggcagct cacaagtgtg ggcagctca 240
 gatggatttg tccagaaaag ggcgtggtgc acctggcgac agcggccgtc ctaaacgcgg 300
 tgtgggactt gtgggccaag caggaggga agcctgtctg gaagttactt gtggacatgg 360
 atcccaggat gctggtatcc tgcatagatt tcaggtacat cactgatgtc ctgactgagg 420
 aggatgccct agaaatactg cagaaaggtc aaattggtaa aaaagaaaga gagaagcaaa 480
 tgctggcaca aggataccct gcttacacga catcgtgcgc ctggctgggg tactcagatg 540
 acacgttgaa gcagctctgt gccacggcgc tgaaggatgg ctggaccagg tttaaagtaa 600
 aggtgggtgc tgatctccag gatgacatgc gaagatgcca aatcatccga gacatgattg 660


```

gaccggaaaa gactttgatg atggatgcca accagcgctg ggatgtgcct gaggcggtgg 720
agtggatgtc caagctggcc aagttcaagc cattgtggat tgaggagcca acctcccctg 780
atgacattct ggggcacgcc accatttcca aggcactggt cccattagga attggcattg 840
ccacaggaga acagtggcac aatagagtga tatttaagca actcctacag gcgaaggccc 900
tgcagttcct ccagattgac agttgcagac tgggcagtgt caatgagaac ctctcagtat 960
tgctgatggc caaaaagttt gaaattcctg tttccccca tgctggtgga gttggcctct 1020
gtgaactggt gcagcacctg atttatattg actacatata agtttctgca agccttgaaa 1080
ataggggtgtg tgagtatgtt gaccacctgc atgagcattt caagtatccc gtgatgatcc 1140
agcgggcttc ctacatgcct cccaaggatc cgggctactc aacagaaatg aaggaggaat 1200
ctgtaaagaa acaccagtat ccagatgggtg aagtttgaa gaaactcctt cctgctcaag 1260
aaaattaagt gctcagcccc aacaactttt ttctttctga agtgaaaggg cttaaaattt 1320
cttgaaaata gttttacaaa aatggattta aaaaatccta ccgatcaaga tgagttcagc 1380
tagaagtcac accaccctca ggaatcagct aagtaattat tacttgattc ttttagcaaa 1440
tcaatgcacg ttatcctact taatccttaa ataagtttag atttaactaa cccaaagtcc 1500
aggaggatgt tcttacaaaa atagctatat caagggtggt cacctagaca ttaaactgta 1560
ctttgaaaat aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1613

```

```

<210> 43
<211> 619
<212> DNA
<213> Homo sapiens

```

```

<400> 43
agcagttcta agggaccata cagagtattc ctctcttcac accaggacca gccactgttg 60
cagcatgagt tcccagcagc agaagcagcc ctgcatccca cccctcagc ttcagcagca 120
gcagggtgaaa cagccttgcc agcctccacc tcaggaacca tgcatccca aaaccaagga 180
gccctgccac cccaaggtgc ctgagccctg ccaccccaaa gtgcctgagc cctgccagcc 240
caagcttcca gagccatgcc accccaaggt gcctgagccc tgcccttcaa tagtcactcc 300
agcaccagcc cagcagaaga ccaagcagaa gtaatgtggt ccacagccat gcccttgagg 360
agccggccac cagatgtga atcccctatc ccattctgtg tatgagtccc atttgccttg 420
caattagcat tctgtctccc ccaaaaaaga atgtgtatg aagctttctt tctacacac 480
tctgagtctc tgaatgaagc tgaaggtctt agtaccagag ctagttttca gctgctcaga 540
attcatctga agagagactt aagatgaaag caaatgattc agctccctta taccctcatt 600
aaattcactt tcaattcca 619

```

```

<210> 44
<211> 762
<212> DNA
<213> Homo sapiens

```

```

<400> 44
atggcaagat cccttctcct gccctgcag atcttactgc tacccttagc cttggaaact 60
gcaggagaag aagcccaggg tgacaagatt attgatggcg ccccatgtgc aagaggctcc 120
caccatggc aggtggccct gctcagtggc aatcagctcc actgaggagg cgtcctggtc 180
aatgagcgtt ggggtctcac tgccgccac tgcaagatga atgagtacac cgtgcacctg 240
ggcagtgata cgctgggcca caggagagct cagaggatca aggcctcgaa gtcattccgc 300

```

caccgccggt actccacaca gacctatggt aatgaccca tgcctctgaa gctcaatagc 360
 caggccaggc tgtcatccat ggtgaagaaa gtcaggctgc cctcccgtg cgaaccccct 420
 ggaaccacct gtactgtctc cggtctgggc actaccacga gccagatgt gacctttccc 480
 tctgacctca tgtcgtgga tgcgaagctc atctccccc aggactgcac gaagggttac 540
 aaggacttac tggaaaattc catgctgtgc gctggcatcc ccgactccaa gaaaaacgcc 600
 tgcaatgggt actcaggggg accgttgggt tgcagaggt cctgcaagg tctgggtgcc 660
 tggggaactt tcccttgctg ccaacccaat gaccaggag tctacctca agtgtgcaag 720
 ttcaccaagt ggataaatga caccatgaaa aagcatcgct aa 762

<210> 45
 <211> 322
 <212> DNA
 <213> Homo sapiens

<400> 45
 atttaggtga cactatagaa tactcaagct atgcatcaa cgcgttggga gctctcccat 60
 atggtcgacc tgcaggcggc cgcactagtg attaagctcc aactgcctac gacaaacaga 120
 cccaaaatcg ctcatgtcat actcttcaat cagccacata gccctcgtag taacagccat 180
 tctcatcaa accccctgaa gcttcaccgg cgcagtcatt ctcataatcg cccacggact 240
 tacatctca ttactattct gcctagcact ctccagctc tcaccgcacc gccacaataa 300
 agatcgcccc cacctcaaaa aa 322

<210> 46
 <211> 799
 <212> DNA
 <213> Homo sapiens

<400> 46
 cgacgttcgc agcgtaccc tttccgctc caggtgacc tccgtgcggc cgggtgcggg 60
 cggagtcttc ctcatcccg tgggtctccg cggcgcgggc ttgctctctt ccggtcgcgg 120
 gacaccgggt gtatagggcg gtcgcggcgg gcagtggcgg cagaatgtt gctaccaggg 180
 tatttagcct agttggcaag cgagcaattt ccacctctgt gtgtgtacga gctcatgaaa 240
 gtgttgtgaa gagcgaagac tttcgcctc cagcttatat ggatcggcgt gaccaccct 300
 tgccggaggt ggccatgtc aagcacctgt ctgccagcca gaaggcactg aaggagaagg 360
 agaaggcctc ctggagcagc ctctccatgg atgagaaagt cgagttgtat cgcattaagt 420
 tcaaggagag ctttgctgag atgaacaggg gtcgaacga gtggaagacg gttgtggcg 480
 gtgccatgtt ctcatcgggt ttcaccgcgc tcgttatcat gtggcagaag cactatgtgt 540
 acggccccct ccgcaaagc tttgacaaag agtgggtggc caagcagacc aagaggatgc 600
 tggacatgaa ggtgaacccc atccagggt tagcctccaa gtgggactac gaaaagaacg 660
 agtgaagaa gtgagagatg ctggcctcgc cctgcacctg cgcctggctc tgtcaccgcc 720
 atgcaactcc atgcctatct actggaacc tgttatgcca aacagttgta ccactgctaa 780
 taaatgacca gtttacctg 799

<210> 47
 <211> 3579
 <212> DNA
 <213> Homo sapiens

<400> 47
 ctgaggccca cgcaggcct aggggtggaa gatggcagg gggggcggcg acctgagcac 60

caggaggctg aatgaatgta tttcaccagt agccacagag agccacagag agccacagag 120
 cagccacgat ttgcaaagga tgttcacgga agaccagggt gtagatgaca ggctgctcta 180
 tgacattgta ttcaagcact tcaaaagaaa taagggtggag atttcaaatg caataaaaaa 240
 gacatttcca ttctctgagg gcctccgtga tcgtgatctc atcacaaata aaatgtttga 300
 agattctcaa gattcttgta gaaacctggt ccctgtacag agagtgggtg acaatgttct 360
 tagtgaactg gagaagacat ttaacctgcc agttctggaa gcactgttca gcgatgtcaa 420
 catgcaggaa taccctgatt taattcacat ttataaaggc ttgaaaatg taatccatga 480
 caaattgcct ctccaagaaa gtgaagaaga agagaggag gagaggtctg gcctccaact 540
 aagtcttgaa caaggaaactg gtgaaaactc ttttcgaagc ctgacttggc caccttcggg 600
 ttccccatct catgctggta caacccacc tgaaaatgga ctctcagagc acccctgtga 660
 aacagaacag ataatgcaa agagaaaaga tacaaccagt gacaaagatg attcgctagg 720
 aagccaacaa acaaatgaac aatgtgtca aaaggctgag ccaacagagt cctgcgaaca 780
 aattgctgtc caagtgaata atggggatgc tggaggagag atgccctgcc cgttgccctg 840
 tgatgaagaa agcccagagg cagagctaca caacctgga atccaaatta attcctgttc 900
 tgtgcgactg gtggatataa aaaaggaaaa gccattttct aattcaaaag ttgagtcca 960
 agcccaagca agaactcatc ataaccaggc atctgacata atagtcatca gcagtgagga 1020
 ctctgaagga tccactgacg ttgatgagcc cttagaagtc ttcattctcag caccgagaag 1080
 tgagcctgtg atcaataatg acaacctttt agaatcaaat gatgaaaagg agggccaaga 1140
 agccacttgc tcacgacccc agattgtacc agagcccatg gatttcagaa aattatctac 1200
 attcagagaa agttttaaga aaagagtgtat aggacaagac cagactttt cagaatccag 1260
 tgaggaggag gcgcccagag aagcctcaag cggggcactg agaagcaagc atggtgagaa 1320
 ggctcctatg acttctagaa gtacatctac ttggagaata cccagcagga agagacgttt 1380
 cagcagtagt gacttttcag acctgagtaa tggagaagag cttcaggaaa cctgcagctc 1440
 atccctaaga agagggtcag gatcacagcc acaagaacct gaaaataaga agtgctcctg 1500
 tgtcatgtgt ttccaaaag gtgtgccaag aagccaagaa gcaaggactg aaagtagtca 1560
 agcatctgac atgatggata ccatggatgt tgaaaacaat tctactttgg aaaaacacag 1620
 tgggaaaaga agaaaaaaga gaaggcatag atctaaagta aatggctctc aaagaggag 1680
 aaagaaagac agacctagaa aacatttaac tctgaataac aaagtccaaa agaaaagatg 1740
 gcaacaaaga ggaagaaaag ccaacactag acctttgaaa agaagaaga aaagaggtcc 1800
 aagaattccc aaagatgaaa atattaattt taaacaatct gaacttcctg tgacctgtgg 1860
 tgagggtgaag ggcactctat ataaggagcg attcaaaca ggaacctcaa agaagtgtat 1920
 acagagtgaag gataaaaagt ggttactcc cagggaattt gaaattgaag gagaccgagg 1980
 agcatccaag aactggaagc taagtatacg ctgcggtgga tataccctga aagtcctgat 2040
 ggagaacaaa tttctgccag aaccaccaag cacaagaaaa aagagaatac tggaatctca 2100
 caacaatacc ttagttagc cttgtgagga gcataagaag aagaaccag atgcttcagt 2160
 caagttctca gagtttttaa agaagtgtc agagacatgg aagaccattt ttgctaaga 2220
 gaaaggaaaa ttgaaagata tggcaaaggc ggacaaggcc cattatgaaa gagaaatgaa 2280
 aacctatc cctcctaaag ggagaaaaa aaagaagttc aaggatccca atgcacccaa 2340
 gaggcctcct ttggcctttt tctgttctg ctctgagtat cgcccaaaaa tcaaaggaga 2400
 acatcctggc ctgtccattg atgatgttgt gaagaaactg gcagggatgt ggaataacac 2460

cgctgcagct gacaagcagt tttatgaaaa gaaggctgca aagctgaagg aaaaatacaa 2520
aaaggatatt gctgcatatc gagctaaagg aaagcctaata tcagcaaaaa agagagttgt 2580
caaggctgaa aaaagcaaga aaaagaagga agaggaagaa gatgaagagg atgaacaaga 2640
ggaggaaaat gaagaagatg atgataaata agttgcttct agtgcagttt ttttcttgtc 2700
tataaagcat ttaagctgcc tgtacacaac tctctccttt taaagaaaaa aacttcaacg 2760
taagactgtg taagatttgt ttttaaaccg tacactgtgt tttttgtat agttaaccac 2820
taccgaatgt gtcttcagat agccctgtcc tgggtgtatt tagccactaa cctttgcctg 2880
gtacagatg ggggttgtaa attggcatgg aaatttaag caggttcttg ttagtgaca 2940
gcacaaatta gttgtatagg aggatgtag tttttcacc ttcagttgtc tctgatgtag 3000
cttatacaaa acatttggtg ttctgttaac tgaatgccac tctgtaattg caaaaaaaaa 3060
aaacagttgc agctgttttg ttgacattct gaatgcttct aagtaatac aatttttaa 3120
aaaccgtatg agggaactgt gtagacaagg taccaggtca gtcttcttcc atgttctatt 3180
agctccacaa agccaatctc aatccctcaa aacaatcttg tcatactga aaatatgaca 3240
ctctagtcaa agccttggtg aaataatcag tgtttccaat ctgtcctgtt acaaaagaaa 3300
cagattatta ttgaacttat gcaataaacc attgtcataa gaatgtttat gaatagtttc 3360
caaattatgg caaattcatg tagagagaga aaagtaactg ttttggtttt gtcacaaaa 3420
gtctacttta cctaagggtc gtcagatata agtaacttaa aagaaagaga agttttcttg 3480
acttttgaaa acaaaatag aaaagaatcg gcaatgttcc aaacaaaaag tcataaaagt 3540
cactttattc ctccatcaaa aaaaaaaaaa aaaaaaaaaa 3579

<210> 48
<211> 1594
<212> DNA
<213> Homo sapiens

<400> 48
ggaattcctc tctttattgt cagggctctc tccctaggag gcctgcccc gctaaccggc 60
tttttgccca aatgggccat tatcgaagaa ttcacaaaaa acaatagcct catcatcccc 120
accatcatag ccaccatcac cctccttaac ctctacttct acctacgcct aatctactcc 180
acctcaatca cactactccc catatctaac aacgtaaaaa taaatgaca gttaacata 240
caaaaccac cccattcctc cccacactca tcgcccttac cagctactc ctacctatct 300
ccccttttat actaataatg tctgttggtg cttgttgctg gcaccgcagt cgcctgaag 360
atggcgtcta ccagccgttt ggatgctctt ccaagagtca catgtccaaa ccattccagat 420
gcgattttag tggaggacta cagagccggt gatatgatct gtcctgaatg tggcttggtt 480
gtaggtgacc ggggttattga tgtgggatct gaatggcgaa ctttcagcaa tgacaaagca 540
acaaaagatc catctcgagt tggagattct cagaatcctc ttctgagtga tggagatttg 600
tctacatga ttggcaaggg cacaggagct gcaagttttg acgaatttgg caattctaag 660
taccagaatc ggagaacaat gagcagttct gatcgggcaa tgatgaatgc attcaaagaa 720
atcactacca tggcagacag aatcaatcta cctcgaaata tagttgatcg aacaaataat 780
ttattcaagc aagtatatga acagaagagc ctgaaggga gagctaata tgctatagct 840
tctgctgtgc tctatattgc ctgtagacaa gaaggggttc ctaggacatt taaagaaata 900
tgtgccgtat cacgaatttc taagaaagaa attggctcgt gttttaaaact tattttgaaa 960
gcgctagaaa ccagtgtgga tttgattaca actggggact tcatgtccag gttctgttcc 1020

aacctttgtc ttcctaaaca agtacagatg gcagctacac atatagcccg taaagctgtg 1080
 gaattggact tggttcctgg gaggagcccc atctctgtgg cagcggcagc tatttacatg 1140
 gcctcacagg catcagctga aaagaggacc caaaaagaaa ttggagatat tgctgggtgtt 1200
 gctgatgtta caatcagaca gtcctataga ctgatctatc ctcgagcccc agatctgttt 1260
 cctacagact tcaaatgtga caccgccagt gacaaactac cacagctata aattgaggca 1320
 gctaactgca aattcttgaa taaaaaactt tgcctgttgt acatagccta taaaaaatgc 1380
 tgggttgagc ctttcatgag gaaaaacaaa agacatggta cgattccag ggctgaatac 1440
 tattgcttgg cattctgtat gtatatacta gtgaaacata tttaatgatt taaatttctt 1500
 atcaaatttc tttgtagca atctaggaaa ctgtattttg gaagatattt gaaattatgt 1560
 aattcttgaa taaaacattt ttcaaacg aatt 1594

<210> 49
 <211> 2969
 <212> DNA
 <213> Homo sapiens

<400> 49
 ggctgacttc ctggatgcac taatcgtgag catggatgtg attcaacatg aaacaatagg 60
 aaagaagttt gagaagaggc atattgaaat attcactgac ctcagcagcc gattcagcaa 120
 aagtcagctg gatattataa ttcatagctt gaagaaatgt gacatctccc tgcaattctt 180
 cttgcctttc tcacttgcca aggaagatgg aagtggggac agaggagatg gcccccttcg 240
 cttaggtggc catgggcctt cctttccact aaaaggaatt accgaacagc aaaaagaagg 300
 tcttgagata gtgaaaatgg tgatgatatc tttagaaggc gaagatgggt tggatgaaat 360
 ttattcatc agtgagagtc tgagaaaact gtgcgtcttc aagaaaattg agaggcattc 420
 cattcactgg ccttgccgac tgaccattgg ctccaatttg tctataagga ttgcagccta 480
 taaatcgatt ctacaggaga gagttaaaaa gacttggaca gttgtggatg caaaaaccct 540
 aaaaaagaa gatatacaaa aagaaacagt ttattgctta aatgatgatg atgaaactga 600
 agttttaaaa gaggatatta ttcaagggtt cctctatgga agtgatatag ttctttctc 660
 taaagtggat gaggaacaaa tgaaatataa atcggagggg aagtgttct ctgttttggg 720
 attttgtaaa tcttctcagg ttcagagaag attcttcatg ggaaatcaag ttctaaaggc 780
 ctttcagca agagatgatg aggcagctgc agttgcactt tctccctga ttcagtcttt 840
 ggatgactta gacatggtg ccatagttcg atatgcttat gacaaaagag ctaatcctca 900
 agtcggcgtg gcttttctc atatcaagca taactatgag tgtttagtgt atgtgcagct 960
 gcctttcatg gaagacttgc ggcaatacat gttttcatcc ttgaaaaaca gtaagaaata 1020
 tgctcccacc gaggcacagt tgaatgctgt tgatgctttg attgactcca tgagcttggc 1080
 aaagaaagat gagaagacag acacccttga agacttgttt ccaaccacca aaatcccaa 1140
 tcctcgattt cagagattat ttcagtgtct gctgcacaga gctttacatc cccgggagcc 1200
 tctaccccca atcagcagc atatttgaa tatgctgaat cctcccgctg aggtgacaac 1260
 gaaaagtcat attcctctct ctaaaataaa gacccttttt cctctgattg aagccaagaa 1320
 aaaggatcaa gtgactgtc aggaaatttt ccaagacaac catgaagatg gacctacagc 1380
 taaaaatta aagactgagc aagggggagc ccacttcagc gtctccagtc tggctgaagg 1440
 cagtgtcacc tctgttgaa gtgtgaatcc tgctgaaaac ttccgtgttc tagtgaaca 1500
 gaagaaggcc agctttgagg aagcgagtaa ccagctcata aatcacatcg aacagttttt 1560

ggataactaat gaaacaccgt attttatgaa gagcatagac tgcattccgag ccttccggga 1620
 agaagccatt aagttttcag aagagcagcg ctttaacaac ttcctgaaag cccttcaaga 1680
 gaaagtggaa attaaacaat taaatcattt ctgggaaatt gttgtccagg atggaattac 1740
 tctgatcacc aaagaggaag cctctggaag ttctgtcaca gctgaggaag ccaaaaagtt 1800
 tctggccccc aaagacaaac caagtggaga cacagcagct gtatttgaag aaggtggtga 1860
 tgtggacgat ttattggaca tgatataggt cgtggatgta tggggaatct aagagagctg 1920
 ccatcgctgt gatgctggga gttctaacaa aacaagttgg atgcggccat tcaaggggag 1980
 ccaaaatctc aagaaattcc cagcaggtta cctgcaggcg gatcatctaa ttctctgttg 2040
 aatgaatata cacatatata ttacaaggga taatttagac cccatacaag ttataaaga 2100
 gtcattgtta ttttctggtt ggtgtattat ttttctgtg gtcttactga tctttgtata 2160
 ttacatacat gctttgaagt ttctggaaag tagatctttt ctgacctag tatatcagt 2220
 acagttgcag cccttgtgat gtgattagtg tctcatgttg aacctggca tggttattga 2280
 tgagtttctt aaccctttcc agagtcctcc ttgcctgat cctccaacag ctgtcacaac 2340
 ttgtgttgag caagcagtag catttgcttc ctccaacaa gcagctgggt taggaaaacc 2400
 atgggtaagg acggactcac ttctctttt agttgaggcc ttctagttac cacattactc 2460
 tgccctgtga tatagggtt tttctttaag tgggtggga aggggagcac aatttccctt 2520
 cactactcctt ttaagcagtg agttatggtg gtggtctcat gaagaaaaga ccttttgcc 2580
 caatctctgc catatcagtg aacctttaga aactcaaaaa ctgagaaatt tactacagta 2640
 gttagaatta tatcacttca ctgttctcta cttgcaagcc tcaaagagag aaagtctctg 2700
 tatattaata cacttaggta acttttcgat cttccatt tctacctaag tcagcttca 2760
 tctttgtgga tgggtgtctc ttactaaat aagaaaataa caagccctt attctctttt 2820
 tttctgtgcc tcattcttgc cttgagttcc agtctctctt tgggtgtacag acttcttgg 2880
 acccagtcac ctctgtcttc agcacctca taagtcgtca ctaatacaca gttttgtaca 2940
 tgtaacatta aaggcataaa tgactcaaa 2969

<210> 50
 <211> 5360
 <212> DNA
 <213> Homo sapiens

<400> 50
 ttgagtgca ttgaaatgtt ccaagctgtt acttacctta acatgttctt gaggtaccat 60
 ggcattgatt aaaaggaaat ttggtaagt gctccactt aaacgactta ctagggaagc 120
 tatgtgaaat tatttaaaag ggcgagggga tcaaatagta cttatccttc atgcaaaagt 180
 tgtacagaag tcatatggaa tgaaaaaggt tttttgccct ccccttgtg tatatcttat 240
 gggcagtgga tggaagaaaa taaaattaca aatgaaatgc gatggttgtt ctgaacaagg 300
 ctctcatcca tgtgcattta ttgggatagg aaatagtgac caagaaatgc agcagctaaa 360
 cttggaagga aagaactatt gcacagccaa aacattgtac atatctgatt cagacaagca 420
 aaagcacttc atgttgtctg taaaggtgtt ctatggcaac ggtgatgaca ttggtgtgtt 480
 cctcagcaag tcgtccaaac ctccaaaaa gaagcagtc tggaaaaatg ctgacttatg 540
 cattggctca ggaacaaagg tggctctgtt taatcgacta cgatcccaga cagttagtac 600
 cagatacttg catgtagaag gagggaaatt tcatgccagt tcacagcagt ggggagcatt 660
 tacattatc ttggatgatg atggatcaga aggagaagaa ttcacagtc gagatggcta 720

cattcattat ggacaaacag tcaagcttgt gtgctcagtt actggcatgg cactcccaag 780
attgataatt aggaaagtgt ataagcagac cacattattg gatgcagatg atcctgtgtc 840
acaactccat aaatgtgcat ttgaccttga ggatacagaa agaattgtact tatgcctttc 900
tcaagaaaga ataattcaat ttcaggccac tccatgcccac acagaaccaa ataaagagat 960
gataaatgat ggtgcttcct gggcaatcat tagcacacat aaggcgaagt atacatttta 1020
tgagagaatg gggcctgtcc ttgccctggt catgcctatg cctgtcgtag agagccttaa 1080
gttgaatggc ggtggggacg aagcaatgct tgaacttaca ggacagaatt tcaactccaa 1140
tttacgagtg tggtttgggg atgtagaagc tgaactatg tacagggtgtg gagagagtat 1200
gctccgtgtt gtcccagacg ttctgcattc tgagaagggt ggagatagtt cccagcaacc 1260
agtccagggt tcagtaactt tggccgaaa tgatggaatc atatattcca ccagccttac 1320
ctttacctac acaccagaag cagggccgcg gccacattgc agtgtagcag gcgcaatcct 1380
taaggccagt tcaagccacg tggcccttaa tgaattaaac acaaacagcg atggaagtta 1440
cacaaatgcc agcacaat caaccagtgt cacatcatct acaccaacag tggtatcctg 1500
aactaccgtc tttttgctaa gactcaaacg gcttgagtgc agcaaaaagt tgacaaaaaa 1560
ggaaaaaaa atgaacagtc ttttgggtt tattgggaaa ctttctacac caggtgatac 1620
tattctaaaa ccccggtgtc tccctgcaag tgctgatttg aaatgcagaa gccacagtaa 1680
aaaaaaaaa aaaaaaaaaa aaaaaagaaa aaaaaatcaa aatgtataaa tattggaaat 1740
caagtttttc agctgtttt tgggttgggt ggttgggttt tgtttgggtt tgtttaaagg 1800
gacaagaagt aaataatgtg gctggaatac aagtgaaca aactagaaga cacaaatcta 1860
acatagtttt tatggacca ggaacttgta tattgtataa gctttagtaa aaggtagatt 1920
ttcaccatac ctttttttat atcacggtat tatagtacac cttgttacca ataggttggt 1980
ctcttcccca cctctctttg agctttgtc taaaatacat tctggttcca agcctgacca 2040
tccttgttta atctatcata ctctccaggt tttttttttt tggctcaagg ctggaacttt 2100
ttctttttt ttccagctga agtcttatga ctttttcatg agtcaaaatt gtttgattt 2160
cacgaagtca aatcttgcaa aggcctgcat atttttttta agattatatg aagtctgtgc 2220
aaaaagcttt aaaaaattgc ctctgccttg cctgcataca tgcaatgtat gtaacttagt 2280
ctctcttctc agacactgtt gggtagttat ttctgtgtt tcttttttta aaaaaaata 2340
tggacttatt tgggtttatc tgagaggttc taacattcac atgcaatttg gtgtggcatt 2400
tagctattat gagttatttg cgcgaacttg ttgatattt gaagtgtctc tccccctttc 2460
ccatgacgta atacataggt gtgttccagg attgttcag gtttttcccc cctcctaatt 2520
cttgtagata acttgattt tgtgtaagtt aaacatttta tttgaacttg gaatgttccc 2580
agtgatttca ttcagcaggg tattttctgc cttgttgga agtagcaaaa aatatgggaa 2640
gtatttgcta ccagttgta gatggtgccc cttattgga gaatcaggaa aatgtccgca 2700
aaagcatgtt ttattatctt tacttttttg gggggttga gggggtagcc tagccagaca 2760
tcatgtaatc ttaaaacata agatgctttt attagatgat caactaaaaa tagctggaag 2820
acagtacttt agaaacaaaa tagttagtaa gatataat gcaaatgtaa cttatgtttt 2880
catttttttc tctgcctttt tttttgttt ttttctttt tttccagtac tgagcatctc 2940
cacaaatgtc tctactcag aaaatgtttc ttttctttca gttgagattt ggtgcattca 3000
gggttgtagg ttggccttgc ttgctaacc gccggtttta ccgtgcttta ttcctgaact 3060

ttgtttatgc ctttgtttgg ttcttctgaa attgcagcag acccattggy cccacattag 3120
 tacaggaacc acgtgtgtaa tgttatataca cacagtcagt aatacaatca tccctcttag 3180
 agtaaaaact acctctagat tgtgtaagct ttttactgtc cataaaacag gagccacagt 3240
 accttatgaa tgcaaaactg taacttccta cagtgtttcc ccacagaaca ttgtctttct 3300
 ggtgtctggg ctgtttttga aaaagtttcc attaatagac tttttagaaa ttattattag 3360
 tagcattttt tttccagctt tgcgtcttca tcactcactc aagtgtcaga ctatgcactg 3420
 taaatatctt cctaacatct ttaaatacgcc ttttcctcag tttcaaggg gaaggctcatt 3480
 tgtaaagcac gttaggtggt taaatcagtt attgcggttt tctcttacag caagcctttt 3540
 taatcacccc caggctgcat tttattctat atcgcccttt ttcttcaaat ctgctccaat 3600
 catccacttc tctcttataa gctattcctg cctcacacct aaatctgttt cagtgatcaa 3660
 gggcagaact cattgtggcc ttatctttct ttgttgtaat tgttactgt ctctttctta 3720
 cagaccactt attctgagta gtagttattc ctccctatgg agtcatggca ggaatcatta 3780
 cacagtgett ttgttcagag catggacatg ttccaggtgc tgctttgctt taacggccac 3840
 aagtttctc cacttctcag gtttggatt tagtaaggaa tcaattaaat taaccaataa 3900
 caaaagagat acttttgaag acaaaactat tctttaccca tttgtagct caaaaaaat 3960
 tttcaagtt catgacctta ttaaaatgaa cttgtgtttt ttttaacaaac gtctatttta 4020
 ttttgatagt ttctttccga agataattga aatattatac tgtaaccctt ttcttttctt 4080
 tttgaaaag tccaagaatg tacttatata ggatttttcc ccacctattt ttggccattc 4140
 tcataccaca gacaaaagag tgaatgattg tcattgtagc ttattgttta tcagtagttc 4200
 tttgtagct gcttacattt tttctttcat ggtttgtaa tcatttcagt atgtaattta 4260
 taggaacctt gtcctctggt atagtagact gtgtgccctc ctccaggatg gcattattag 4320
 acatgctggt catttacct cagaaagact ctcttataga atggtgagtg cttcagttat 4380
 agtatgtttg aattttaaaa aattcctggt tagaatgtat ctatgctctc atgactatgc 4440
 agtttctaac atacacatag aagctgagtc tctgatccaa tatgttttta tttgttccat 4500
 taatttatca catagattgg gaaggcaagc taaaagcctt aaaaatgcc tttatatattt 4560
 gagtgatttc agcgttgaac acagtatact atctaaattt gctgctcact ttcttaaact 4620
 gttgcaatta aaggcatggt tatacatgac taatcgtgaa atgtttgtca ctcttactgc 4680
 acagacttat ctgcaatcaa actggtagt ttttttggtt tgttttggtt tattgttttt 4740
 aatgaatctg gtaccatctg tgctttcaca aaaaacttcc aatgccattt ttgagaacta 4800
 acctaacagt catgctaacc agaaaatcca ctggggagga ggttcctttg aaacaaaatg 4860
 ctgttcagtt agtaaccaag ttactttgat tgcaaaagca gctgtgtttc tgataagtac 4920
 tgaacaaatg tgtgtaattt tctgtgccag acttatgact ttgttttcaa gactgtaat 4980
 gtgggatgga tgggttagaaa caataatata tagggtttct gtttaaccctt tcaggactca 5040
 actgtatctc cttttgttaa tttccctctg tgtgtgata aattgtttgc cagcattcag 5100
 tactgtgttg gtgcagatga ggtttatata tcatttttagc ttatttcttg tacctttcag 5160
 catgcctacg cattcagtc ttaaggggtt tattttacaa actgtgcgcc tgaagtttat 5220
 tagcaataag atagaaaatg agcaagtta taccataatt ttgagaaaaa aagaatctgc 5280
 tcagttccat atttcatccg tgaaaaactt gcaatacgag cagtttcaag gaataaataa 5340
 aaaggaaatg aaaccattgt 5360

<210> 51
 <211> 863
 <212> DNA
 <213> Homo sapiens

<400> 51
 ggagtctcca actgggagag ctgcagctgc cgagaggagg agaacgctga ggtcggctcg 60
 accaacggac gcgctgaccg ctgccaaactg cagctcgcg tgcctcctgc tcgcgccgtg 120
 ccactaaggt cactcccgcc tccgagagcc cagagccgag atggaaacgg tccaggagct 180
 gatccccctg gccaaaggaga tgatggccca gaagcgcaag ggaagatgg tgaagctgta 240
 cgtgctgggc agcgtgctgg ccctcttcgg cgtggtgctc ggcctgatgg agactgtgtg 300
 cagccccttc acggccgcca gacgtctgcg ggaccaggag gcagccgtgg cggagctgca 360
 ggccgcccctg gagcgacagg ctctccagaa gcaagccctg caggagaaag gcaagcagca 420
 ggacacggtc ctgcccggcc gggccctgtc caaccggcag cagcctcct aggaactgtg 480
 ggagaccagc ggagtgggag ggagacgcag tagacagaga cagaccgaga aggaaggag 540
 agacagaggg ggccgcccga caggagcctg actccgctgg gagagtgcag gacacgtgc 600
 tgttttttat ttgacttaa ctccagagaa accgctgaca tctagaactg acctaccaca 660
 agcatccacc aaaggagttt gggattgagt tttgctgctg tgcagcactg cattgtcatg 720
 acatttccaa cactgtgtga attatctaaa tgcgtctacc attttgact agggagggaag 780
 gataaatgct ttttatgtta ttattattaa ttattacaat gaccaccatt ttgcattttg 840
 aaataaaaaa ctttttatac cat 863

<210> 52
 <211> 3921
 <212> DNA
 <213> Homo sapiens

<400> 52
 atgggggccc cctcggggcc cggggggccc gggctgctgc tgcccctgcc gctgctgttg 60
 ctgctgccgc cgcagcccgc cctggcgttg gaccccgggc tgcagcccgc caacttttct 120
 gctgacgagg ccggggcgca gctcttcgcg cagagctaca actccagcgc cgaacagggtg 180
 ctgttccaga gcgtggccgc cagctgggag cagcacacca acatcaccgc ggagaatgca 240
 aggcgccagg aggaagcagc cctgctcagc caggagtttg cggaggcctg gggccagaag 300
 gccaggagc tgtatgaacc gatctggcag aacttcacgg acccgagct gcgcaggatc 360
 atcggagctg tgcgcaccct gggctctgcc aacctgcccc tggctaagcg gcagcagtac 420
 aacgccctgc taagcaacat gagcaggatc tactccaccg ccaaggctctg cctccccaac 480
 aagactgcca cctgctggtc cctggaccca gatctcacca acatcctggc ttcctcgca 540
 agctacgcca tgcctctgtt tgccctggag ggctggcaca acgctgcggg catcccgctg 600
 aaaccgctgt acgaggattt cactgccctc agcaatgaag cctacaagca ggacggcttc 660
 acagacacgg gggcctactg gcgctcctgg tacaactccc ccaccttcga ggacgatctg 720
 gaacacctct accaacagct agagcccctc tacctgaacc tccatgcctt cgtccgccgc 780
 gcactgcac gccgatcagc agacagatac atcaacctca ggggacccat ccctgctcat 840
 ctgctgggag acatgtgggc ccagagctgg gaaaacatct acgacatggt ggtgccttcc 900
 ccagacaagc ccaacctcga tgcaccagt actatgctgc agcagggtg gaacgccacg 960
 cacatgttcc gggtggcaga ggagttcttc acctccctgg agctctcccc catgcctccc 1020
 gagttctggg aagggtcgat gctggagaag ccggccgacg ggcgggaagt ggtgtgccac 1080

gcctcggcctt gggacttcta caacaggaaa gacttcagga tcaaycagtg cacacgggtc 1140
acgatggacc agctctccac agtgcacat gagatgggcc atatacagta ctacctgcag 1200
tacaaggatc tgcccgtctc cctgcgtcgg ggggccaacc cggcttcca tgaggccatt 1260
ggggacgtgc tggcgctctc ggtctccact cctgaacatc tgcacaaaat cggcctgctg 1320
gaccgtgtca ccaatgacac ggaaagtgc atcaattact tgctaaaaat ggactggaa 1380
aaaattgcct tcctgccctt tggctacttg gtggaccagt ggcgtgggg ggtcttagt 1440
gggctaccc cccctcccg ctacaacttc gactggtgt atcttcgaac caagtatcag 1500
gggatctgtc ctctgttac ccgaaacgaa acccactttg atgctggagc taagtttcat 1560
gttccaaatg tgacaccata catcaggta tttgtgagtt ttgtcctgca gttccagttc 1620
catgaagccc tgtgaagga ggcaggctat gagggccac tgaccagtg tgacatctac 1680
cggtcacca aggcaggggc caagctccg aaggtgctgc aggtggctc ctccaggccc 1740
tggcaggagg tgcgaagga catggtcggc ttagatgcc tggatgcca gccgtgctc 1800
aagtacttcc agccagtcac ccagtggctg caggagcaga accagcagaa cggcgaggtc 1860
ctgggctggc ccgagtacca gtggcaccg cgttgctg acaactaccc ggagggcata 1920
gacctggtga ctgatgaggc tgaggccagc aagtttgtg aggaatatga ccggacatcc 1980
caggtggtgt ggaacgagta tgcagagcc aactggaact acaacaccaa catcaccaca 2040
gagaccagca agattctgct gcagaagaac atgcaaatag ccaaccacac cctgaagtac 2100
ggcaccagg ccaggaagtt tgatgtgaac cagttgcaga acaccactat caagcgatc 2160
ataaagaagg ttcaggacct agaacgggca gactgcctg cccaggagct ggaggagtac 2220
aacaagatcc tgttgatat ggaaccacc tacagcgtg ccactgtgtg caccgccaat 2280
ggcagctgcc tgcagctcga gccagatctg acgaatgtga tggccacatc ccggaatat 2340
gaagacctgt tatgggcatg ggagggctg cgagacaagg cgggagagc catcctccag 2400
ttttaccga aatacgtga actcatcaac caggctgccc ggctcaatg ctatgtagat 2460
gcaggggact cgtggaggc tatgtacgag acaccatccc tggagcaaga cctggagcgg 2520
ctcttcagg agctgcagc actctacctc aacctgcatg cctacgtgc cggggcctg 2580
caccgtaact acggggccca gcacatcaac ctggaggggc ccattcctgc tcacctgctg 2640
gggaacatgt gggcgagac ctggtccaac atctatgact tgggtgtgcc cttccctca 2700
gccccctga tggacaccac agaggctatg ctaaagcagg gctggagcc caggaggatg 2760
tttaaggagg ctgatgattt cttcacctcc ctggggctgc tgcccgtgcc tcctgagttc 2820
tgaacaagt cgtgctgga gaagccaacc gacgggcggg aggtggtctg ccacgcctc 2880
gcctgggact tctacaacgg caaggacttc cggatcaagc agtgcaccac cgtgaacttg 2940
gaggacctg tggtgccca ccacgaaatg ggccacatcc agtatttcat gcagtacaaa 3000
gacttacctg tggccttgag ggagggtgcc aaccccggt tccatgaggc cattggggac 3060
gtgctagccc tctcagtgc tacgccaag cacctgcaca gtctcaacct gctgagcagt 3120
gaggggtgca gcgacgagca tgacatcaac tttctgatga agatggccct tgacaagatc 3180
gcctttatcc ccttcagcta cctcgtcgat cagtggcgt ggagggtatt tgatggaagc 3240
atcaccaagg agaactataa ccaggagtgg tggagcctca ggctgaagta ccagggcctc 3300
tgccccccag tgcccaggac tcaaggtgac tttgaccag gggccaagtt ccacattcct 3360
tctagcgtgc cttacatcag gtacttcgtc agcttcatca tccagttcca gttccacgag 3420
gcactgtgcc aggcagctg ccacacgggc cccctgcaca agtgtgacat ctaccagtcc 3480

aaggaggccg ggcagcgcct ggcgaccgcc atgaagctgg gcttcagtag gccgtggccg 3540
gaagccatgc agctgatcac gggccagccc aacatgagcg cctcgcccat gttgagctac 3600
ttcaagccgc tgctggactg gctccgcacg gagaacgagc tgcattggga gaagctgggc 3660
tgcccgagcgt acaactggac gccgaactcc gctcgctcag aagggccctt cccagacagc 3720
ggccgcgtca gcttctggg cctggacctg gatgcgcagc agggccgcgt gggccagtgg 3780
ctgctgctct tcctgggcat cgccctgctg gtagccaccc tgggcctcag ccagcggctc 3840
ttcagcatcc gccaccgag cctccaccgg cactccacg gggccagtt cggtccgag 3900
gtggagctga gacactctg a 3921

<210> 53
<211> 5297
<212> DNA
<213> Homo sapiens

<400> 53
gggcccggcc gggctgggct ggagcagcgg cggccgggag ccgagcttgc agcgaggagc 60
cggctgaggg gcgcgggagg gaaggaggca agggctccgc ggcgctgtcg cgctgccgct 120
cactctcggg gaagagatgg cggcggagcg gggagcccgg cgactcctca gacccccctc 180
cttctggctc tactgcctgc tgctgctcgg gcgccgggcg ccgggcgcccg cggcggccag 240
gagcggctcc gcgccgagc cccagggagc cagcattcga acgttctctc cattttatct 300
tctggtggag ccggtggata cactctcagt tagaggctct tctgttatat taaactgttc 360
agcatattct gagccttctc caaaaattga atggaaaaa gatggaactt ttttaaactt 420
agtatcagat gatcgacgcc agcttctccc ggatggatct ttatttatca gcaatgtggg 480
gcattccaaa cacaataaac ctgatgaagg ttattatcag tgtgtggcca ctgttgagag 540
tcttggaact attatcagta gaacagcgaa gctcatagta gcaggctctc caagatttac 600
cagccaacca gaaccttctc cagtttatgc tgggaacgga gcaattctga attgtgaagt 660
taatgcagat ttggtcccat ttgtgagggt ggaacagaac agacaacccc ttcttctgga 720
tgatagagtt atcaaacttc caagtggat gctggttatc agcaatgcaa ctgaaggaga 780
tgccgggctt tatcgctcgc tagtggaagg tggggggcca ccaaagtata gtgatgaagt 840
tgaattgaag gttcttcag atcctgaggt gatatcagac ttggtatctt tgaacagacc 900
ttctccctta gtcagagtca ttggtcagga ttagtggttg ccatgtgttg cttcaggact 960
tcctactcca accattaaat ggatgaaaaa tgaggaggca cttgacacag aaagctctga 1020
aagattggta ttgctggcag gtggtagcct ggagatcagt gatgttactg aggatgatgc 1080
tgggacttat tttgtatag ctgataatgg aaatgagaca attgaagctc aagcagagct 1140
tacagtgcaa gctcaacctg aattcctgaa gcagcctact aatatatatg ctcacgaatc 1200
tatggatatt gtatttgaat gtgaagtgc tggaaaacca actccaactg tgaagtgggt 1260
caaaaatggg gatatgggta tccaagtga ttattttaag attgtaaagg aacataatct 1320
tcaagttttg ggtctggtga aatcagatga agggttctat cagtgcattg ctgaaaatga 1380
tgttggaat gcacaagctg gagcccaact gataatcctt gaacatgcac cagccacaac 1440
gggaccactg cttcagctc ctcgggatgt cgtggcctcc ctggtctcta cccgcttcat 1500
caaattgacg tggcggacac ctgcacaga tcctcacgga gacaacctta cctactctgt 1560
gttctacacc aagggaagga ttgctagggg acgtgttgag aataccagtc acccaggaga 1620
gatgcaagta accattcaaa acctaatgcc agcgaccgtg tacatcttta gagttatggc 1680

tcaaaataag catggctcag gagagagttc agctccactg cgagtagaaa cacaacctga	1740
ggttcagctc cctggcccag cacctaacct tcgtgcatat gcagcttcgc ctacctccat	1800
cactgttacg tgggaaacac cagtgtctgg caatggggaa attcagaatt ataagttgta	1860
ctacatggaa aaggggactg ataaagaaca ggatgttgat gtttcaagtc actcttacac	1920
cattaatggg ttgaaaaaat atacagagta tagtttccga gtggtggcct acaataaaca	1980
tggtcctgga gtttccacac cagatgttgc tgttcgaaca ttgtcagatg tttccagtgc	2040
tgctcctcag aatctgtcct tggaagttag aaattcaaag agtattatga ttcactggca	2100
gccacctgct ccagccacac aaaatgggca gattactggc tacaagattc gctaccgaaa	2160
ggcctcccga aagagttagt tcaactgagac cttggttaagc gggacacagc tgtctcagct	2220
gattgaaggt cttgatcggg ggactgagta taatttccga gtggctgctc taacaatcaa	2280
tggtacaggc ccggcaactg actggctgtc tgctgaaact tttgaaagt acctagatga	2340
aactcgtgtt cctgaagtgc ctgactctct tcacgtacgc ccgctcgtta ctgacatcgt	2400
agttagctgg actcctccag agaatcagaa catttgtgtc agaggttacg ccattgggta	2460
tggcattggc agccctcatg cccagaccat caaagtggac tataaacagc gctattacac	2520
cattgaaaat ctggatccca gctctcacta tgtgattacc ctgaaagcat ttaataacgt	2580
gggtgaaggc atccccctgt atgagagtgc tgtgaccagg cctcacacag acacttctga	2640
agttgattta tttgttatta atgctccata cactccagtg ccagatccca ctcccatgat	2700
gccaccagtg ggagttcagg ctccattctc gagtcatgac accatcagga ttacgtgggc	2760
agacaactcg ctgccaagc accagaagat tacagactcc cgatactaca ccgtccgatg	2820
gaaaaccaac atcccagcaa acaccaagta caagaatgca aatgcaacca ctttgagtta	2880
tttggtgact ggtttaaagc cgaatacact ctatgaattc tctgtgatgg tgaccaagg	2940
tcgaagatca agtatcagga gtatgacagc ccatgggacc accttgat tagttccgac	3000
ttctccacc aaggatgtga ctgttgtag taaagagggg aaacctaga ccataattgt	3060
gaattggcag cctccctctg aagccaatgg caaaattaca ggttacatca tatattacag	3120
tacagatgtg aatgcagaga tacatgactg ggttattgag cctgttgtag gaaacagact	3180
gactcaccag atacaagagt taactcttga cacaccatac tacttcaaaa tccaggcacg	3240
gaactcaaag ggcattggac ccatgtctga agctgtccaa ttcagaacac ctaaagcggg	3300
ctcctctgat aaaatgccta atgatcaagc ctcagggtct ggagggaag gaagccggct	3360
gccagacctg ggatccgact acaaacctcc aatgagcggc agtaacagcc ctcattggag	3420
ccccacctct cctctggaca gtaatatgct gctggtcata attgtttctg ttggcgctcat	3480
caccatcgtg gtgggttgta ttatcgctgt cttttgtacc cgctgtacca cctctacca	3540
gaaaaagaaa cgagctgcct gcaaatcagt gaatggctct cataagtaca aagggaattc	3600
caaagatgtg aaacctccag atctctggat ccatcatgag agactggagc tgaaacccat	3660
tgataagtct ccagacccaa accccatcat gactgatact ccaattcttc gcaactctca	3720
agatatcaca ccagttgaca actccatgga cagcaatgc catcaaaggc gaaattcata	3780
cagagggcat gagtacagag acagcatgtc tacactggct ggaaggcgag gaatgagacc	3840
aaaaatgatg atgccctttg actcccagcc accccagcct gtgattagtg cccatcccat	3900
ccattccctc gataaccctc accatcatct ccaactccagc agcctcgctt ctccagctcg	3960
cagtcatctc taccaccggc gcagcccatg gccattggc acatccatgt ccctttcaga	4020

cagggccaat tccacagaat ccgttcgaaa tacccccagc acgacacca tgcagagctc 4080
 ttcgtctcaa acatgctgca ctgatcacca ggaccctgaa ggtgctacca gtcctcttta 4140
 cttggccagc tccaagagg aagattcagg ccagagtctt cccactgccc atgttcgccc 4200
 tccccacca ttgaagagct tcgccgtgcc agcaatcccg cctccaggac ctcccaccta 4260
 tgatcctgca ttgccaagca caccattact gtcccagcaa gctctgaacc atcacattca 4320
 ctcagtgaag acagcctcca tcgggactct aggaaggagc cggcctccta tgccagtgtt 4380
 tgttcccagt gccctgaag tgcaggagac cacaaggatg ttggaagact ccgagagtag 4440
 ctatgaacca gatgagctga ccaagagat ggcccactg gaaggactaa tgaaggacct 4500
 aaacgctatc -acaacagcat- gacgaccttc accaggacct gacttcaaac ctgagtctgg 4560
 aagtcttggg acttaaccct tgaacaag gaattgtaca gagtacgaga ggacagcact 4620
 tgagaacaca gaatgagcca gcagactggc cagcgcctct gtgtagggtt ggctccaggc 4680
 atggccacct gccttccctt ggtcagcctg gaagaagcct gtgtcaggc agcttccctt 4740
 tgctgtctga tattctgcag gactgggcac catgggcaa aattttgtgt ccagggaaga 4800
 ggcgagaagt gcaacctgca ttctactttg tggtcaggcc gtgtctttgt gctgtgactg 4860
 catcaccttt atggagtgtg gacattggca tttatgtaca attttatttg tgtcttattt 4920
 tattttacct tcaaaaacaa aaacgccatc caaaaccaag gaagtccttg gtgttctcca 4980
 caagtgttg acatttgact gctgttcca attatgtatg gaaagcttt gacagtgtgg 5040
 gtcgttcttg gggttgctt gtttttgggt ttcattttta tttttaatt ctgagtcatt 5100
 gcacctccta ccagctgtta atccatcact ctgaggggga ggaatgttg cattgctgtt 5160
 tgtaagcttt ttttattatt tttttattat aattattaaa ggcctgactc tttcctctca 5220
 tcaactgtgag attacagatc tatttgaatt gaatgaaatg taacattgaa aaaaaaaaaa 5280
 aaaaaaaaaa aaaaaaa 5297

<210> 54
 <211> 2366
 <212> DNA
 <213> Homo sapiens

<400> 54
 ggcacgagcg agggagccg aaagatggtg gttaccagat ctgcacgggc taaggccagc 60
 atccaagccg cgtcggtgca aagttccggg caaaagagtt ttgctgctaa tgggattcaa 120
 gcgcatccag aaagtagtac tggatctgat gccgaacta ctgatgaatc acagaccact 180
 gggagcaaaa gtttaatccc tagaactcct aaagctagaa agagtaagag cagaactaca 240
 ggctcactac caaaggggac tgaaccatct acggatggag agacctctga ggcagagtca 300
 aattattctg tgtctgagca ccatgatacc attttaaggg taactaggag aaggcagatc 360
 ttaattgcat gtcctccagt gtccagtgtt aggaagaaag cgaaagtaac tccaacaaag 420
 gagtcttaca ctgaagaaat agtgtctgaa gcagaatctc atgtttcagg tatttctaga 480
 attgtgcttc ctacagaaaa aactacagga gccagaagaa gtaaggctaa atctctgaca 540
 gatccaagcc aagaatctca tacagaagct atatctgatg ctgagacatc aagctcagac 600
 atttcattct ctggaattgc aactagaaga accaggagta tgcagaggaa attaaaggca 660
 caaactgaaa agaaagatag taagattgta ccaggaaatg agaaacagat cgtgggtaca 720
 cctgtgaatt cagaggatc agataccaga caaacttccc atttacaagc aagatctctt 780
 tctgagataa ataagccaaa tttctataat aatgactttg atgatgattt ctcccacaga 840

```

agttcagaaa atatattaac agtgcacgaa cagggccaatg ctgaatctct caaayaaaca 900
aaacagaatt gtaaggattt ggatgaagat gccaatggaa taacagatga ggggaaagaa 960
attaatgaga aaagtcttca gctgaagaat ctttctgaac ttcaggacac tagccttcaa 1020
cagttagttt ctccagagaca ttcaaccccc caaaataaaa atgctgtatc agtgcactct 1080
aatctgaact ctgaggctgt aatgaaatca ttaactcaaa catttgcaac tgtggaagta 1140
ggcagatgga ataacaacaa aaagagcccc ataaaagcaa gtgacttgac aaagtttgg 1200
gattgtggtg gtagtgatga tgaagaagag tccacagtta taagtgtcag tgaagacatg 1260
aacagtgaag ggaatgtaga ttttgaatgt gataccaaac tatacacgtc tgcgcccaac 1320
acatctcagg gtaaagataa ttctgtctta ctagtcttca gcagtgatga aagccaacag 1380
tctgaaaaa gtgagaatga agaggatact ttatgttttg ttgaaaatag tggccaaagg 1440
gagtcattaa gtggagacac aggaagtctg tcatgtgaca atgcattgtt tghtaattgac 1500
acaactcctg gaatgagtgc tgataaaaat ttttacttgg aagaggaaga caaggcaagt 1560
gaggttgcca ttgaggaaga aaaagaagag gaagaggatg aaaaaagtga agaagattca 1620
tcagaccatg acgaaaatga agatgagttt agtgatgaag aagacttcct aaatagcaca 1680
aaggctaaac ttctgaagtt gacaagcagc agcatagacc ctggtctgag tatcaagcag 1740
ttgggtggtt tgtatattaa ttttaatgca gataaactac agtctaacaa gagaacccta 1800
acacagatca aggagaaaaa gaaaaatgag cttctgcaga aagccgtcat tacacctgat 1860
tttgaaaaaa accactgtgt tccaccatat agtgaatcaa agtatcaact tcagaaaaaa 1920
cgcagaaaaa aacgacaaaa aacagcaggg gatggctggt ttggtatgaa agctccagaa 1980
atgacaaatg aactgaaaaa tgatctcaaa gcactgaaga tgagagccag catggaccg 2040
aaaagatttt acaagaaaaa tgatagagat ggcttcccca agtacttcca gattggaacc 2100
attgttgaca atccagctga tttctaccat tcacgaattc ccaagaagca aaggaaaaga 2160
actattgtgg aagactgctg gctgattctg aattcagaga tacaaccgaa ggaagtactc 2220
agagatcatg gctgaaaaa cagcaaatgc agcaggaaaa aagttccgaa agaagaagaa 2280
atttcgcaat taagatttac caagcaaact gcaacatttt acattgctcc tttatttact 2340
tattaaagac gtttgaaaaa ctaaaa 2366

```

```

<210> 55
<211> 3018
<212> DNA
<213> Homo sapiens

```

```

<400> 55
gaattccggg ccaggcatgg tagcgcacg ctgtaatccc agctactcgg gaaactgagg 60
tgggagaatc gattgaacct ggaagtggag gttgcggtga gccaatgca tcctgtcgca 120
ctccagcctg ggcaacaaga gcgaaactcc atctcaaaaa gaaaaaaaaa gatatatatg 180
tgtgacttac aggtacaggt aaagttgctt ctggttttct gggtgttgca tggattttcc 240
tatgcagcca caggtcttta ttttcttact taagtgcctc caacttccca taacacaaat 300
taaggcatga tgaacatcct ctctgtgctg aacatcctgt gtatgtcact tcagaagcct 360
gtgtgacggt ttcttttagt tttataccta ggggtgggat ttctgggtca taggacagta 420
atttatattt atttactaa gtattctctt tctctggctt ttgttacata ttacctgttt 480
gtcctccaga aaacttgac caatttcat tcctaccaat agggtaggag agtgacaaat 540
gggtggattc taactccaaa tctaacacct cttcttttct ttgtttctag cagccatggc 600

```

```

aatgacaggc tcaacacctt gctcatccat gagcaaccac acaaaaggaa gyytyacaat 660
gaccaaaagt acactggaga atttttatag caaccttata gctcaacatg aagaacgaga 720
aatgagacaa aagaagttag aaaaggtgat ggaagaagaa ggcctaaaag atgaggagaa 780
acgactccgg agatcagcac atgctcggaa ggaacagag tttcttcgtt tgaagagaac 840
aagacttga ttggaagatt ttgagtcctt aaaagtaata ggagaggag catttggtga 900
ggtacggctt gttcagaaga aagatacggg acatgtgtat gcaatgaaaa tactccgtaa 960
agcagatatg cttgaaaaag agcaggttgg ccacattcgt gcggagcgtg acattctagt 1020
ggaggcagac agttttgtgg ttgtgaaat gttctatagt ttccaggata agctaaacct 1080
ctacctaatc atggagttcc tgcttgagg ggacatgatg acctgttga tgaaaaaaga 1140
cactctgaca gaagaggaga ctgagtttta tatagcagaa acagtattag ccatagactc 1200
tattcaccaa ctggattca tccacagaga catcaacca gacaaccttc ttttgacag 1260
caagggccat gtgaaacttt ctgactttgg tctttgcaca ggactgaaaa aagcacatag 1320
gacagaattt tataggaatc tgaaccacag cctccccagt gatttcactt tccagaacat 1380
gaattccaaa aggaaagcag aaacctggaa aagaaataga cgtcagctag ccttctccac 1440
agtaggcact cctgactaca ttgctcctga ggtgttcag cagaccgggt acaacaagct 1500
ctgtgattgg tggtcgctt gggtgatcat gtatgagatg ctcatcggct acccacctt 1560
ctgttctgag acccctcaag agacatataa gaaggtgatg aactggaaag aaactttgac 1620
tttctctcca gaagtccca tctctgagaa agccaaggat ctaattttga ggttctgctg 1680
tgaatgggaa catagaattg gagctcctgg agttgaggaa ataaaaagta actcttttt 1740
tgaaggcgtt gactgggaac atatcagaga gagacctgt gcaatatcta ttgaaatcaa 1800
aagcattgat gataacctca acttcgatga gttccagaa tctgatattc ttaagccaac 1860
agtggccaca agtaatcatc ctgagactga ctacaagaac aaagactggg tctcatcaa 1920
ttacacgtac aagcgcttg agggcctgac tgcaagggg gcaatacctt cctacatgaa 1980
agcagcaaaa tagtactct gccacggaat cctatgtgga gcagagttct ttgtataaca 2040
tcatgctttt cctctcacac tctgaagag ctccaagaa gttgatggaa cccaccaata 2100
tgtcatagta aagtctcctg aaatgtggta gtaagaggat tttcttccat aatgcactg 2160
aaaaactgta acaaaagaca accatttcta ctacgtcggc cataaacagc tatectgctt 2220
tggaagagaa gcatcatgag ccaatttgat aggtgtttta aaaataactt gagtttctt 2280
aagttcatca gaatgaagg gaaaaacagc catcatcaa cattattgag attgtcgtgt 2340
atagtcacg aatatcagcc agttcctgta atttgtgac acgctctctg ccaagcccac 2400
caagtatttc ctttatagct aaaagtcca tagtactaag gaaataaagc aataaagaca 2460
gtctcagcag ccaggattct ggctgaagga aatgatccgc caccctgagg gtggtgatgg 2520
tagtttctac ccatacctca gcctcaggcg agtggettat agcctccatt catggtgcac 2580
tttatttatg gtactaagat aaagactgtc aatccattga tttatctct cctgtcccc 2640
atctaaaata cccatgctgc tttctgagt gttgatggg gttaccagct tgatccactg 2700
ttgctcttag aaggccaga aagtctttg gcattgcaag aaatcccga ttagtgga 2760
aaccctcact tctcttcac ggctgtacca gaaaatccct aagacagatc ttgccgtgga 2820
ctagcaatac ctgcaagtgc tgccaatgg aactcaattt attcctggga acctaacgag 2880
gagagcccag gcctaggcag gaggcctgga accctcttg ctaagggtgt gttcctgttc 2940
ctgcaaggtc tccagaacct ctttggaat ggtgaaggaa ccagccaat agaagtacag 3000

```

agccagctga cggaattc 3018

<210> 56
 <211> 1846
 <212> DNA
 <213> Homo sapiens

<400> 56
 cgctcatgga gccctggcat tgagtgtgag cacttcacac tctacctctc tcagttggcc 60
 ctccgaaatg cctcaattta ggagtgggtgc cccactgtgg aggggtatattt caggaccatc 120
 ttacaaatta ttgtgaagtg ttggaaacaa agagcttcct gcttcttttc aacctgggtc 180
 taccatgttc caagctgtag ccaaaaggaa aataaatcag agcttgaaac tagcctttct 240
 gatgggaata tctatctggg acaccctcc ctttttgtct ctgccccca tacgtctcct 300
 ccttacagca caggctgttt gggaaggagg acaggatag tcatctaact tttttccatc 360
 cctagctgag tcatgatta aaaacaaatg aacaaacaaa aacctaaaaa accttcaga 420
 aatacaagg aaaagggttt gtttgtttt tattttaatt tttattctg taggtttttg 480
 gggaacagat ggtatttagt tacatgagaa agttatttag tggtgatttg tgagattctg 540
 gtgcacccat caccgagca gccttcactg tacccaatat gtagtctttt atccctcact 600
 tacctccac ctttccctc gagtcccaa agtccattgt gttattctta tgcctttgca 660
 tcctcatagc tttagtccca cttgtgagtg agaacatatg atgtttggtt ttccattcct 720
 gagttacttc acttagaata atagtctcca tccagggtgc tgcaaatgcc attaatgtgt 780
 tcttttttat ggctgagtag tattccatgg tgtatatata ccacaatttc tttatccact 840
 cattgattga tgggcatttg ggctggttcc atatctttgc agctgtgaat tgtgctgcta 900
 taaacatgcg tgtgcaagta tcttttctgt ataatgactt atttctctct gggtagatac 960
 ccagtagtgg gattactgga tcaaatggta gttctttcta cttttagttc tttaaagaat 1020
 ctccacattg tttccatag tggttgtact agtttacatt ccaccagct gtgtaaacgt 1080
 gttccttttt caccgcatcc acgccaacat ctgttatttt ttgatttttg gattaaggcc 1140
 attcttgctg agtaacgtgg tattgcattg tagttttgat ttgcatttcc cagatcatta 1200
 gtgatgttga gcattttttc ctatatttgt tggccatttg tatatcttct tctgagaatt 1260
 gtctactcat gtccctcagc cagtttttga tgggattggt tgttattttt tcttgctaatt 1320
 ttgtttgagt tccttgtaga ttatagatat tagtcctttg tcagatgtat agattgtgaa 1380
 gattttctcc cactctgtgg gttgtctgtt tactctgctg actgttcctt ttgctgtgca 1440
 gaagttttta tgaagcaagt ctttggggag gatattttgt ctcataaaag ttattacaaa 1500
 catcaagaaa gtggattcca gccgggcgca gtggctcacg cctgtaatcc cagcactttg 1560
 ggaggccaag acgggtggat cacgaggtca ggagatccag accatcctgg gtaacacggg 1620
 gaaacctgtc tctactaaaa atacaaaaaa ttagctgggc atggtggcgg gcgcctgtag 1680
 tcccagctac ttgggaggct gaggcaggag aatagcgtga acctggggagg tggagcttgc 1740
 agtgagccga gattgtgcca ctgcactcca gcctggggga cagagcgaga ctctgtctca 1800
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1846

<210> 57
 <211> 4006
 <212> DNA
 <213> Homo sapiens

<400> 57


```

ccgattcctg gcttttgcaa ggctgtggtc ggtggcacc agtgcctctg acccagytcc 60
agcgagcctt ttccctgggt ttgcagctgt tgtgtaccg ccgccgtcgc cgccgtcgcc 120
gcctgctctg cggggctcat gtgtgcttcc gcctcttccc ggttccgggc tcagggtctg 180
ttctggctct cctagtctct ggagctgtgc ggtcttatgc attggaactt aatttgacag 240
attcagaaaa tgccacttgc ctttatgcaa aatggcagat gaatttcaca gtacgctatg 300
aaactacaaa taaaacttat aaaactgtaa ccatttcaga ccatggcact gtgacatata 360
atggaagcat ttgtggggat gatcagaatg gtcccaaat agcagtgcag ttcggacctg 420
gcttttctct gattgcgaat ttaccaagg cagcatctac ttattcaatt gacagcgtct 480
cattttctca caacactggg gataacacaa catttcctga tgcagaagat aaaggaattc 540
ttactgttga tgaacttttg gccatcagaa ttccattgaa tgaccttttt agatgcaata 600
gtttatcaac ttggaaaag aatgatgttg tccaacacta ctgggatgtt cttgtacaag 660
cttttgtcca aaatggcaca gtgagcacia atgagttcct gtgtgataaa gacaaaactt 720
caacagtggc acccaccata cacaccactg tgccatctcc tactacaaca cctactccaa 780
aggaaaaacc agaagctgga acctattcag ttaataatgg caatgatact tgtctgctgg 840
ctaccatggg gctgcagctg aacatcactc aggataaggt tgcttcagtt attaacatca 900
acccaatac aactcactcc acaggcagct gccgttctca cactgctcta cttagactca 960
atagcagcac cattaagtat ctgacttttg tctttgctgt gaaaaatgaa aaccgatttt 1020
atctgaagga agtgaacatc agcatgtatt tggtaatgg ctccgttttc agcattgcaa 1080
ataacaatct cagctactgg gatgcccccc tgggaagttc ttatatgtgc aacaaagagc 1140
agactgttcc agtgtctgga gcatttcaga taaatacctt tgatctaagg gttcagcctt 1200
tcaatgtgac acaaggaaag tattctacag ccaagagtg ttcgctggat gatgacacca 1260
ttctaatccc aattatagtt ggtgctggtc ttcaggctt gattatcggt atagtgttg 1320
cttacgtaat tggcagaaga aaaagttagt ctggatatca gactctgtaa cactaatcaa 1380
tacgtgatct ctgttacaaa agaaaaaagc aagtacaagt tccaacatgc aatactggtc 1440
aacttaaggt atatttagtt gcagtcacgc tctttagaat gggtggtatg ggggatttca 1500
aacttaacaa aaaaactatc aactacaaat tagttgcctg actttggttt ttccaaccaa 1560
ggaatttaaa actgttattt ttacagcaaa agatgtgcaa aatcactgga ttataagttc 1620
tattttactg tcttgaatta gtatttcagt gttttcattt tagacattca gactaaaaat 1680
acaccgttta gaaaaacaa tttttgaaa agagattttt tttccctgca ggtagttag 1740
ttgaacaaca tgttctaccg tggatttga cttgctcctt ttgctctttt tgtgtgtgtg 1800
tgtgtgtgtg tgtgtgtgtg tgtgattttt gttgcaggt taacttagct actttggcat 1860
tgctgcatat ttgaccttgg agagatataa tagtagattt gaacaggggc tggattatt 1920
atgttcttag caataaatgc ttttctaatg ctttttgaat acatttgtat ttatgtggct 1980
gtaatgacaa aagatacaaa agctttttta aatttagagt aggtattaat cttattgttt 2040
aatctttttt ttaaaaaaac tggatatttc aatcttttaa attgcaatat ataagactat 2100
tccaactggg catttcaatc catttttttag gtgctttaga gataattgct tgccagtgcc 2160
aattgagggc attagtactt tgtgctcata aattggcctc tgtatgcagt actaaaatta 2220
atgcagattt ctcttttagc ttccaacatt tctgttgat agtgatgtat ttattattt 2280
tctttttctt aagaaatgcc agtgtgtcct agaacctaga taacgaagtg cacttacact 2340
tataaaataa cttgcatcta ggctgggcgt ggcggctcac gcctgtaac ccagcacttt 2400

```

```

gggaggccga agtgggtgga tcacttgagg ccaggagttt gagaccagcc tggccaacat 2460
ggtgaaaccc catctctatc agaaatacaa aaaattagct gggcatggtg gtgggcgcct 2520
gtaatcccag ttactcggga ggctgaggca ggagaatcac ttgaaccggg gaggcagagg 2580
ttgcggtgag ccaagagcgc accattgcac tccagccttg ggcgacaaaa acgaaactcc 2640
atcttcaaaa caaaacaaaa caaaacaaac aaacaaacaa aacttgcatc ttaacaaaaa 2700
gtcttggttt tatcttaatc cattaaaagt tggctctggt tccagcttgc attgattgct 2760
acaacatcac taatttggtt ttcacattta aatgggtctg tgctaataca aactttcggt 2820
gttattattc gttatggtag aatcattttt aattcacgtg ctttgtgttc agttttgtgg 2880
tctgagagat gtaccaattg tcaaattacc gtgtaccacc taatgtttat aggagaaagc 2940
aaaatacatc agcttggtag ttaacacatc aaatatttct tgctgcttct aggagaactt 3000
ttttggtgtg tgttggaatg gctgagcaaa tattaataat gttaatatgc agccatatat 3060
ggaaggttcc tgtggggttg tttttctgtg tttttttttt ttgtggtggg attatgtgcc 3120
tcccattcac tagaaaatga gaaaattgtc tgggttccaa aatattgaca ttgaatggat 3180
caatacacac acacagacat atatataat atatgcacac atatataggc agttgcatgc 3240
ctagcatggg tattttataa ccatataact gagttatatt ggaattataa atattttccg 3300
tcacttaaat ttgttctttg tttagcctga aaacctttat ggctcaagat cagattcctg 3360
actaaccctt ctcttagagc tacagcgagc tgcattacca gcttaaaaca cttcttaggg 3420
attaaatata gatgtaattt ttcaaatcg tttttaattt aaactgtgtt ttagtgtaaa 3480
attgttaacc ttgtaagatg gataatgtgt ataagaatgt aggccttaac tatttcacat 3540
gagtcaaac aaagcagctt taaaaaata attggaagca caatgcatgg cactgactga 3600
atgctgttaa tatttctaaa agtttctaca ttcagattat atgcctgatt catagtaaaa 3660
tacctctaataaacactgtt ttatagaaaa cctgacttca gtgaatatatt ttgtatttta 3720
catgggccag tttatatact gctatttaca ctattatttc ctatagctac atgttctttg 3780
taccttttgt agttttattt gtattactag attcatacct tgatggtaac gctctatctg 3840
gttttggtg tttttcatgt tttagcattt gtataaagaa actgggtccat gtaaaactt 3900
tccatgtttt ttcttcaaat gtttaaacca ctagttagt tatggatct ttagatatatt 3960
gcctgtctgt ttgctcaaaa ttgcttctaa aacaataaag attctt 4006

```

<210> 58
<211> 1879
<212> DNA
<213> Homo sapiens

```

<400> 58
ctgaggccca cgcagggcct aggggtggga gatggcaggt gggggcggcg acctgagcac 60
caggaggctg aatgaatgta ttccaccagt agcaaatgag atgaaccatc ttcctgcaca 120
cagccacgat ttgcaaagga tgttcacgga agaccagggt gtagatgaca ggctgctcta 180
tgacattgta ttcaagcact tcaaaagaaa taagggtggag atttcaaatg caataaaaaa 240
gacatttcca ttcctcgagg gcctccgtga tcgtgatctc atcacaaata aaatgtttga 300
agattctcaa gattcttgta gaaacctggt ccctgtacag agagtgtgtg acaatgttct 360
tagtgaactg gagaagacat ttaacctgcc agttctggaa gcactgttca gcgatgtcaa 420
catgcaggaa tccccgatt taattcacat ttataaaggc tttgaaaatg taatccatga 480
caaattgcct ctccaagaaa gtgaagaaga agagaggag gagaggtctg gcctccaact 540

```

```

aagtcttgaa caaggaactg gtgaaaaactc ttttcgaagc ctgacttggc caccttcggg 600
ttccccatct catgctggtg caacccacc tgaaaatgga ctctcagagc acccctgtga 660
aacagaacag ataatgcaa agagaaaaga tacaaccagt gacaaagatg attcgctagg 720
aagccaacaa acaaatgaac aatgtgtctc aaaggctgag ccaacagagt cctgcgaaca 780
aattgctgtc caagtgaata atggggatgc tggaaaggag atgccctgcc cgttgccctg 840
tgatgaagaa agcccagagg cagagctaca caaccatgga atccaaatta attcctgttc 900
tgtgcgactg gtggatataa aaaaggaaaa gccattttct aattcaaaag ttgagtcca 960
agcccaagca agaactcatc ataaccaggc atctgacata atagtcatca gcagtggagg 1020
ctctgaagga tccactgacg ttgatgagcc cttagaagtc ttcattctcag caccgagaag 1080
tgagcctgtg atcaataatg .acaacccttt agaatcaat gatgaaaagg agggccaaga 1140
agccacttgc tcacgacccc agattgtacc agagcccatg gatttcagaa aattatctac 1200
attcagagaa agttttaaga aaagagtgat aggacaagac cagcactttt cagaatccag 1260
tgaggaggag gcgcccgcag aagcctcaag cggggcactg agaagcaagc atggtgagaa 1320
ggctcctatg acttctagaa gtacatctac ttggagaata cccagcagga agagacgttt 1380
cagcagtatg gacttttcag acctgagtaa tggagaagag cttcaggaaa cctgcagctc 1440
atccctaaga agagggtcag gtaagaaga ttaggatgcc aagacttggc ctgcagaatg 1500
tcaggaaatg gaattaaaag ctgctgtttc cagacgcttt ttattctgag caccttact 1560
accttgtatc cagttcatct gggaaactcct ttttgcatth tagaaaatgg aaagaggcag 1620
gaaattatga taaactcatg ttaacagaa agagtttcac tgactaaatg tatgtaatta 1680
tattttgttg ttgtagaaga aataaatagc aaatttgttg tattcttttt ttaaacctg 1740
ctctcattcc tattaacact aagatcttag atttttatag tgataaatgg gttgacatca 1800
ttgtcgtttg taattgtaaa gcctcaaaag acaactgttc ctactatgta attatagaca 1860
gaaataaaaa cttcagatc 1879

```

```

<210> 59
<211> 2286
<212> DNA
<213> Homo sapiens

```

```

<400> 59
cctgtgagca ccacgtcaac ggctccggc ccccatgcac gggggaggga gatacccca 60
agtgtagcaa gatctgtgag cctggctaca gcccgacctc caaacaggac aagcactagc 120
gatacaattc ctacagcgtc tccaatagcg agaaggacat catggccgag atctacaaaa 180
acggccccgt ggaggagct ttctctgtgt attcggactt cctgctctac aagtcaggag 240
tgtaccaaca cgtcaccgga gagatgatgg gtggccatgc catccgcatc ctgggctggg 300
gagtggagaa tggcacaccc tactggctgg ttgccaactc ctggaacact gactggggtg 360
acaatggctt ctttaaaata ctacagaggc aggatcactg tggaaatcga tcagaagtgg 420
tggtggaat tccacgcacc gatcagtact gggaaaagat ctaatctgcc gtgggcctgt 480
cgtgccagtc ctgggggcga gatcggggta gaaatgcatt ttattcttta agttcacgta 540
agatacaagt ttacagacag gtctgaagga ctggattggc caaacatcag acctgtcttc 600
caaggagacc aagtcctggc tacatcccag cctgtgggta cagtgcagac aggccatgtg 660
agccaccgct gccagcacag agcgtccttc cccctgtaga ctagtgccgt aggagtacct 720
gctgccccag ctgactgtgg cccctccgt gatccatcca tctccaggga gcaagacaga 780

```

```

gacgcaggaa tggaaagcgg agttcctaac aggatgaaag tcccccatc agttcccca 840
gtacctccaa gcaagtagct ttccacattt gtcacagaaa tcagaggaga gacggtgttg 900
gagccctttg gagaacgcca gtctcccagg cccctgcat ctatcgagtt tgcaatgtca 960
caacctctct gatcttgtgc tcagcatgat tctttaatag aagttttatt ttttcgtgca 1020
ctctgcta at catgtgggtg agccagtggg acagcgggag acctgtgcta gttttacaga 1080
ttgctcctt atgacgcggc tcaaaaggaa accaagtggg caggagtgtg ttctgacca 1140
ctgatctcta ctaccacaag gaaaatagtt taggagaaac cagcttttac tgttttgaa 1200
aaattacagc ttcacctgt caagttaaca aggaatgcct gtgccaataa aaggtttcgg 1260
aattccgtcc cctttcaagt tttagggaaa ttttaactgaa gtgtatacaa attagacatt 1320
gctaataatgt acaaaagtat tttatacggg ttttgaacga tctagctatt tgcaataaac 1380
aggatgttac aaaacagtc caataatgca tttcctatta agaagcaca tacacaacat 1440
aattcaattt tattaaaaa taacttcaaa atgtagaaca atcccctta ggaagaaaag 1500
ctattttctg agttcactct gtcagtaaac acacaagttg aacgctgcag cagagggctg 1560
tccttttcca tggagaaaag aaatgaggct tctagggcct atcttttctg ggtaaaaatt 1620
ccacctacag ctgagatggg cagttattgc ctgtggtagg cagaatttga aaatgccct 1680
tcccccttc aatgagctaa tctccagaac cgtgaatat gatgagatga gacagtactc 1740
ctgcaattat gttctatcgc acaatcaacc ttaaaatata tctgtgggct tgagctaatac 1800
atatgccctt aaaacaggag gacgggagag agatatgaag catgagaaag agcaggaagg 1860
ctggtttgaa gctggagggg accacataag aaggaatgca ggcagccttg aggtgagaga 1920
ggggcctcca gctgagagcc agcaaagaac tgaattccgc caacaacctg aatgaactta 1980
gaagcagatt cttcccaga gcctccatga aggaatgttg tctgccaac ctttatttca 2040
gcctttaaga cctgagcag agaatccagc cactgtgc cagactcatg agctacagaa 2100
ctgctatggg tattgtttt taaactgcta aatttgggt aatttgtcac acagcaatag 2160
aaaactaata cactgccc aa ggttaactt tcttaaccta attacattg gcagtttctg 2220
cttgggttct gaatgcattt ttttacaaa agctctgctg gaaaaactga ataacgcgct 2280
ggcagc 2286

```

```

<210> 60
<211> 7680
<212> DNA
<213> Homo sapiens

```

```

<400> 60
gaagagcaag aggcaggctc agcaaatggt tcagccccag tccccggtgg ctgtcagtc 60
aagcaagccc ggtgttatg acaatggaaa aactatcag ataaatcaac agtgggagcg 120
gacctaccta ggtaatgtgt tggttgtac ttgttatgga ggaagccgag gttttaactg 180
cgaaagtaaa cctgaagctg aagagacttg ctttgacaag taaactggga acacttaccg 240
agtgggtgac acttatgagc gtcctaaaga ctccatgac tgggactgta cctgcacg 300
ggctggcgga gggagaataa gctgtacat cgcaaaccgc tgccatgaag ggggtcagtc 360
ctacaagatt ggtgacacct ggaggagacc acatgagact ggtggttaca tgttagagtg 420
tgtgtgtctt ggtaatggaa aaggagaatg gacctgaag cccatagctg agaagtgtt 480
tgatcatgct gctgggactt cctatgtgt cgagaaaacg tgggagaagc cctaccaagg 540
ctggatgatg gtatgtgta cttgcctggg agaaggcagc ggacgcatca cttgcacttc 600

```

tagaaataga tgcaacgac aggacacaag gacatcctat agaattggag acacctggag 660
 caagaaggat aatcgaggaa acctgctcca gtgcatctgc acaggcaacg gccgaggaga 720
 gtggaagtgt gagaggcaca cctctgtgca gaccacatcg agcggatctg gcccttcac 780
 cgatgttcgt gcagctgttt accaaccgca gcctcaccct cagcctcctc cctatggcca 840
 ctgtgtcaca gacagtgtg tggctactc tgtggggatg cagtgggtga agacacaagg 900
 aaataagcaa atgctttgca cgtgcctggg caacggagtc agctgccaag agacagctgt 960
 aaccagact tacggtggca acttaaatgg agagccatgt gtcttaccat tcacctacaa 1020
 tggcaggacg ttctactcct gcaccacgga agggcgacag gacggacatc tttggtgcag 1080
 cacaacttcg aattatgagc aggaccagaa atactctttc tgcacagacc aactgtttt 1140
 ggttcagact caaggaggaa attccaatgg tgccttgtgc cacttccctc tcctatacaa 1200
 caaccacaat tacactgatt gcacttctga gggcagaaga gacaacatga agtgggtgtg 1260
 gaccacacag aactatgatg ccgaccagaa gtttgggttc tgcccatggt ctgccacga 1320
 ggaaatctgc acaaccaatg aaggggtcat gtaccgatt ggagatcagt gggataagca 1380
 gcatgacatg ggtcacatga tgaggtgcac gtgtgttggg aatggctgtg gggaaatggac 1440
 atgcattgcc tactcgcaac ttcgagatca gtgcattgtt gatgacatca cttacaatgt 1500
 gaacgacaca ttccacaagc gtcatgaaga ggggcacatg ctgaactgta catgcttcg 1560
 tcagggtcgg ggcaggtgga agtgtgatcc cgtcgaccaa tgccaggatt cagagactgg 1620
 gacgttttat caaattggag attcatggga gaagtatgtg catggtgtca gataccagt 1680
 ctactgttat ggccgtggca ttggggagtg gcattgcaa cctttacaga cctatccaag 1740
 ctcaagtgtt cctgtcgaag tatttatcac tgagactccg agtcagcca actcccacc 1800
 catccagtgg aatgcaccac agccatctca catttccaag tacattctca ggtggagacc 1860
 taaaaattct gtaggccgtt ggaaggaagc taccatacca ggccactaa actcctacac 1920
 catcaaaggc ctgaagcctg gtgtggtata cgagggccag ctcacagca tccagcagta 1980
 cggccaccaa gaagtgactc gctttgactt caccaccacc agcaccagca cacctgtgac 2040
 cagcaacacc gtgacaggag agacgactcc cttttctcct cttgtggcca cttctgaatc 2100
 tgtgaccgaa atcacagcca gtagctttgt ggtctcctgg gtctcagctt ccgacaccgt 2160
 gtcgggattc cgggtggaat atgagctgag tgaggaggga gatgagccac agtacctgga 2220
 tcttccaagc acagccactt ctgtgaacat ccctgacctg cttcctggcc gaaaatacat 2280
 tgtaaatgtc tatcagatat ctgaggatgg ggagcagagt ttgatcctgt ctacttcaca 2340
 aacaacagcg cctgatgccc ctcctgaccc gactgtggac caagttgatg acacctcaat 2400
 tgttgttcgc tggagcagac cccaggctcc catcacaggg tacagaatag tctattcgcc 2460
 atcagtagaa ggtagcagca cagaactcaa ccttcctgaa actgcaaact ccgtcaccct 2520
 cagtgacttg caacctggtg ttcagtataa catcactatc tatgtgtgg aagaaatca 2580
 agaaagtaca cctgtttgca ttcaacaaga aacctgtgc accccacgct cagatacagt 2640
 gccctctccc agggacctgc agtttgtgga agtgacagac gtgaaggatc ccatcatgtg 2700
 gacaccgctt gagagtgcag tgaccggcta ccgtgtggat gtgatcccg tcaacctgcc 2760
 tggcgagcac gggcagaggc tgcccatcag caggaacacc tttgcagaag tcaccgggct 2820
 gtcccctggg gtcacctatt acttcaaagt ctttgcatg agccatggga gggagagcaa 2880
 gcctctgact gctcaacaga caaccaaact ggatgtctcc actaacctcc agtttgtcaa 2940

tgaaactgat tctactgtcc tggtagatg gactccacct cgggccaga taacaggata 3000
ccgactgacc gtgggcctta cccgaagagg ccagcccagg cagtacaatg tgggtccctc 3060
tgtctccaag taccctctga ggaatctgca gcctgcatct gactacaccg tatccctcgt 3120
ggccataaag ggcaaccaag agagcccca agccactgga gtctttacca cactgcagcc 3180
tgggagctct attccacctt acaacaccga ggtgactgag accaccatcg tgatcacatg 3240
gacgcctgct ccaagaattg gttttaagct ggggtgacga ccaagccagg gaggagaggc 3300
accacgagaa gtgacttcag actcaggaag catcgttggt tccggcttga ctccaggagt 3360
agaatacgtc tacaccatcc aagtctgag agatggacag gaaagagatg cgccaattgt 3420
aacaagaatg gtgacacatc tgtctccacc acaaaacttg catctggagg caaacctga 3480
cactggagtg ctacagctct cctgggagag gagcaccacc ccagacatta ctggttatag 3540
aattaccaca acccttaca acggccagca gggaaattct ttggaagaag tgggccatgc 3600
tgatcagagc tctgcactt ttgataacct gactccggc ctggagtaca atgtcagtgt 3660
ttacactgtc aaggatgaca aggaaagtgt ccctatctct gataccatca tcccagctgt 3720
tctctctccc actgacctgc gattcaccaa cattggtcca gacaccatgc gtgtcacctg 3780
ggctccaccc ccattcattg atttaaccaa ctctctggtg cgttactcac ctgtgaaaaa 3840
tgaggaagat gttgcagagt tgtcaatttc tccttcagac aatgcagtgg tcttaacaaa 3900
tctctgcct ggtacagaat atgtagttag tgtctccagt gtctacgaac aacatgagag 3960
cacacctctt agaggaagac agaaaacagg tcttgattcc ccaactggca ttgacttttc 4020
tgatattact gccaactctt ttactgtgca ctggattgct cctcgagcca ccactactgg 4080
ctacaggatc cgcatcatc ccgagcactt cagtgggaga cctcgagaag atcgggtgcc 4140
ccactctcgg aattccatca cctcaccaa cctcactcca ggcacagagt atgtggtcag 4200
catcgttgct cttaatggca gagaggaaag tcccttattg attggccaac aatcaacagt 4260
ttctgatgtt ccgagggacc tggaaagtgt tgctgcgacc cccaccagcc tactgatcag 4320
ctgggatgct cctgctgtca cagttagata ttacaggatc acttacggag aaacaggagg 4380
aaatagccct gtccaggagt tctactgtgc tgggagcaag tctacagcta ccactcagcg 4440
ccttaaacct ggagttgatt ataccatcac tgtgtatgct gtcactggcc gtggagacag 4500
ccccgaagc agcaagccaa tttccattaa ttaccgaaca gaaattgaca aacctccca 4560
gatgcaagt accgatgttc aggacaacag cattagtgtc aagtggctgc cttcaagttc 4620
ccctgttact ggttacagag taaccaccac tccccaaaat ggaccaggac caacaaaaac 4680
taaaactgca ggtccagatc aaacagaaat gactattgaa ggcttgagc ccacagtgga 4740
gtatgtggtt agtgtctatg ctcagaatcc aagcggagag agtcagcctc tggttcagac 4800
tgcagtaacc aacattgatc gccctaaagg actggcattc actgatgtgg atgtcgattc 4860
catcaaaatt gcttgggaaa gcccacagg gcaagtttcc aggtacaggg tgacctactc 4920
gagccctgag gatggaatcc atgagctatt ccctgcacct gatggtgaag aagacactgc 4980
agagctgcaa ggcctcagac cgggttctga gtacacagtc agtgtggttg ccttgacaga 5040
tgatattgag agccagcccc tgattggaac ccagtccaca gctattcctg caccaactga 5100
cctgaagttc actcaggtca caccacaag cctgagcgcc cagtggacac caccatgt 5160
tcagctcact ggatatcag tgcgggtgac cccaaggag aagaccggac caatgaaaga 5220
aatcaacctt gctcctgaca gctcatccgt ggttgatca ggacttatgg tggccacca 5280
atatgaagtg agtgtctatg ctcttaagga cactttgaca agcagaccag ctccagggtg 5340

tgtcaccact ctggagaatg tcagcccacc aagaagggt cgtgtgacag atgctactga 5400
 gaccaccatc accattagct ggagaaccaa gactgagacg atcactggct tccaagtga 5460
 tgccgttcca gccaatggcc agactccaat ccagagaacc atcaagccag atgtcagaag 5520
 ctacaccatc acaggtttac aaccaggcac tgactacaag atctacctgt acaccttgaa 5580
 tgacaatgct cggagctccc ctgtggtcat cgacgcctcc actgccattg atgcaccatc 5640
 caacctgcgt ttcttgccca ccacacccaa ttctttgctg gtatcatggc agccgccacg 5700
 tgccaggatt accggctaca tcatcaagta tgagaagcct gggctcctc ccagagaagt 5760
 ggtccctcgg ccccgccctg gtgtcacaga ggctactatt actggcctgg aaccgggaac 5820
 cgaatataca atttatgtca ttgccctgaa gaataatcag aagagcgagc ccctgattgg 5880
 aaggaaaaag acagacgagc ttcccaact ggtaaccctt ccacaccca atcttcatgg 5940
 accagagatc ttggatgttc ctccacagt tcaaaagacc cctttcgtca cccaccctgg 6000
 gtatgacact ggaatggtta ttacgttcc ttgacattct ggtcagcaac ccagtgttg 6060
 gcaacaaatg atctttgagg aacatggttt taggcggacc acaccgcca caacggccac 6120
 ccccataagg cataggccaa gaccataccc gccgaatga ggacaagaag ctctctctca 6180
 gacaaccatc tcatgggccc cattccagga cacttctgag tacatcattt catgtcatcc 6240
 tgttggcact gatgaagaac ccttacagtt cagggttcc ttgaaactta ccagtgccac 6300
 tctgacaggc ctcaccagag gtgccaccta caacatcata gtggaggcac tgaagacca 6360
 gcagaggcat aaggttcggg aagaggttgt tacctgggc aactctgtca acgaaggctt 6420
 gaaccaacct acggatgact cgtgctttga cccctacaca gtttccatt atgccgttg 6480
 agatgagtgg gaacgaatgt ctgaatcagg ctttaactg ttgtgccagt gcttaggctt 6540
 tggaagtgg catttcagat gtgattcatc tagatgtgc catgacaatg gtgtgaacta 6600
 caagattgga gagaagtggg accgtcaggg agaaaatggc cagatgatga gctgcacatg 6660
 tcttgggaac ggaaaaggag aattcaagtg tgaccctcat gaggcaacgt gttacgatga 6720
 tgggaagaca taccacgtag gagaacagtg gcagaaggaa tatctcgtg ccatttgctc 6780
 ctgcacatgc tttggaggcc agcggggctg gcgctgtgac aactgccga gacctgggg 6840
 tgaacccagt cccgaaggca ctactggcca gtcctacaac cagtattctc agagatacca 6900
 tcagagaaca aacactaatg ttaattgccc aattgagtgc ttcatgcctt tagatgtaca 6960
 ggctgacaga gaagattccc gagagtaaat catctttcca atccagagga acaagcatgt 7020
 ctctctgcca agatccatct aaactggagt gatgttagca gaccagctt agagttcttc 7080
 tttctttctt aagcccttg ctctggagga agttctccag cttcagctca actcacagct 7140
 tctccaagca taccctggg agtttctga gggtttctc ataaatgagg gctgcacatt 7200
 gcctgttctg cttcgaagta ttcaataccg ctcatgttt taaatgaagt gattctaaga 7260
 tttggtttgg gatcaatagg aaagcatatg cagccaacca agatgcaa atgtttgaaat 7320
 gatatgacca aaattttaag taggaaagtc acccaaacac ttctgctttc acttaagtgt 7380
 ctggcccgca atactgtagg aacaagcatg atcttggtac tgtgatattt taaatatcca 7440
 cagtactcac tttttccaaa tgatcctagt aattgcctag aaatatctt ctcttacctg 7500
 ttatttatca atttttccca gtatttttat acggaaaaa ttgtattgaa aacacttagt 7560
 atgcagtga taagaggaa ttggtataat tatggtgggt gattattttt tatactgtat 7620
 gtgcaaaagc ttactactg tggaaagaca actgttttaa taaaagattt acattccaca 7680

<210> 61
 <211> 570
 <212> DNA
 <213> Homo sapiens

<400> 61
 gcctgcagcc gcagagatgt tgatgcctaa gaagaaccgg attgccatct atgaactcct 60
 ttttaaggag ggagtcattg tggccaagaa ggatgtccac atgcctaagc acccgagct 120
 ggcagacaag aatgtgcccc accttcattg catgaaggcc atgcagtctc tcaagtcccg 180
 aggctacgtg aaggaacagt ttgcctggag acatttctac tggtagctta ccaatgaggg 240
 tatccagtat ctccgtgatt accttcattg gccccggag attgtgcctg ccaccctacg 300
 ccgtagccgt ccagagactg gcaggcctcg gcctaaaggt ctggagggtg agcgacctgc 360
 gagactcaca agaggggaag ctgacagaga tacctacaga cggagtgtg tgccacctgg 420
 tgccgacaag aaagccgagg ctggggctgg gtcagcaacc gaattccagt ttagaggcgg 480
 atttggctgt ggacgtggtc agccacctca gtaaaattgg agaggattct tttgcattga 540
 ataaacttac agccaaaaaa ccttaaaaaa 570

<210> 62
 <211> 560
 <212> DNA
 <213> Homo sapiens

<400> 62
 atggcgacga aggccgtgtg cgtgctgaag ggcgacggcc cagtgcaggg catcatcaat 60
 ttcgagcaga aggaaagtaa tggaccagtg aagggtgtgg gaagcattaa aggactgact 120
 gaaggcctgc atggattcca tgttcattg tttggagata atacggcagg ctgtaccagt 180
 gcaggctctc actttaatcc tctatccaga aaacacggtg ggccaaagga tgaagagagg 240
 catgttggag acttgggcaa tgtgactgct gacaaagatg gtgtggccga tgtgtctatt 300
 gaagattctg tgatctcact ctccaggagc cattgcatca ttggccgcac actggtggtc 360
 catgaaaaag cagatgactt gggcaaaggt ggaatgaag aaagtacaaa gacaggaaac 420
 gctggaagtc gtttggcttg tgggtgaatt gggatcggcc aataaacatt cccttgatg 480
 tagtctgagg ccccttaact catctgttat cctgctagct gtagaaatgt atcctgataa 540
 acattaaaca ctgtaattct 560

<210> 63
 <211> 9771
 <212> DNA
 <213> Homo sapiens

<400> 63
 atgtggccca cgagacgcct gggtactatc aaaaggagcg gggtcgacgg tccccacttt 60
 cccctgagcc tcagcacctg cttgtttgga aggggtattg aatgtgacat ccgtatccag 120
 cttctgttg tgtcaaaaca acattgcaaa attgaaatcc atgagcagga ggcaatatta 180
 cataatttca gttccacaaa tccaacacaa gtaaatgggt ctgttattga tgagcctgta 240
 cggctaaaac atggagatgt aataactatt attgatcgtt ccttcaggta tgaatgaa 300
 agtcttcaga atggaaggaa gtcaactgaa tttccaagaa aaatacgtga acaggagcca 360
 gcacgtcgtg tctcaagatc tagcttctct tctgaccctg atgagaaagc tcaagattcc 420
 aaggcctatt caaaaatcac tgaaggaaaa gtttcaggaa atcctcaggt acatatcaag 480
 aatgtcaaag aagacagtac cgcagatgac tcaaaagaca gtgttgctca ggaacaact 540

aatgttcatt cctcagaaca tgctggacgt aalygcayaa atgcagctga ccccaattct 600
 ggggatttta aagaaatttc cagcgtaaa ttagtgagcc gttatggaga attgaagtct 660
 gttcccaacta cacaatgtct tgacaatagc aaaaaaatg aatctccctt ttggaagctt 720
 tatgagtcag tgaagaaaga gttggatgta aaatcacaaa aagaaatgt cctacagtat 780
 tgtagaaaat ctggattaca aactgattac gcaacagaga aagaaagtgc tgatggttta 840
 cagggggaga cccaactgtt ggtctcgcgt aagtcaagac caaaatctgg tgggagcggc 900
 cacgctgtgg cagagcctgc ttcacctgaa caagagcttg accagaacaa ggggaaggga 960
 agagacgtgg agtctgttca gactcccagc aaggctgtgg gcgccagctt tcctctctat 1020
 gagccggcta aaatgaagac ccctgtacaa tattcacagc aacaaaattc tccacaaaaa 1080
 cataagaaca aagacctgta tactactggt agaagagaat ctgtgaatct gggtaaaagt 1140
 gaaggcttca aggctgtgta taaaactctt actcccagga agctttcaac tagaaatcga 1200
 acaccagcta aagttgaaga tgcagctgac tctgccacta agccagaaaa tctctcttcc 1260
 aaaaccagag gaagtattcc tacagatgtg gaagttctgc ctacggaaac tgaaattcac 1320
 aatgagccat ttttaactct gtggtcact caagttgaga ggaagatcca aaaggattcc 1380
 ctgagcaagc ctgagaaatt gggcactaca gctggacaga tgtgctctgg gttacctggt 1440
 cttagttcag ttgatatcaa caactttggt gattccatta atgagagtga gggaaacct 1500
 ttgaaaagaa ggcgtgtgtc ctttgggtggg cacctaagac ctgaactatt tgatgaaaac 1560
 ttgcctccta atacgcctct caaaagggga gaagcccaa ccaaagaaa gtctctggtta 1620
 atgcacactc cacctgtcct gaagaaaatc atcaaggaac agcctcaacc atcaggaaaa 1680
 caagagtcag gttcagaaat ccatgtggaa gtgaaggcac aaagcttgggt tataagccct 1740
 ccagctccta gtcctaggaa aactccagtt gccagtgatc aacgccgtag gtcctgcaaa 1800
 acagccccctg cttccagcag caaatctcag acagaggttc ctaagagagg aggagaaaga 1860
 gtggcaacct gccttcaaaa gagagtgtct atcagccgaa gtcaacatga tattttacag 1920
 atgatatgtt ccaaaagaag aagtgggtgtc tcggaagcaa atctgattgt tgcaaaatca 1980
 tgggcagatg tagtaaaact tgggtcaaaa caaacacaaa ctaaagtcac aaaacatggt 2040
 cctcaaagggt caatgaacaa aaggcaaaga agacctgcta ctccaaagaa gcctgtgggc 2100
 gaagttcaca gtcaatttag tacaggccac gcaaactctc cttgtaccat aataataggg 2160
 aaagctcata ctgaaaaagt acatgtgcct gctcgacct acagagtgtc caacaacttc 2220
 atttcaacc aaaaaatgga ctttaaggaa gatctttcag gaatagctga aatgttcaag 2280
 accccagtgag aggagcaacc gcagttgaca agcacatgtc acatcgctat ttcaaattca 2340
 gagaatttgc ttggaaaaca gtttcaagga actgattcag gagaagaacc tctgctcccc 2400
 acctcagaga gttttggagg aaatgtgttc ttcagtgac agaatgcagc aaaacagcca 2460
 tctgataaat gctctgcaag ccctccctta agacggcagt gtattagaga aaatggaaac 2520
 gtgcaaaaa cgcccaggaa cacctacaaa atgacttctc tggagacaaa aacttcagat 2580
 actgagacag agccttcaaa aacagtatcc actgtaacaa ggtcagggaag gtctacagag 2640
 ttcaggaata tacagaagct acctgtggaa agtaagagtg aagaaacaaa tacagaaatt 2700
 gttgagtga tcctaaaaag aggtcagaag gcaacactac tacaacaaag gagagaagga 2760
 gagatgaagg aaatagaag accttttgag acatataagg aaaatattga attaaaagaa 2820
 aacgatgaaa agatgaaagc aatgaagaga tcaagaactt gggggcagaa atgtgcacca 2880
 atgtctgacc tgacagacct caagagcttg cctgatacag aactcatgaa agacacggca 2940

cgtggccaga atctcctcca aacccaagat catgccaagg caccaaagag tgagaaaggc 3000
 aaaatcacta aaatgccctg ccagtcatta caaccagaac caataaacac cccaacacac 3060
 acaaaacaac agttgaaggc atccctgggg aaagtaggtg tgaaagaaga gtccttagca 3120
 gtcggcaagt tcacacggac gtcaggggag accacgcaca cgcacagaga gccagcagga 3180
 gatggcaaga gcatcagaac gtttaaggag tctccaaagc agatcctgga cccagcagcc 3240
 cgtgtaactg gaatgaagaa gtggccaaga acgcctaagg aagaggccca gtcactagaa 3300
 gacctggctg gcttcaaaga gctcttcag acaccaggtc cctctgagga atcaatgact 3360
 gatgagaaaa ctaccaaagt agcctgcaaa tctccaccac cagaatcagt ggacactcca 3420
 acaagcacia agcaatggcc taagagaagt ctcaggaaag cagatgtaga ggaagaattc 3480
 ttagcactca ggaactaac accatcagca gggaaagcca tgcttacgcc caaaccagca 3540
 ggaggtgatg agaagacat taaagcattt atgggaactc cagtgcagaa actggacctg 3600
 gcagggaactt tacctggcag caaaagacag ctacagactc ctaaggaaaa ggcccaggct 3660
 ctagaagacc tggctggctt taaagagctc ttccagactc ctggtcacac cgaggaatta 3720
 gtggtgctg gtaaaaccac taaaatcccc tgcgactctc cacagtcaga cccagtggac 3780
 accccaacia gcacaaagca acgacccaag agaagtatca ggaagcaga tgtagaggga 3840
 gaactcttag cgtgcaggaa tctaagcca tcagcaggca aagccatgca cagcctaaa 3900
 ccatcagtag gtgaagagaa agacatcatc atatttgtgg gaactccagt gcagaaactg 3960
 gacctgacag agaacttaac cggcagcaag agacggccac aaactcctaa ggaagaggcc 4020
 caggctctgg aagacctgac tggctttaaa gagctcttcc agaccctgg tcatactgaa 4080
 gaagcagtg ctgctggcaa aactactaaa atgccctgag aatcttctcc accagaatca 4140
 gcagacaccc caacaagcac aagaaggcag cccaagacac ctttgagaaa aaggagcgtg 4200
 cagaaggagc tctcagccct gaagaagctc acacagacat caggggaaac cacacacaca 4260
 gataaagtac caggaggtga ggataaaagc atcaacgcgt ttagggaaac tgcaaaacag 4320
 aaactggacc cagcagcaag tgtaactggt agcaagaggc acccaaaaac taaggaaaag 4380
 gcccaacccc tagaagacct ggctggctgg aaagagctct tccagacacc agtatgact 4440
 gacaagccca cgactcacga gaaaactacc aaaatagcct gcagatcaca accagaccca 4500
 gtggacacac caacaagctc caagccacag tccaagagaa gtctcaggaa agtggacgta 4560
 gaagaagaat tcttcgact caggaaacga acaccatcag caggcaaaag catgcacaca 4620
 cccaaaccag cagtaagtgg tgagaaaaac atctacgcat ttatgggaac tccagtgcag 4680
 aaactggacc tgacagagaa cttaactggc agcaagagac ggctacaaac tcctaaggaa 4740
 aaggcccagg ctctagaaga cctggctggc tttaaagagc tcttcagac acgaggtcac 4800
 actgaggaat caatgactaa cgataaaact gccaaagtag cctgcaaatc ttcacaacca 4860
 gacctagaca aaaacccagc aagctccaag cgacggctca agacatccct ggggaaagtg 4920
 ggcgtgaaag aagagctcct agcagttggc aagctcacac agacatcagg agagactaca 4980
 cacacacaca cagagccaac aggagatggt aagagcatga aagcatttat ggagtctcca 5040
 aagcagatct tagactcagc agcaagtcta actggcagca agaggcagct gagaactcct 5100
 aagggaagt ctgaagtccc tgaagacctg gccggcttca tcgagctctt ccagacacca 5160
 agtcacacta agaatcaat gactaatgaa aaaactacca aagtatccta cagagcttca 5220
 cagccagacc tagtggacac cccaacaagc tccaagccac agcccaagag aagtctcagg 5280

aaagcagaca ctgaagaaga atttttagca ttlaygaac aaacyccac agcayycaaa 5340
 gccatgcaca cacccaaacc agcagtaggt gaagagaaag acatcaacac gtttttgga 5400
 actccagtgc agaaactgga ccagccagga aatttacctg gcagcaatag acggctacaa 5460
 actcgttaagg aaaaggccca ggctctagaa gaactgactg gcttcagaga gcttttcag 5520
 acaccatgca ctgataaccc cacagctgat gagaaaacta ccaaaaaaat actctgcaa 5580
 tctccgaat cagaccagc ggacacccca acaaacacaa agcaacggcc caagagaagc 5640
 ctcaagaag cagacgtaga ggaagaattt ttagcattca ggaactaac accatcagca 5700
 ggcaagcca tgcacacgcc taaagcagca gtaggtgaag agaaagacat caacacattt 5760
 gtggggactc cagtggagaa actggacctg ctaggaaatt tacctggcag caagagacgg 5820
 ccacaaactc ctaagaaaa ggccaaggct ctagaagatc tggctggctt caaagagctc 5880
 ttccagacac caggtcacac tgaggaatca atgaccgatg aaaaaatcac agaagtatcc 5940
 tgcaaatctc cacaaccaga ccagtcacaa accccaacaa gctccaagca acgactcaag 6000
 atatccttg ggaaagtagg tgtgaaagaa gaggtcctac cagtcggcaa gctcacacag 6060
 acgtcaggga agaccacaca gacacacaga gagacagcag gagatggaaa gagcatcaa 6120
 gcgtttaagg aatctgcaa gcagatgctg gaccagcaa actatggaac tgggatggag 6180
 aggtggccaa gaacaccta ggaagaggcc caatcactag aagacctggc cggcttcaa 6240
 gagctcttcc agacaccaga ccacactgag gaatcaacaa ctgatgacaa aactaccaa 6300
 atagcctgca aatctccacc accagaatca atggacactc caacaagcac aaggaggcgg 6360
 cccaaacac ctttggggaa aagggatata gtggaagagc tctcagccct gaagcagctc 6420
 acacagacca cacacacaga caaagtacca ggagatgagg ataaaggcat caacgtgttc 6480
 agggaaactg caaacagaa actggaccca gcagcaagt taactggtag caagaggcag 6540
 ccaagaactc ctaagggaag agccaaccc ctagaagact tggctggctt gaaagagctc 6600
 ttccagacac cagtatgcac tgacaagccc acgactcag agaaaactac caaatagcc 6660
 tgcagatctc cacaaccaga ccagtggtt accccaacaa tctcaagcc acagtccaag 6720
 agaagtctca ggaagcaga cgtagaggaa gaatccttag cactcaggaa acgaacacca 6780
 tcagtaggga aagctatgga cacacccaaa ccagcaggag gtgatgagaa agacatgaaa 6840
 gcatttatgg gaactccagt gcagaaattg gacctgccag gaaatttacc tggcagcaaa 6900
 agatggccac aaactccta ggaagaggcc caggctctag aagacctggc tggcttcaa 6960
 gagctcttcc agacaccag cactgacaag cccacgactg atgagaaaac taccaaaata 7020
 gcctgcaaat ctccacaacc agaccagtg gacacccag caagcacaaa gcaacggccc 7080
 aagagaaacc tcaggaaagc agacgtagag gaagaattt tagcactcag gaaacgaaca 7140
 ccacagcag gcaaaagccat ggacacccca aaaccagcag taagtatga gaaaaatc 7200
 aacacatttg tggaaactcc agtgcagaaa ctggacctgc taggaaattt acctggcagc 7260
 aagagacagc cacagactcc taaggaaaag gctgaggctc tagaggacct ggttggttc 7320
 aaagaactct tccagacacc aggtcacact gaggaatcaa tgactgatga caaaatcaca 7380
 gaagtatcct gtaaatctcc acagccagag tcattcaaaa cctcaagaag ctccaagcaa 7440
 aggtcacaaga taccctggt gaaagtggac atgaaagaag agcccctagc agtcagcaag 7500
 ctcacacgga catcagggga gactacgcaa acacacacag agccaacagg agatagtaag 7560
 agcatcaaag cgtttaagga gtctccaaag cagatcctgg acccagcagc aagtgttaact 7620
 ggtagcagga ggcagctgag aactcgttaag gaaaaggccc gtgctctaga agacctggtt 7680

gacttcaaag agctcttctc agcaccaggt cacactgaag agtcaatgac tattgacaaa 7740
 aacacaaaaa ttccctgcaa atctcccca ccagaactaa cagacactgc cagcagcaca 7800
 aagagatgcc ccaagacacg tcccaggaaa gaagtaaaag aggagctctc agcagttgag 7860
 aggctcagc aaacatcagg gcaaagcaca cacacacaca aagaaccagc aagcgggtgat 7920
 gagggcatca aagtattgaa gcaacgtgca aagaagaaac caaaccagc agaagaggaa 7980
 cccagcagga gaaggccaag agcacctaag gaaaaggccc aaccctgga agacctggcc 8040
 ggcttcacag agctctctga aacatcaggt cacactcagg aatcactgac tgctggcaaa 8100
 gccactaaaa taccctgcaa atctcccca ctagaagtgg tagacaccac agcaagcaca 8160
 aagaggcatc tcaggacacg tgtgcagaag gtacaagtaa aagaagagcc ttcagcagtc 8220
 aagttcacac aaacatcagg ggaaccacg gatgcagaca aagaaccagc aggtgaagat 8280
 aaaggcatca aagcattgaa ggaatctgca aaacagacac cggtccagc agcaagtga 8340
 actggcagca ggagacggcc aagagcacc agggaaagtg cccaagccat agaagaccta 8400
 gctggcttca aagaccagc agcaggtcac actgaagaat caatgactga tgacaaaacc 8460
 actaaaatac cctgcaaatc atcaccagaa ctagaagaca cgcacaag ctcaaagaga 8520
 cggcccagga cagtgccca gaaagtagaa gtgaaggagg agctgttagc agttggcaag 8580
 ctcacacaaa cctcagggga gaccacgac accgacaaag agccggtagg tgagggcaaa 8640
 ggcacgaaag catttaagca acctgcaaag cggaacgtgg acgcagaaga tgtaattggc 8700
 agcaggagac agccaagagc acctaaggaa aaggccaac ccctggaaga cctggccagc 8760
 ttccaagagc tctctcaaac accaggccac actgaggaac tggcaaatgg tgctgctgat 8820
 agctttacaa gcgtccaaa gcaaacacct gacagtggaa aacctctaa aatatccaga 8880
 agagttcttc gggccctaa agtagaacc gtgggagacg tggtgaagcag cagagacct 8940
 gtaaatcac aaagcaaaag caacacttcc ctgccccac tgccttcaa gaggggaggt 9000
 ggcaaagatg gaagcgtcac ggaaccaag aggcgtcgct gcatgccagc accagaggaa 9060
 attgtggagg agtgccagc cagcaagaag cagagggttg ctcccaggc aagaggcaaa 9120
 tcatccgaac ccgtggtcat catgaagaga agtttgagga cttctgcaa aagaattgaa 9180
 cctgcggaag agctgaacag caacgacatg aaaaccaaca aagaggaaca caaattacaa 9240
 gactcgttcc ctgaaaataa ggaatatcc ctgcgtcca gacccaaga taagactgag 9300
 gcagaacagc aaataactga ggtcttga ttagcagaaa gaatagaaat aaacagaaat 9360
 gaaaagaagc ccatgaagac ctcccagag atggacattc agaatccaga tgatggagcc 9420
 cggaaccca tacctagaga caaagtcact gagaacaaa ggtgcttgag gtctgctaga 9480
 cagaatgaga gctcccagc taaggaggca gagagagcg gagggcagaa gagtgcgaag 9540
 gttctcatgc agaatcagaa agggaaagga gaagcaggaa attcagactc catgtgcctg 9600
 agatcaagaa agacaaaaag ccagcctgca gcaagcactt tgagagcaa atctgtgcag 9660
 agagtaacgc ggagtgtcaa gaggtgtgca gaaaatcaa agaaggctga ggacaatgtg 9720
 tgtgtcaaga aaataacaac cagaagtcac agggacagtg aagatatttg a 9771

<210> 64
 <211> 2569
 <212> DNA
 <213> Homo sapiens

<400> 64
 tccctcgtct ctctcgggca acatggcggg cgtggaggag gtagcggcct ccgggagcca 60

cctgaatggc gacctggatc cagacgacag ggaagaagga gctgcctcta cggctgagga	120
agcagccaag aaaaaaagac gaaagaagaa gaagagcaaa gggccttctg cagcagggga	180
acaggaacct gataaagaat caggagcctc agtggatgaa gtagcaagac agttggaaag	240
atcagcattg gaagataaag aaagagatga agatgatgaa gatggagatg gcgatggaga	300
tggagcaact ggaagaaga agaaaaagaa gaagaagaag agaggaccaa aagttcaaac	360
agaccctccc tcagttccaa tatgtgacct gtatccta atgtgtatttc ccaaaggaca	420
agaatgcgaa taccacacca cacaagatgg gcgaacagct gcttgagaa ctacaagtga	480
agaaaagaaa gcattagatc aggcaagtga agagatttgg aatgattttc gagaagctgc	540
agaagcacat cgacaagtta gaaaatacgt aatgagctgg atcaagcctg ggatgacaat	600
gatagaaatc tgtgaaaagt tgggaagactg ttcacgcaag ttaataaaag agaattgatt	660
aatgcaggc ctggcatttc ctactggatg ttctctcaat aattgtgctg cccattatac	720
tcccaatgcc ggtgacacaa cagtattaca gtatgatgac atctgtaaaa tagactttgg	780
aacacatata agtggtagga ttattgactg tgcttttact gtcactttta atcccaata	840
tgatacgtta ttaaaagctg taaagatgc tactaacact ggaataaagt gtgctggaat	900
tgatgttcgt ctgtgtgatg ttggtgaggc catccaagaa gttatggagt cctatgaagt	960
tgaaatagat ggggaagacat atcaagtga accaatccgt aatctaagt gacattcaat	1020
tgggcaatat agaatacatg ctggaaaaac agtgccgatt gtgaaaggag gggaggcaac	1080
aagaatggag gaaggagaag tatatgcaat tgaacacctt ggtagtacag gaaagggtgt	1140
tgttcatgat gatatggaat gttcacatta catgaaaaat tttgatgttg gacatgtgcc	1200
aataaggctt ccaagaacaa aacacttggt aatgtcatc aatgaaaact ttggaacctt	1260
tgccttctgc cgcagatggc tggatcgctt gggagaaaagt aaatactga tggctctgaa	1320
gaatctgtgt gacttgggca ttgtagatcc atatccacca ttatgtgaca ttaaaggatc	1380
atatacagcg caatttgaac ataccatcct gttgcgtcca acatgtaaag aagttgtcag	1440
cagaggagat gactattaaa cttagtccaa agccacctca acacctttat tttctgagct	1500
ttgttgaaa acatgatacc agaattaatt tgccacatgt tgtctgtttt aacagtggac	1560
ccatgtaata cttttatcca tgtttaaaaa agaaggaatt tggacaaaag caaacgtct	1620
aatgtaatta accaacgaaa aagctttccg gacttttaaa tgctaactgt tttcccctt	1680
cctgtctagg aaaatgctat aaagctcaaa ttagttagga atgacttata cgttttgttt	1740
tgaataccta agagatactt tttggatatt tatattgcca tattcttact tgaatgcttt	1800
gaatgactac atccagtctt gcacctatac cctctggtgt tgctttttaa ccttcctgga	1860
atccattttc taaaaataa agacacattc ttctcagcac cacacaacac ctattccaaa	1920
atcgaccaca ttttggag taaagctctc ctcagcaaat gtaaaagaac agaaattata	1980
acaaactgtc tctcagacca cagtataacc aaactagaac tcaggattaa gaaactcact	2040
caaaaccaca caactacatg gaaactgaac aacctgctcc tgaatgacta ctggatacat	2100
aacaaaatga aggcagaaat aaagatgttc tttaaaacca atgagaacaa agacacaaca	2160
taccagaatc tctgggacac attcaaagca gtgtgtagag ggaattttat agcactaaat	2220
gccacaaga gaaagcagga aatatctaaa attgacaccc taacatcaca attaaaagaa	2280
ctagagaagc aagagcaaac acattgaaaa gctaagagaa ggcaagaaat aactaagatc	2340
agagcagaac tgaaggaaat agagacacaa aaaactcttc aaaaaatcaa tgaatccagg	2400

agctgggtttt ttgaaacgat caacaaaatt gatagacact agcaagacca ataaagaaga 2460
aaggagagaa gaatcaaata gaagcaataa aaaatgataa aggggatatc accaccaatc 2520
ccacagaaat aaaccaccat cagagaatac tacaacacc tctacgcaa 2569

<210> 65
<211> 2204
<212> DNA
<213> Homo sapiens

<400> 65
agaaaaatgt acatgactcc cagtgtctgt ggaacatga ttgaagacat tataagcgag 60
tgcgtgtgac ctataaggaa agtctcattg gtagaagaga catgcatggt agaaaggatg 120
atgcacaaaa gcagcctggt aaaaatcagc ttggattaaa cccgcagtca catctaccag 180
aactgcagct atttcaagct gaagggaaaa tatataata tgatcacatg gaaaaatctg 240
tcaacagtag ttcccttagtt tccccacccc aacgtatttc ttctactgtc aaaaccacaca 300
tttctcatat atatgaatgt aattttgtgg attcattatt cacacaaaaa gagaaagcaa 360
atattgggac agaacactac aaatgtaatg agcgtggcaa ggcctttcat caaggcttac 420
attttactat acatcaaata atccatacta aagagacgca atttaaagt gatatatgtg 480
gcaagatctt caataaaaaa tcaaaccttg caagtcatca aagaattcat actggagaga 540
agccatataa atgtaatgaa tgtggcaagg tcttcataa tatgtcacac cttgcacagc 600
atcgcaggat tcatactgga gagaaaccat ataaatgtaa tgaatgtggc aaggtcttta 660
atcaaatttc acaccttgca caacatcaaa gaattcatc cggagagaaa ccttataaat 720
gtaatgaatg tggaaaggtc ttccatcaaa ttccacacct tgcacaacat cggacaattc 780
atactggaga aaaaccttac gaatgtaaca aatgtggcaa ggtgttcagt cgcaattcct 840
accttgtaca acatctgatc attcatactg gagagaaacc ttacagatgt aatgtatgtg 900
gcaaggtctt cagtcacaag tcatccctag taaatcactg gagaattcat actggagaga 960
aaccttacaa atgtaatgag tgtggcaagg tcttcagtca caagtcatcc ctagtataatc 1020
actggagaat ccacactgga gagaaacctt acaaatgtaa tgaatgtggc aaggtcttca 1080
gtcgaattc ataccttgcc caacatctga taattcatgc cggtgagaaa ccttataagt 1140
gtgatgaatg tgacaaagca ttcagtcaaa attcacatct tgtacaacat cacagaatcc 1200
atactggaga gaaaccttac aaatgtgatg aatgtggcaa agtcttcagt caaaattcat 1260
accttgcata tcattggaga attcatactg gagaaaaagc ttataaatgt aatgaatgtg 1320
ggaaggtctt cggcttaaac tcatccctag cacatcatcg gaaaattcac actggagaga 1380
aacctttcaa atgtaatgaa tgtggcaagg cttttagtat gcgttcaagc ctactaatc 1440
atcatcgcat ccacactgga gagaaacatt tcaaatgtaa tgaatgtggc aaactcttcc 1500
gcgacaattc atatcttgta cgtcatcaga gatttcatgc cggaaagaaa tctaacacat 1560
gtaattaatg tggcagagtg ttcagttagc attaaagcct tgaagacat acaataattt 1620
atactggaga aaaactttgc aagtataatg aatgtagcag agcctttagt tttgttcaa 1680
ggcttaataa ccgttagcta gaccatagag gacagaaact ttactaatgt actgaatgtg 1740
gcaaggtctt aaggtaaaat ctgagaccag gatttttcaa agaattcttg ctggtgagaa 1800
acctaacaaa tgtaatgaat gtggcaaggt cttctggcac aattctcaca ttgtacaata 1860
ttgcaaaaat tcatgcttga gagaaacaaa aacactgaga gtgggaaacc attatgactt 1920
caaacattca tcaacatcag agaattcata ctaaagagca tttataataa ttatatgtga 1980

tagagatttt ccgcaggcca aagtctcact aggcacaaaa aacccccctt atyaaaccat 2040
 acaaatgtaa cgtgcatgct taagctttta cccaggcatc aaaaccggaa catcacaggg 2100
 ttatatacagg agagtaacta cacaagata atgtaataag cctttcagtg taatattcat 2160
 gattttgtcg tgagagatcc actcaataaa aaccaggcaa atgt 2204

<210> 66
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 66
 gtcccagtcg gtccggaggc tgcggctgca gaagtaccgc tgcggagtaa ctgcaaagat 60
 gctgtccgtg cgcgttctg cggccgtggt ccgcgccctt cctcggcggg ccggactggt 120
 ctccagaaat gctttgggtt catctttcat tgcgtcaagg aacttccatg cctctaacac 180
 tcatcttcaa aagactggga ctgctgagat gtcctctatt cttgaagagc gtattcttgg 240
 agctgatacc tctgttgatc ttgaagaaac tggcggtgtc ttaagtattg gtgatggtat 300
 tgcccgcgta catgggctga ggaatgttca agcagaagaa atggtagagt tttcttcagg 360
 cttaaagggt atgtccttga acttggaacc tgacaatgtt ggtgttctcg tgtttgaaa 420
 tgataaacta attaaaggag gagatatagt gaagaggaca ggagccattg tggacgttcc 480
 agttggtgag gagctgttgg gtcgtgtagt tgatgccctt ggtaatgcta ttgatgaaa 540
 ggggtccaatt ggtccaaga cgcgtaggcg agttggtctg aaagcccccg gtatcattcc 600
 tcgaatttca gtgcgggaac caatgcagac tggcattaag gctgtggata gcttgggtgcc 660
 aattggtcgt ggtcagcgtg aactgattat tggtgaccga cagactggga aaacctcaat 720
 tgctattgac acaatcatta accagaaacg tttcaatgat ggatctgatg aaaagaagaa 780
 gctgtactgt atttatgttg ctattgttca aaagagatcc actgttgcct agttggtgaa 840
 gagacttaca gatgcagatg ccatgaagta caccattgtg gtgtcggcta cggcctcgga 900
 tgctgccccca cttcagtaacc tggctcctta ctctggctgt tccatgggag agtatttttag 960
 agacaatggc aaacatgctt tgatcatcta tgacgactta tccaaacagg ctgttgctta 1020
 ccgtcagatg tctctgttgc tccgccgacc ccctggctgt gaggcctatc ctggtgatgt 1080
 gttctaccta cactcccggg tgctggagag agcagccaaa atgaacgatg cttttggtgg 1140
 tggctccttg actgctttgc cagtcataga aacacaggct ggtgatgtgt ctgcttacat 1200
 tccaacaaat gtcatttcca tcaactgacg acagatcttc ttgaaacag aattgttcta 1260
 caaaggatc cgccttgcaa ttaacgttgg tctgtctgta tctcgtgtcg gatccgctgc 1320
 ccaaaccagg gctatgaagc aggtagcagg taccatgaag ctggaattgg ctcagtatcg 1380
 tgaggttgct gcttttgcct agttcgggtc tgacctgat gctgccactc aacaactttt 1440
 gagtcgtggc gtgcgtctaa ctgagttgct gaagcaagga cagtattctc ccatggctat 1500
 tgaagaacaa gtggctgtta tctatgcggg tgtaagggga tatcttgata aactggagcc 1560
 cagcaagatt acaaaatttg agaattgctt cttgtctcat gtcgtcagcc agcaccaagc 1620
 cttgttgggc actatcaggg ctgatggaaa gatctcagaa caatcagatg caaagctgaa 1680
 agagattgta acaaaattct tggctggatt tgaagcttaa actcctgttg attcacatca 1740
 aataccagtt cagttttgtc attgttctag taaattagtt ccatattgtaa aagggttact 1800
 ctcatactcc ttatgtacag aaatcacatg aaaaataaag gttccataat gcaaaaaaaaa 1860
 aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 67
 <211> 1696
 <212> DNA
 <213> Homo sapiens

<400> 67
 cacctaaaag ccaaaatggg aaaggaaaag actcatatca acattgtcgt cattggacac 60
 gtagattcgg gcaagtccac cactactggc catctgatct ataaatgcgg tggcatcgac 120
 aaaagaacca ttgaaaaatt tgagaaggag gctgctgaga tgggaaaggg ctccctcaag 180
 tatgcctggg tcttggataa actgaaagct gagcgtgaac gtggtatcac cattgatatc 240
 tccttgtgga aatttgagac cagcaagtac tatgtgacta tcattgatgc cccaggacac 300
 agagacttta tcaaaaacat gattacaggg acatctcagg ctgactgtgc tgcctgatt 360
 gttgctgctg gtgttggtga atttgaagct ggtatctcca agaattgggca gacccgagag 420
 catgcccttc tggcttacac actgggtgtg aaacaactaa ttgtcgggtg taacaaatg 480
 gattccactg agccacccta cagccagaag agatatgagg aaattgttaa ggaagtcagc 540
 acttacatta agaaaattgg ctacaacccc gacacagtag catttgtgcc aatttctggt 600
 tggaatggtg acaacatgct ggagccaagt gctaacatgc cttggttcaa gggatggaaa 660
 gtcaccgcta aggatggcaa tgccagtga accacgctgc ttgaggctgt ggactgcatc 720
 ctaccaccaa ctgcgtcaac tgacaagccc ttgcgcctgc ctctccagga tgtctacaaa 780
 attggtggtg ttggtactgt tcctgttggc cgagtggaga ctggtgttct caaaccggt 840
 atggtggtca cctttgctcc agtcaacgtt acaacggaag taaaatctgt cgaatgcac 900
 catgaagctt tgagtgaagc tcttctctgg gacaatgtgg gcttcaatgt caagaatgtg 960
 tctgtcaagg atgttcgtcg tggcaacgtt gctggtgaca gcaaaaatga cccaccaatg 1020
 gaagcagctg gcttactgac tcagggtgatt atcctgaacc atccaggcca aataagcgcc 1080
 ggtatgccc ctgtattgga ttgccacacg gtcacattg catgcaagtt tgctgagctg 1140
 aaggaaaaga ttgatcgccg ttctgtgtaa aagctggaag atggccctaa attcttgaag 1200
 tctggtgatg ctgccattgt tgatatggtt cctggcaagc ccatgtgtgt tgagagcttc 1260
 tcagactatc cacctttggg tcgctttgct gttcgtgata tgagacagac agttgcggtg 1320
 ggtgtcatca aagcagtga caagaaggct gctggagctg gcaaggtcac caagtctgcc 1380
 cagaaagctc agaaggctaa atgaatatta tccctaatac ctgccacccc actettaatc 1440
 agtggtgga gaacggtctc agaactgttt gtttcaattg gccatttaag ttagtagta 1500
 aaagactggt taatgataac aatgcatcgt aaaaccttca gaaggaaagg agaattttt 1560
 gtggaccact ttggttttct tttttgcgtg tggcagtttt aagttattag tttttaaatt 1620
 cagtactttt taatggaaac aacttgacca aaaattgtc acagaatttt gagaccatt 1680
 aaaaaagtta atgag 1696

<210> 68
 <211> 4648
 <212> DNA
 <213> Homo sapiens

<400> 68
 gaatgcaggt gagaaaaggc acggactctg cggctgcgaa cccaaacttg ggcaccgcac 60
 ggtgcgcact gctcagcctt cgtcccgctg ggcgaaaggc tgctgcggtt tcaggcggct 120
 gcttcgtgac taatgacctt gcgcagagtt gttaagaaaa aagagaaacc cgcgctctcc 180
 ggggtgagaa gggactgact ctgggcgtct ctgaagatgg ctccggcttc tctttggcgc 240

gccgggggga ccctgacact gaccgctctg tgacgcgagt agtctccctt gcaccgtgcc 300
 cgaagcgacg tgccggggga tttttcattc tcgatctgtt gactggctcc cccgctgcat 360
 gagcagatcg gagttgagac tggcttggtg ctggccccag cgcttggtgc aggaagcgac 420
 tcacgtttgt ctgggtggcc ggagccggag ccggagcaga gctgggcttt ggagttagtg 480
 cctggaacgt gaattggact caactcgagt agcagcaaag accagcgggc tggcagcgcg 540
 gggaggctgc aggtcattc cccacctctt cccagcccca ctgcccgtct gccggagcgg 600
 ttctggcccc ttccgacaga gcggggacta gagccgggga ttctccgcc gctgagggga 660
 tgactctggg ttgggggagc gccgaacccg cggcgcgagc tgtcccgta actgtgagta 720
 ctgcgactga acggcgagc gcgagcgggc gattagcacc cattgcatga attatgaaac 780
 aataactttc ggaagaagca ggaggaaaaa aagaagcacc taccgctgcc ctcccacccc 840
 cattccgggc caactctcca cgcgctttt gcccctccc tcccctccct ctgctcctt 900
 cctttccggg agaggggaga ggactcggg gagggcaggc gggcgccccc ggaggagggg 960
 ggcgcgagg gggtgtggt tagaaggagc agtagcagca gcaggagaag atgctgagga 1020
 tgcggaccgc gggatggcg cgcggctggt gcttgggtg ctgcctctc ctgcccgtct 1080
 cgttcagcct ggcggccgcc aagcagctcc tccggtaccg gctggccgag gagggcccg 1140
 ccgacgtccg catcggaac gtggtctcag acctgggcat cgtgaccgga tcgggtgagg 1200
 tgactttcag cctggagtcc ggttccgagt acctgaagat cgacaacctc actggcgagc 1260
 tgagcacgag cgagcggcgc atcgaccgcg agaagctgcc ccagtgtcag atgatcttcg 1320
 acgagaacga gtgcttctc gacttcgagg tgcggtgat cgggccctc cagagctggg 1380
 tggacctgtt tgagggtcag gtcacgtgc ttgacatcaa cgacaacacg cccaccttc 1440
 cgtcgccctg gtcacgctc acggtggagg agaatcgcc ggtgggcaca cttacctgc 1500
 tgcccacagc caccgaccgc gacttcggcc gcaacggcat cgagcgctac gagctgctcc 1560
 aggagcccg aggcggcggc agcggcgcg agagccggc cgcggggcg gccgacagcg 1620
 ccccttccc cggggcggc gggaacggc cgagcggcg cggctcggga ggctccaagc 1680
 ggcggctgga cgcatcagag ggcggcgcg gcaccaaccc cgcggccgc agcagcgtgt 1740
 tcgagctgca ggtggcgac accccggagc gcgagaagca gccgcagctg atcgtgaagg 1800
 ggcggctgga ccgagcagc cgcgactcct acgagctgac cctgcgagtg cgcgacggcg 1860
 gcgaccgcc tcgctcctc caggccatcc tacgggtcct catcaccgac gtgaacgaca 1920
 acagccccc cttcgagaag agcgtgtacg aggcgactt ggctgagaac agcggcccg 1980
 ggaccccat cctgcaactg cgcgcagcgc acttgagctt gggggtcaac gggcagatcg 2040
 aatactgtt cggggcgcc accgagtcgg tagggcgct gctgcgctt gacgagacgt 2100
 ccggctggct cagcgtcctg caccggatcg accgcgagga ggtgaaccag ctgcgcttca 2160
 cggatcatgg ccgcgaccgc gggcagcccc ccaagaccga caaggccacc gtggtcctta 2220
 acatcaaaga cgagaacgac aacgtgacct ccattgaaat ccgcaagatt gggcgcatcc 2280
 cctcaagga cgggtggcc aacgtggcg aggacgttct ggtcgacacc cccatcgctc 2340
 tgggtcaggt gtccgaccga gaccaaggcg agaacggggt ggtcacctgc accgtggtg 2400
 gcgacgtgcc cttcagctc aagccagcca gcgacaccga gggcgaccag aacaagaaaa 2460
 agtacttctt gcacacctc acccctctgg actatgaggc caccgggag ttcaacgtgg 2520
 tcacgtggc ggtggactca ggcagcccca gcctctcgag caagaactcc ctgattgtca 2580

```

aggtgggaga caccaacgac aaccgccc tttcggcca gtcggtggtg gaggtttact 2640
tccttgagaa caacatcccg ggcgagaggg tggccacggt gctggcgaca gacgcagaca 2700
gcggtaagaa cgccgagatc gcctactcgc tggactcctc tgtgatgggg atctttgcca 2760
tcgatcccg tttcggggac atcctggtca ataccgtgct ggaccgcgag cagactgaca 2820
ggtatgagtt taaagttaac gccaaagaca aaggcatccc cgtgctgcag ggcagcacta 2880
cggtgattgt gcaggtggct gataaaaatg acaatgaccc taagtttatg caggacgtct 2940
tcacctttta tgtaaagaa aacttcgagc ccaacagccc tgtggggatg gtcaccgtga 3000
tggatgctga caaggggagg aatgcagaga tgagcctgta catagaggag aacaataaca 3060
ttttttctat tgaaaatgac acggggacca ttactccac aatgtctttt gaccgggaac 3120
atcagaccac atacactttc agagtcaagg ctgtggatgg gggagatcct cccagatctg 3180
ccacagctac agtctcgctt tttgtgatgg atgaaaatga caatgctccc acagttaccc 3240
ttcccaaaaa catttctac actttactgc caccttcgag taatgtcagg acagtagtag 3300
ctacagtgtt ggcaacagac agtgatgatg gcatcaatgc agacctgaac tacagcattg 3360
tggggagaaa tcccttcaag ctgtttgaaa ttgatccac tagtggtgtg gtttccttag 3420
tgggaaaact caccaaaag cattatggct tgcacagggt ggtggtgcaa gtgaatgaca 3480
gtgggcagcc ttcccagtc accacgactg tggcgcagct gtttgtcaat gaaagtgttt 3540
ctaagcaac tgcgattgac tcccagatag ctagaagttt gcacatcca ctcaccagg 3600
atatagctgg tgaccaagc tatgaaatta gcaaacagag actcagtatt gtcattggcg 3660
tagttgctgg cattatgacg gtgattctaa tcatcttaat tgtagtgatg gcaaggtact 3720
gcaggtccaa aataaaaaat ggctatgaag ccggcaaaaa agatcacgaa gactttttta 3780
caccacaaca gcatgacaaa tctaaaaagc ctaaaaagga caagaaaaac aaaaaatcta 3840
agcagcctct ctacagcagc attgtcactg tggaggcttc taagccaaat ggacagaggt 3900
atgatagtgt caatgagaag ctgtcagaca gcccaagcat ggggcgatac agatccgtta 3960
atgggtgggc cgccagtcct gacctggcaa ggcattacaa atctagttcc ccattgccta 4020
ctgttcagct tcatccccag tcaccaactg caggaaaaaa acaccaggcc gtacaagatc 4080
taccaccagc caacacattt gtgggagcag gagacaacat ttcaattgga tcagatcact 4140
gctctgagta cagctgtcaa accaataaca agtacagcaa acagatgcgt ctacatccat 4200
acattactgt gtttgctga attccactct aatatgatgc tccattatgc accatactgt 4260
gatgaccttt ctactccgaa acctgctgga gcctgccctt ggccgtgggg tgtcagccaa 4320
tcactgcttg ttccacttgt tgtacatttt atttttgagt ctttttcttt ctcatataca 4380
gaaaaatagt atgaaaataa aataaatgta tgaacagta ttaatgcaga aatgtgctac 4440
taatggatgt ctgagtcacc agaaattcca ttcttaaga ggcggttagc acctattaga 4500
cgtaacagtg atgtctttta aaaaatccaa aagcatattg caacaataag tttgagactt 4560
tgtgtgaaca aagggaatt cagcctctta tgtctttgtc tttaatacat taaatactga 4620
ttttgaataa aaatctaaat tgatcaat 4648

```

<210> 69
 <211> 2386
 <212> DNA
 <213> Homo sapiens

<400> 69
 aagaattcgg cagcaggatg acttctcttt ggaaaagaaa accattgagt ggcctgaaga 60

gattaagaaa atcgaagaag ccgagcggga agcagaglyc aaaattcygy aagcagaagc	120
taaagtgaat tctaagagtg gccagaggg cgatagcaaa atgagcttct ccaagactca	180
cagtacagcc acaatgccac ctctatttaa ccccatctc gccagcttgc agcacaacag	240
catctcaca ccaactcggg tcagcagtag tgccacgaaa cagaaagttc tcagcccacc	300
tcacataaag gcggatttca atcttgctga ctttgagtgt gaagaagacc catttgataa	360
tctggagtta aaaactattg atgagaagga agagctgaga aatattcttg taggaaccac	420
tggaccatt atggctcagt tattggacaa taacttgccc aggggaggct ctgggtctgt	480
gttacaggat gaggaggtcc tggcatcctt ggaacgggca accctagatt tcaagcctct	540
tcataaacc aatggcttta taaccttacc acagttgggc aactgtgaaa agatgtcact	600
gtcttccaaa gtgtccctcc cccctatacc tgcagtaagc aatatcaaat ccctgtcttt	660
ccccaaactt gactctgatg acagcaatca gaagacagcc aagctggcga gcactttcca	720
tagcacatcc tgcctccgca atggcacgtt ccagaattcc ctaaagcctt ccacccaaag	780
cagtgccagt gagctcaatg ggcacacac tcttgggctt tcagctttga acttgacag	840
tggcacagag atgccagccc tgacatctc ccagatgcct tccctctctg ttttgtctgt	900
gtgcacagag gaatcatcac ctccaaatac tggccccacg gtcacccctc ctaatttctc	960
agtgtcacia gtgccaaca tgcacagctg tccccaggcc tattctgaac tgcagatgct	1020
gtccccacg gagcggcagt gtgtggagac ggtggtcaac atgggctact cgtacgagtg	1080
tgtctcaga gccatgaaga agaaaggaga gaattattgag cagattctcg actatctctt	1140
tgcacatgga cagctttgtg agaagggtt cgacctctt ttagtggaag aggtcttgga	1200
aatgcaccag tgttcagaag aaaagatgat ggagtttctt cagttaatga gcaaatata	1260
ggagatggg tttgagctga aagacattaa ggaagttttg ctattacaca acaatgacca	1320
ggacaatgct ttggaagacc tcatggctcg ggcaggagcc agctgagacc aggccctgcc	1380
taggccctgc cgcagaacca ccacccctgg gaggccctgc agagcccacc tgtggggaaa	1440
gagaagggg agcttccgga tttcttttg ggggttagaa ggtcaggtgt ggagactgct	1500
cgccagctc tgtgagccta ggccctgagc tggggaggtg gggagattc gggcatgtga	1560
gtgccccag aactgtcctg gctcctccg tattaaacgc atttgcatth tgagaagtgt	1620
ccttccact tcagccctcc ggagagacta cctagtctt tctgggtgt ttatgtctc	1680
agctgaagcc tggcctagtt gctgagagg gctggggaga tggggcgga gggccagact	1740
cagtgtgct gtggagctag gtgcttcccc cttccctga gactggtga ctgaactcca	1800
gtcaagtga gttcaagtga aagattctt cagggtttta ttttttccc tcctaacaaa	1860
gtctcatagt gttaacactg gttctgcaat atctctgagg tgcaaagaat gcacttttcc	1920
ctatggggcc cagagtttgc ctttctgcc aggcagtcac cagcttccc taccacagcc	1980
tgtttctttt ggcttggtt ggaccacagt cctctgtac ccagggttt agagcccctg	2040
ctctagggaa cagtttaaga aatcattggc cccttcccag cacattgaat gggtaagcag	2100
acaggccatg atttagttg ccagcactaa ctccacctt gttctcctt aacagcttcc	2160
cctccagccc actgctttag gatgacacaa tgaataacac ctagtcatag aaatcagctt	2220
ctctggtttg ttttgattta tgtgtacat cattaaagat ctaaatataa aggatataca	2280
gtcttgaatc taaaataatt tgctaactat tttgattctt cagagagaac tactaataaa	2340
aatctaaaag gtaaaaaaaa aaaaaaaaaa aaaaaaaa aaaaaa	2386

<210> 70
 <211> 1399
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1399)
 <223> n=A,T,C,or G

```

<400> 70
gtcgtatttc caaggactcc aaagcgaggc cggggactga aggtgtgggt gtcgagccct    60
ctggcagagg gttaacctgg gtcaaatgca cggattctca cctcgtacag ttacgctctc    120
ccgcggcacg tccgaaggat ttggaagtcc tgagcgcctc agtttgtccg tagtcgagag    180
aaggccatgg aggtgccgcc accggacgcn gggagctttc tctgtagagc attgtgccta    240
tttccccgag tctttgtctg cgaagctgtg actgccgatt cggaagtcct tgaggagcgt    300
cagaagcggc ttcctacgtg cccagagccc tattaccgga aatctggatg ggaccgcctc    360
cgggagctgt ttggcaaaga tgaacagcag agaatttcaa aggacctgac taatatctgt    420
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt    480
catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa ccggtttgat    540
gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca ttcgttatgg ctggcgtggtg    600
ggttggagaa ctgcagtgtt tgtgactata ttcaacacag tgaacactag tctgaatgta    660
taccgaaata aagatgcctt aagccatttt gtaattgcag gagctgtcac ggggaagtctt    720
tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg agccttgctg    780
ggcactctct taggaggcct gctgatggca tttcagaagt actctggtga gactgttcag    840
gaaagaaaac agaaggatcg aaaggcactc catgagctaa aactggaaga gtggaaaggc    900
agactacaag ttactgagca cctccctgag aaaattgaaa gtagtttaca ggaagatgaa    960
cctgagaatg atgctaagaa aattgaagca ctgctaaacc ttcctagaaa cccttcagta   1020
atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg gagagctgaa   1080
gggagctgcc atgtccgatg aatgccaaca gacaggccac tctttggtca gcctgctgac   1140
aaatttaagt gctggtacct gtggtggcag tggcttgctc ttgtcttttt cttttctttt   1200
taactaagaa tggggctggt gtactctcac tttacttata cttaaattta aatacatact   1260
tatgtttgta ttaatctatc aatatatgca tacatgaata tatccacca cctagatttt   1320
aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt aaaaaaaaaa   1380
aaaaaaaaaa aaaaaaaaaa                                     1399

```

<210> 71
 <211> 1014
 <212> DNA
 <213> Homo sapiens

```

<400> 71
gcagaaatag cctagggaga tcaaccccgga gatgctgaac aaagtgtgtg cccgggtggg    60
ggtcgccggc cagtggcgct tcgtggacgt gctggggctg gaagaggagt ctctgggctc    120
gggtccagcg cctgectgcg cgctgctgct gctgtttccc ctacggccc agcatgagaa    180
cttcaggaaa aagcagattg aagagctgaa gggacaagaa gttagtccta aagtgtactt    240
catgaagcag accattggga attcctgtgg cacaatcgga cttattcacg cagtggccaa    300
taatcaagac aaactgggat ttgaggatgg atcagttctg aaacagtttc tttctgaaac    360

```

```

agagaaaaatg tccccgaag acagagcaaa atgctctgaa aagaaatgagc ccaacagggc 420
agcccatgat gccgtggcac aggaaggcca atgtcgggta gatgacaagg tgaatttcca 480
ttttattctg ttttaacaacg tggatggcca cctctatgaa cttgatggac gaatgccttt 540
tccggtgaac catggcgcca gttcagagga caccctgctg aaggacgctg ccaagggtg 600
cagagaattc accgagcgtg agcaaggaga agtcgccttc tctgccgtgg ctctctgcaa 660
ggcagcctaa tgctctgtgg gagggacttt gctgatttcc cctcttccct tcaacatgaa 720
aatatatacc ccccatgcag tctaaaatgc ttcagtactt gtgaaacaca gctgttcttc 780
tgttctgcag acacgccttc ccctcagcca caccagga ctttaagcaca agcagagtgc 840
acagctgtcc actgggccaat tgtggtgtga gcttcagatg gtgaagcatt ctccccagt 900
tatgtcttgt atccgatatc taacgcttta aatggctact ttggtttctg tctgtaagtt 960
aagaccttg atgtggttat gttgtcctaa agaataaatt ttgctgatag tagc 1014

```

```

<210> 72
<211> 3179
<212> DNA
<213> Homo sapiens

```

```

<400> 72
cccccccttt ttgaaattat gtgctgctgt ttaaaacaac aaacaaaaaa aacaacaaaa 60
acacagcaac tgcggatttt gtccccggt ggagcccagc gccccgctg gaatggatga 120
gcctctccat gagagatccg gtcattcctg ggacaagcat ggcctaccat ccgttcttac 180
ctcaccgggc gccggacttc gccatgagcg cgggtgctgg tcaccagccg ccgttcttcc 240
ccgcgctgac gctgcctccc aacggcgcg cggcgctctc gctgccgggc gccctggcca 300
agccgatcat ggatcaattg gtggggcgcg ccgagaccgg catcccgctc tcctccctgg 360
ggccccaggc gcactctgag cctttgaaga ccatggagcc cgaagaagag gtggaggagc 420
accccaaggt gcacctggag gctaaagaac tttgggatca gtttcacaag cggggcaccg 480
agatggctcat taccaagtcg ggaaggcgaa tgttctctcc atttaagtg agatgttctg 540
ggctggataa aaaagccaaa tacattttat tgatggacat tatagctgct gatgactgtc 600
gttataaatt tcacaattct cggtggatgg tggctggtaa ggccgacccc gaaatgcaa 660
agaggatgta cattcaccgc gacagcccg ctactgggga acagtggatg tccaaagtcg 720
tcactttcca caaactgaaa ctaccaaca acatttcaga caaacatgga ttactttgg 780
ccttcccaag tgatcacgct acgtggcagg ggaattatag ttttggtact cagactatat 840
tgaactccat gcacaaatac cagccccggt tccacattgt aagagccaat gacatcttga 900
aactccctta tagtacattt cgacatact tgttccccga aactgaattc atcgctgtga 960
ctgcatacca gaatgataag ataaccagt taaaaataga caacaaccct ttgcaaaaag 1020
gtttccggga cactggaat ggccgaagag aaaaagaca acagctcacc ctgcagtcca 1080
tgagggtgtt tgatgaaaga cacaaaaagg agaatgggac ctctgatgag tcctccagt 1140
aacaagcagc tttcaactgc ttcgcccagg cttcttctcc agccgcctcc actgtaggga 1200
catcgaacct caaagattta tgtcccagcg aggggtgagag cgacgccgag gccgagagca 1260
aagaggagca tggccccgag gcctgcgacg cgccaagat ctccaccacc acgtcggagg 1320
agccctgccg tgacaagggc agcccccgcg tcaaggctca ccttttcgct gctgagcggc 1380
cccgggacag cgggcgctg gacaaagcgt cgcccactc acgccatagc cccgccacca 1440
tctcgccag cactcgcggc ctgggcgcg aggagcgag gagcccggt cgcgagggca 1500

```

cagcgccggc caaggtggaa gaggcgcgcg cgccccyyg caayyayycc cccgcgcgc 1560
 tcacgggtgca gacggacgcg gctcgcagct cggcgcaccg ccaccccttc cgcaatctga 1620
 acaccatgcg cccgcggctg cgctacagcc cctactccat cccggtgccg gtcccggacg 1680
 gcagcagctct gctcaccacc gccctggccg ccagcccgcc ctcggtggca gtggactcgg 1740
 gctctgaact caacagccgc tctccacgc tctctccag ctccatgtcc ttgtcgccca 1800
 aactctgcgc ggagaaagag gcggccacca gcgaactgca gagcatccag cggttggtta 1860
 gcggcttgga agccaagccg gacagggtccc gcagcgcgtc cccgtagacc cgtcccagac 1920
 acgtcttttc attccagtc agttcaggct gccgtgcact ttgtcggata taaaataaac 1980
 cacgggcccg ccattggcgtt agcccttctt ttgcagttg cgtctgggaa ggggccccgg 2040
 actccctcga gagaatgtgc tagagacagc ccctgtcttc ttggcgtggt ttatatgtcc 2100
 gggatctgga tcagattctg ggggtcaga aacgtcgggt gcattgagct actgggggta 2160
 ggagttccaa catttatgtc cagagcaact tccagcaagg ctggtctggg tctctgccac 2220
 caggcgggga ggtgttcaaa gacatctcct cagtgcggat ttatatatat atttttcttc 2280
 actgtgtcaa agtggaaaca aaaacaaat cttcaaaaa aaaaatccgg acaagtgaac 2340
 acattaacat gattctgttt gtgcagatta aaaactttat agggacttgc attatcgggt 2400
 ctcaataaat tactgagcag cttgttttg ggagggaagt ccctaccatc cttgtttagt 2460
 ctatattaag aaaatctgtg tctttttaat attcttgtga tgttttcaga gccgctgtag 2520
 gtctcttctt gcatgtccac agtaatgtat ttgtggtttt tattttgaac gcttgctttt 2580
 agagagaaaa caatatagcc ccctaccctt ttcccaatcc ttgccctca aatcagtgac 2640
 ccaaggaggg gggggattta aagggaagga gtgggcaaaa cacataaaat gaatttatta 2700
 tatctaagct ctgtagcagg attcatgtcg ttctttgaca gttctttctc ttccctgtat 2760
 atgcaataac aaggttttaa aaaaaaaaa aaaaagttag actattagac aaagtattta 2820
 tgtaattatt tgataactct tgtaaatagg tggaatatga atgcttgga aattaaactt 2880
 taattttatt acattgtaca tagctctgtg taaatagaat tgcaactgtc aggttttggtg 2940
 ttcttgtttt cctttagttg ggtttatttc caggtcacag aattgctgtt aacactagaa 3000
 aacacacttc ctgcaccaac accaataccc ttcaaaaaga gttgtctgca acatttttgt 3060
 tttctttttt aatgtccaaa agtgggggaa agtgctatct cctattttca ccaaaattgg 3120
 ggaaggagtg ccactttcca gctccacttc aaattcctta aaatataact gagattgct 3179

<210> 73
 <211> 1009
 <212> DNA
 <213> Homo sapiens

<400> 73
 gggggacggg cactgggcga ctctgtgcct cgctgaggaa aaataactaa acatgggcaa 60
 aggagatcct aagaagccga gaggcaaaat gtcacatcat gcattttttg tgcaaaacttg 120
 tcgggaggag cataagaaga agcaccacga tgcttcagtc aacttctcag agttttctaa 180
 gaagtgtca gagagggtga agaccatgtc tgctaaagag aaaggaaaat ttgaagatat 240
 ggcaaaagcg gacaaggccc gttatgaaag agaaatgaaa acctatatcc ctcccaaagg 300
 ggagacaaaa aagaagtcca aggatcccaa tgcaccaag aggcctcctt cggccttctt 360
 cctcttctgc tctgagtatc gcccaaaaat caaaggagaa catcctggcc tgtccattgg 420
 tgatgttgcg aagaaactgg gagagatgtg gaataacact gctgcagatg acaagcagcc 480

ttatgaaaag aaggctgcga agctgaagga aaaatacyaa aaggatatac ctgcacatcg 540
 agctaagga aagcctgatg cagcaaaaaa gggagttgtc aaggctgaaa aaagcaagaa 600
 aaagaaggaa gaggaggaag atgaggaaga tgaagaggat gaggaggagg aggaagatga 660
 agaagatgaa gatgaagaag aagatgatga tgatgaataa gttggttcta gcgcagtttt 720
 ttttttcttg tctataaagc atttaacccc cctgtacaca actcactccc ttttaagaa 780
 aaaaattgaa atgtaaggct gtgtaagatt tgtttttaa ctgtacagtg tctttttttg 840
 tatagttaac acactaccga atgtgtcttt agatagccct gtcctggtgg tattttcaat 900
 agccactaac ctgtcctggt acagtatggg ggttgtaa atggcatggaa atttaagca 960
 ggttcttgtt ggtgcacagc acaaattagt tatatatggg gatggtagt 1009

<210> 74
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<400> 74
 agagagaaag gttgtgatgg cggctatagc tgcacccgag gtgctggtgg acagcgcgga 60
 ggagggggtcc ctgcgtgcgg cggcggagct ggcgcctcag aagcgcgaac agagactgcg 120
 caaattccgg gagctgcacc tgatgcggaa tgaagctcgt aaattaaatc accaggaagt 180
 tgtggaagaa gataaaagac taaaattacc tgcaaattgg gaagccaaaa aagctcgttt 240
 ggagtgggaa ctaaaggaag aggaaaagaa aaaggaaatgt gcggcaagag gagaagacta 300
 tgagaaagtg aagttgctgg agatcagtgc agaagatgca gaaagatggg agaggaaaaa 360
 gaagaggaaa aacctgatc tgggattttc agattatgct gctgccagcagc tacgccagta 420
 tcatcggttg accaagcaga tcaaacctga catggaaaca tatgagagac tgagagaaaa 480
 acatggagaa gagtttttcc caacatccaa tagtcttctt catggaacac atgtgccttc 540
 cacagaggaa attgacagga tggatcataga tctggaaaaa cagattgaaa aacgagacaa 600
 atatagccgg agagctcctt ataattgatga tgcatatc gactacatta atgaaaggaa 660
 tgccaaattc aacaagaaag ctgaaagatt ctatgggaaa tacacagctg aaattaaaca 720
 gaatttgaa agaggaaacag ctgtctaata ccttcaagaa ctgtttatag aagcttgaga 780
 atggggtaaa aattttctgct agcaaatca agttctttt gaaattttat cagtaatcca 840
 gaatttagta gtccatgcct tctcactcag catttagaaa taaaaatgtg gtttcttaaa 900
 cgtatacctt ttcattgata tttccacatt tttgtgcttg gatataagat gtatttcttg 960
 tagtgaagt gttttgtaat ctactttgta tacattctaa ttatattatt tttctatgta 1020
 ttttaaatgt atatggctgt ttaatctttg aagcattttg ggcttaagat tgccagcagc 1080
 acacatcaga tgcagtcatt gttgctatca gtgtggaatt tgatagagtc tagactcggg 1140
 ccacttgagg tttgttactc caaagctaag gacagtgatg aggaagatgg cagtggccac 1200
 cggaggactg gagcagtccc tctcatggc ggcctgtgac caagtcggg gaggagtggg 1260
 gctatccctc catgatctga tcatgtacag tcccctttt aaaaagcaat aaatgcttg 1320
 gattagaatt tctaaaaaaa aaaa 1344

<210> 75
 <211> 4058
 <212> DNA
 <213> Homo sapiens

<400> 75
 ccaatgttgg agccgtctgc aaagtgtccc cggcaagaag aggctgccta ccacaaggac 60

tttagcttac tttttaaaga ttgaagaaaa aaaagaagac agaaaaagaa gaactcaaag	120
atacacaaag taatttgaac caaggctcag aagtttttgg agccgtgagg gatacagcag	180
tttggtcaat attgtcttaa catgcttcaa ataaatcaga tgttctcagt gcagctgagt	240
cttggtgagc agacatggga atccgaaggc agcagtataa agaaggctca gcaggctggt	300
gccataaag ctttgactga atctacgctt cccaaaccag ttcagaagcc acccaaaagt	360
aatgttaaca ataaccagg cagtataact ccaactgtgg aactgaatgg gcttgctatg	420
aaaaggggag agcctgccat ctacaggcca ttagatccaa agccattccc aaattataga	480
gctaattaca actttcgggg catgtacaat cagaggatc attgccagc gcctaagatc	540
ttttatgttc agctcactgt aggaaataat gaattttttg ggaaggaaa gactcgacaa	600
gctgctagac acaatgctgc aatgaaagcc ctccaagcac tgcagaatga acctattcca	660
gaaagatctc ctcaaatgg tgaatcagga aaggatatgg atgatgacaa agatgcaa	720
aagtctgaga tcagcttagt gtttgaatg gctctgaagc gaaatatgcc tgcagtttt	780
gaggttatta aagaaagtgg accaccacat atgaaaagct ttgttactcg agtgcagta	840
ggagagtctc ctgcagaagg agaaggaaat agcaaaaaac tctccaagaa gcgcgctgcg	900
accaccgtct tacaggagct taaaaaactt ccacctcttc ctgtggtgga aaagccaaaa	960
ctatttttta aaaaacgccc taaaacaata gtaaggccg gaccagaata tggccaaggg	1020
atgaacccta ttgcccctt ggcgcaaatt caacaggcca aaaaggaaaa ggagccggat	1080
tatgttttgc tttcagaaag aggaatgcct cgacgtcgag aattttgtgat gcagggtgaag	1140
gtaggcaatg aagtgtctac aggaacagga cctaataaaa agatagccaa aaaaaatgct	1200
gcagaagcaa tgctgttaca acttggttat aaagcatcca ctaatcttca ggatcaactt	1260
gagaagacag gggaaaacaa aggatggagt ggtccaaagc ctgggtttcc tgaaccaaca	1320
aataatactc caaaaggaat tcttcatttg tctcctgatg tttatcaaga gatggaagcc	1380
agccgccaca aagtaatctc tggcactact ctaggctatt tgcacccaa agatatgaac	1440
caacctcaa gctctttctt cagtatatct cccacatcga atagttcagc tacaattgcc	1500
agggaactcc ttatgaatgg aacatcttct acagctgaag ccataggttt aaaaggaggt	1560
tctcctactc ccccttggtc tccagtacaa ccttcaaac aactggaata tttagcaagg	1620
attcaaggct ttcaggtatg aattaaaagc aaaaacaaaa aacaaaacaa ttcattagcc	1680
tcagattctt catctgtata catcacaagg ctcatcttg cctgctagta tggcctacat	1740
gccacttacg ttttaagtta tttaggaaca caaaggacag acaaaaaagc catatgcaca	1800
tgccctattt tctcttattt ttgatctatc tagtaattct tttgctgcct gtctcttctc	1860
cattttcctt cttctttttt aagcattttt catattcttc actgtcttct atttggctct	1920
gattaggtgc atctatctct tcgctctgtc ttccacaaac aaaaattctg ccttcagaca	1980
tttggtgta gtatttcaca ctacgtcttc ccttttttta cataaggatt gagtttcttt	2040
ttatgatgat ttaccttta tagcaatttt gaattttgca ttctgttgct agtattgatt	2100
caggtagacc attagatag aacattctag aagtctatta ccttaggagt taattaaaca	2160
tgatatttga agaataatga aatgctttat agttgttga ggcataacaa tgtgtatttg	2220
ttttactgga tcatgttttg aactgactag ggagggtagc acctgcctca gatagtacca	2280
acaattctgt ttcactgggt agtctaaaac tagcttatag ttttaactta cttgttgtgt	2340
atgtgaattt agggatggaa actttttttc ccctatttat tctttgttct cttctgggaa	2400


```

aaaacccac aaaaatcagc actcctttat ggatcacctt gagccttctt aagaacgtgta 2460
aactctagga aggggaaata tctgtgtctt gatttcttag ttgccttgaa aatcatgtac 2520
tgaactgtaa ccgctaactt gactggatga actagtttgc ttgtgtgtag agagtgtatt 2580
gcttctcag atttcaactgt tttcatctcc tttccatct tagtctttat tccttaagac 2640
caaaaactgt aatatccttt agaaatgctc tagaagatct gtattgtgta gaatgatcat 2700
gtatttataa atattttaca agtttagatt ataaaatgaa aaagaaggtc atgtgttttg 2760
gggggtattt tgcattgttc gatttttttt tcccttcacc gaacccttct gattctttca 2820
aactattgcc aggtagtgt tagtgtttct aattggactc ttaatatgaa cttcaagaag 2880
ctgttaccag ttatcggtc tgcattctga aattttaacc acttaattta aagttacaat 2940
tttagaattt gtttttgtt ttttacccta agaaacacaa taaatcactg tttaaaaaag 3000
atctcaattt atataaagta ctggaaaaaa gctaagtaat ttttagttct atctataatc 3060
tccgtaggat gaattagaaa taaattgtga tgaagaagaa ttaactgctt atttatgaat 3120
ctaatactt agaaatgtct gagagtaaca ctgcattctt atagaaacaa agcacaaatt 3180
gcattcaagc tctgaattga ttttttgcct ggagctgttg ttacagtagc tgtaattttg 3240
ctaccagaat gtcttaattt tttaaatttg tttttatttc taagctcttg gcaatgacaa 3300
taattataat tttacatat cttcactgta gtcaacatgt agagtctgct tccctcatta 3360
ttgcattgct aaggcctttt taaaaagctt atgcttacct aatatactct tttttatgga 3420
cacgttatat gtttccaaat ctgtgtattg tgatttttac atactaatga atataaacag 3480
gtgattttta aatattactg tgcttctttg gttgaatgag ctggtattga tgtaaaatac 3540
tctgtcattg atggaccact acctgcagct aagcagttag cagaatctcc gggaaatgac 3600
ttagtctggc cacatgcata gcccatcttc ataatgtcgc agcagaaggc tctttgtggt 3660
taaaagtttt aaagcctatt tctttatagg taaccctctc aggtatatat acctggtaga 3720
aaaacatgta gattgtttct attacttaaa tgttttaatt ggactgtagt ttagaaatta 3780
caggaccagc ttgttacaga ttatacacta ttctgttact tttatttctg aaacttaaaa 3840
acaataaatt ctttttctgt gtttctaggt tagaactttt ttattttatt gcacactgaa 3900
cagatactgt tgcttattga atattgtgta aacccttctt tggctttcct tgcccattgc 3960
aatttgattt aagcctacta gagccattgt atgtgacagc tatattgtat taaaaagtaa 4020
aaatatatga gtgtattgaa aaaaaaaaaa aaaaaaaa 4058

```

```

<210> 76
<211> 3020
<212> DNA
<213> Homo sapiens

```

```

<400> 76
tgaagctcgt cagttcacca tccgccctcg gcttccgcgg ggcgtgggc cgccagcctc 60
ggcaccgtcc tttcctttct ccctcgcgtt aggcaggtga cagcaggac atgtctcggg 120
agatgcagga tgtagacctc gctgaggtga agcctttggt ggagaaagg gagaccatca 180
ccggcctcct gcaagagttt gatgtccagg agcaggacat cgagacttta catggctctg 240
ttcacgtcac gctgtgtggg actcccaagg gaaaccggcc tgtcatctc acctaccatg 300
acatcggcac gaaccacaaa acctgttaca acccctctt caactacgag gacatgcagg 360
agatcaccca gcactttgcc gtctgccacg tggacgcccc tggccagcag gacggcgag 420
cctccttccc cgcagggtac atgtaccctt ccatggatca gctggctgaa atgcttctctg 480

```

gagtccttca acagtttggg ctgaaaagca ttatctgcat yyyacacayya yacyygcct 540
 acaccctaac tcgatttgct ctaaacacac ctgagatggt ggagggcctt gtccttatca 600
 acgtgaaccc ttgtgcggaa ggctggatgg actgggccgc ctccaagatc tcaggatgga 660
 cccaagctct gcccgacatg gtggtgtccc accttttttg gaaggaagaa atgcagagta 720
 acgtggaagt ggtccacacc tacgccagc acattgtgaa tgacatgaac cccggcaacc 780
 tgcacctgtt catcaatgcc tacaacagcc ggcgcgacct ggagattgag cgaccaatgc 840
 cggaaccca cacagtacc ctgcagtcc ctgctctgtt ggtggttggg gacagctgc 900
 ctgcagtga tgccgtggtg gagtgcaact caaaattgga cccaacaaag accactctcc 960
 tcaagatggc ggactgtggc ggccctccgc agatctccca gccggccaag ctgctgagg 1020
 ccttcaagta cttcgtgcag ggcatgggat acatgccctc ggctagcatg acccgctga 1080
 tgccgtcccg cacagcctct ggtccagcg tcacttctct ggatggcacc cgcagccgct 1140
 cccacaccag cgagggcacc cgaagccgct cccacaccag cgagggcacc cgcagccgct 1200
 cgcacaccag cgagggggcc cacctggaca tcaccccaa ctcgggtgct gctgggaaca 1260
 gcgcccggcc caagtccatg gaggtctcct gctaggcggc ctgccagct gccgcccccg 1320
 gactctgac tctgtagtgg cccctcctc cccggccct tttcgcccc tgctgccaat 1380
 actgccccta actcggatatt aatccaaagc ttattttgta agagttagct ctggtggaga 1440
 caaatgaggt ctattacgtg ggtgccctct ccaaaggcgg ggtggcggtg gaccaaagga 1500
 aggaagcaag catctccgca tcgcacctc ttccattaac cagtggccgg ttgccactct 1560
 cctcccctcc ctgagagaca ccaaactgcc aaaaacaaga cgcgtagcag cacacacttc 1620
 acaagccaa gcctaggccg cctgagcat cctggttcaa acgggtgcct ggtcagaagg 1680
 ccagccgccc acttccggtt tcctctttaa ctgaggagaa gctgatccag ctttccggaa 1740
 acaaaatcct tttcttcatt tggggagggg ggtaatagt acatgcaggc acctcttcta 1800
 aacaggcaaa acaggaaggg ggaagagggt ggattcatgt cgaggctaga ggcatttga 1860
 acaacaaatc tacgtagtta acttgaagaa accgattttt aaagtgtgtg catctagaaa 1920
 gctttgaatg cagaagcaaa caagcttgat tttctagca tcctcttaat gtgcagcaaa 1980
 agcaggcaac aaaatctcct ggctttacag acaaaaatat ttcagcaaac gttgggcac 2040
 atggtttttg aaggctttag ttctgcttc tgctctcct ccacagcccc aacctccac 2100
 ccctgataca tgagccagt attattcttg ttcagggaga agatcattta gatttgtttt 2160
 gcattcctta gaatggagg caacattcca cagctgcct ggctgtgatg agtgccttg 2220
 caggggccgg agtaggagca ctgggggtgg ggcggaattg ggttactcg atgtaaggga 2280
 ttcttgttg ttgtgtgag atccagtga gttgtgatt ctgtggatcc cagcttggtc 2340
 caggaatttt gagagatttg cttaaatcca gttttcaatc ttcgacagct gggctggaac 2400
 gtgaactcag tagctgaacc tgcctgaccc ggtcacgttc ttggatcctc agaactctt 2460
 gctcttgctg ggtgggggt gggaaactcac gtggggagcg gtgctgaga aaatgtaagg 2520
 attctggaat acatattcca tggactttcc ttccctctcc tgcttctct tttctgctc 2580
 cctaaccttt cgcgaatgg ggcagacaaa cactgacgtt tctgggtggc cagtgcggct 2640
 gccaggttcc tgtactactg ccttgactt ttcatthttg ctcaccgtgg attttctcat 2700
 aggaagttht gtcagagtga attgaatatt gtaagtcagc cactgggacc cgaggatttc 2760
 tgggaccccg cagttgggag gaggaagtag tccagccttc caggtggcg tgagaggcaa 2820
 tgactcgta cctgccgccc atcaccttg aggccttccc tggccttgag tagaaaagtc 2880

ggggatcggg gcaagagagg ctgagtacgg atgggaaact attgtgcaca agtctttcca 2940
gaggagtttc ttaatgagat atttgtatctt atttcagac caataaattt gtaactttgc 3000
aaaaaaaaa aaaaaaaaaa 3020

<210> 77
<211> 2759
<212> DNA
<213> Homo sapiens

<400> 77
gcctgactga gaggatgac tgacccatga agagcaccat gcagccaaaa ccctggggat 60
tggcaaagcc attgctgtct taacctctgg tggagatgcc caaggtatga atgctgctgt 120
cagggctgtg gttcaggttg gtatcttcac cgtgcccgt gtcttctttg tccatgaggg 180
ttatcaaggc ctggtggatg gtggagatca catcaaggaa gccacctggg agagcgtttc 240
gatgatgctt cagctgggag gcacggatg tggagtgcc cgtgcaagg actttcggga 300
acgagaagga cgactccgag ctgcttaca cctggtgaag cgtgggatca ccaatctctg 360
tgtcattggg ggtgatggca gcctcactgg ggctgacacc ttccgttctg agtggagtga 420
cttggtgagt gacctccaga aagcaggtaa gatcacagat gaggaggcta cgaagtccag 480
ctacctgaac attgtgggcc tggttgggtc aattgacaat gacttctgtg gcactgatat 540
gaccattggc actgactctg ccctgcatcg gatcatgga attgtagatg ccatcactac 600
cactgcccag agccaccaga ggacatttgt gttagaagta atgggccgcc actgtggata 660
cctggccctt gtcacctctc tgcctgttg ggccgactgg gtttttattc ctgaatgtcc 720
accagatgac gactgggagg aacacctttg tcgccgactc agcgagacaa ggaccctgg 780
ttctcgtctc aacatcatca ttgtggctga ggtgcaatt gacaagaatg gaaaaccaat 840
cacctcagaa gacatcaaga atctggtggt taagcgtctg ggatatgaca cccgggttac 900
tgtcttggg catgtgcaga ggggtgggac gccatcagcc ttgacagaa ttctgggcag 960
caggatgggt gtggaagcag tgatggcact ttggagggg accccagata cccagcctg 1020
tgtagtgagc ctctctggta accaggctgt gcgcctgccc ctcatggaat gtgtccagg 1080
gaccaaagat gtgaccaagg ccattgatga gaagaaattt gacgaagccc tgaagctgag 1140
aggccggagc ttcatgaaca actgggagggt gtacaagctt ctactcatg tcagaccccc 1200
ggtatctaag agtggttcgc acacagtgcc tgtgatgaac gtgggggctc cggctgcagg 1260
catgaatgct gctgttcgct ccactgtgag gattggcctt atccagggca accgagtgt 1320
cgttgccat gatggtttcg agggcctggc caaggggcag atagaggaag ctggctggag 1380
ctatgttggg ggtggactg gccaaagggt ctctaaactt gggactaaaa ggactctacc 1440
caagaagagc ttgaacaga tcagtccaa tataactaag tttaacattc agggccttgt 1500
catcattggg ggctttgagg ctacacagg gggcctggaa ctgatggagg gcaggaagca 1560
gtttgatgag ctctgcatcc catttgggt cattcctgct acagtctcca acaatgtccc 1620
tggctcagac ttcagcgttg gggctgacac agcactcaat actatctgca caacctgtga 1680
ccgcatcaag cagtcagcag ctggcaccac gcgtcgggtg ttatcattg agactatggg 1740
tggctactgt ggctacctg ctacctggc tggactggca gctggggccg atgctgccta 1800
catttttgag gagcccttca ccattcgaga cctgcaggca aatgttgaac atctgttgca 1860
aaagatgaaa acaactgtga aaaggggctt ggtgttaagg aatgaaaagt gcaatgagaa 1920
ctataccact gacttcattt tcaacctgta ctctgaggag gggaagggca tcttcgacag 1980

caggaagaat gtgcttggtc acatgcagca ggggtgggagc ccaaccccat ttgataggaa 2040
 ttttgccact aagatgggag ccaaggctat gaactggatg tctgggaaaa tcaaagagag 2100
 ttaccgtaat gggcggtatc ttgccaatac tccagattcg ggctgtgttc tggggatgag 2160
 taagagggct ctggtcttcc aaccagtggc tgagctgaag gaccagacag attttgagca 2220
 tcgaatcccc aaggaacagt ggtggctgaa actgaggccc atcctcaaaa tcctagccaa 2280
 gtacgagatt gacttggaca cttcagacca tgcccacctg gacacatca cccggaagcg 2340
 gtccggggaa gctgccgtct aaacctctct ggagtggagg gaatagatta cctgatcatg 2400
 gtcagctcac accctaataa gtccacatct tctcagtgtt ttagctgttt ttttcattag 2460
 gtttctttt atctgttacc ttgcagccat gaccagtctt ggcaggagc tggaggagca 2520
 ggcagtgggt gggagctcct tttaggtaga atttaacatg acttctgcc cagctttatc 2580
 tgtcacacaa ggtcgggac ctctagtgtc actgctagat atcacttact cagttagaat 2640
 tttcctaaaa ataagcttta tttatttctt tgtgataaca aagagtcttg gttcctctac 2700
 tacttttact acagtgacaa attgtaacta cactaataaa tgccaactgg tcactgtga 2759

<210> 78
 <211> 6133
 <212> DNA
 <213> Homo sapiens

<400> 78
 tgcataaaga caaaaggctc tgtgctcacc tgggaccctt ctggacgttg cctgtgtac 60
 ctcttcgact gctgttcat ctacgacgaa ccccggtat tgacccaga caacaatgcc 120
 acttcataat ggggacttcg tctgggatc caagggtcat tcattgcaaa gttccttaa 180
 tattttctca ctgcttcta ctaaaggagc gacagagcat ttgttcttca gccacatac 240
 ttcttccac tggccagcat tctcctctat tagactaga ctgtggataa acctcagaaa 300
 atggccaccc agcagaaagc ctctgacgag aggatctccc agttgatca caatttgctg 360
 ccagagctgt ctgctcttct gggcctagat gcagttcagt tggcaagga actagaagaa 420
 gaggagcaga aggagcgagc aaaaatgcag aaaggctaca actctcaaat gcgcagtga 480
 gcaaaaagg taaagacttt tgtgacttat gagccgtaca gctcatggat accacaggag 540
 atggcgccg ctgggtttta cttcactggg gtaaaatctg ggattcagt ctctctgtgt 600
 agcctaatec tctttggtgc cggcctcac agactccca tagaagacca caagaggttt 660
 catccagatt gtgggttcct tttgaacaag gatgttggt acattgccaa gtacgacata 720
 aggggtgaag atctgaagag caggctgaga ggaggtaaaa tgaggtagca agaagaggag 780
 gctagacttg cgtccttcag gaactggcca ttttatgtcc aaggatata ccttgtgtg 840
 ctctcagagg ctggcttctg ctttacaggt aaacaggaca cggtagagt ttttctctg 900
 ggtggatgt taggaaattg ggaagaagga gatgatcctt ggaaggaaca tgccaatgg 960
 ttcccaaat gtgaatttct tcggagtaag aaatcctcag aggaattac ccagtatatt 1020
 caaagctaca agggatttct tgacataacg ggagaacatt ttgtgaattc ctgggtccag 1080
 agagaattac ctatggcctc agcttattgc aatgacagca tctttgctta cgaagaacta 1140
 cggctggact cttttaagga ctggcccgga gaatcagctg tgggagttgc agcactggcc 1200
 aaagcaggtc ttttctacac aggtataaag gacatcgtcc agtcttttc ctgtggaggg 1260
 tgtttagaga aatggcagga aggtgatgac ccattagacg atcacaccag atgttttccc 1320
 aattgtccat ttctcaaaa tatgaagtcc tctgcggaag tgactccaga ccttcagagc 1380

cgtggtgaac tttgtgaatt actggaaacc acaagtgaag gcaatcttga agattcaata 1440
 gcagttggtc ctatagtgcc agaaatggca cagggtgaag cccagtgggt tcaagaggca 1500
 aagaatctga atgagcagct gagagcagct tataccagcg ccagtttccg ccacatgtct 1560
 ttgcttgata tctcttccga tctggccacg gaccacttgc tgggctgtga tctgtctatt 1620
 gcttcaaaac acatcagcaa acctgtgcaa gaacctctgg tgctgcctga ggtctttggc 1680
 aacttgaact ctgtcatgtg tgtggagggt gaagctgga gtggaaagac ggtcctctcg 1740
 aagaaaatag cttttctgtg ggcatctgga tgctgtcccc tgttaacag gttccagctg 1800
 gttttctacc tctcccttag ttccaccaga ccagacgagg ggctggccag tatcatctgt 1860
 gaccagctcc tagagaaaga aggatctgtt actgaaatgt gcatgaggaa cattatccag 1920
 cagttaaaga atcaggtctt attcctttta gatgactaca aagaaatag ttcaatccct 1980
 caagtcatag gaaaactgat tcaaaaaaac cacttatccc ggacctgcct attgattgct 2040
 gtccgtacaa acaggggccg ggacatccgc cgatacctag agaccattct agagatcaaa 2100
 gcatttccct ttataatac tgtctgtata ttacggaagc tcttttcaca taatatgact 2160
 cgtctgcgaa agtttatggt ttacttttga aagaaccaa gtttgcagaa gatacagaaa 2220
 actcctctct tttggggc gatctgtgct cattgggttc agtatccttt tgacccatcc 2280
 tttgatgatg tggctgtttt caagtcctat atggaacgcc tttccttaag gaacaaagcg 2340
 acagctgaaa ttctcaaagc aactgtgtcc tctgtggtg agctggcctt gaaagggttt 2400
 tttcatgtt gctttgagtt taatgatgat gatctcgag aagcagggtt tgatgaagat 2460
 gaagatctaa ccatgtgctt gatgagcaaa ttacagccc agagactaag accattctac 2520
 cggtttttaa gtcctgcctt ccaagaattt cttgcgggga tgaggctgat tgaactcctg 2580
 gattcagata ggcaggaaac tcaagatttg ggactgtatc atttgaaca aatcaactca 2640
 cccatgatga ctgtaagcgc ctacaacaat ttttgaact atgtctccag cctcccttca 2700
 acaaaagcag ggcccaaat tgtgtctcat ttgtccatt tagtgataa caaagagtca 2760
 ttggagaata tatctgaaaa tgatgactac ttaaagcacc agccagaaat ttactgcag 2820
 atgcagttac ttaggggatt gtggcaaatt tgtccacaag ctacttttc aatgggttca 2880
 gaacatttac tggttcttgc cctgaaaact gcttatcaaa gcaacactgt tgctgcgtgt 2940
 tctccatttg ttttgaatt cttcaaggg agaactga ctttgggtgc gcttaactta 3000
 cagtactttt tcgaccaccc agaaagcttg tcattgttga ggagcatcca cttcccaata 3060
 cgaggaaata agacatcacc cagagcacat ttttcagttc tggaacatg ttttgacaaa 3120
 tcacaggtgc caactataga tcaggactat gctctgcct ttgaacctat gaatgaatgg 3180
 gagcgaaatt tagctgaaaa agaggataat gtaaagagct atatggatat gcagcgcagg 3240
 gcatcaccag accttagtac tggctatttg aaactttctc caaagcagta caagattccc 3300
 tgtctagaag tcgatgtgaa tgatattgat gttgtaggcc aggatatgct tgagattcta 3360
 atgacagttt tctcagcttc acagcgcac gaactccatt taaaccacag cagaggcttt 3420
 atagaaagca tccgccagc tcttgagctg tctaaggcct ctgtcaccaa gtgctccata 3480
 agcaagtgg aactcagcgc agcgaacag gaactgcttc tcacctgcc ttccctggaa 3540
 tctcttgaag tctcaggac aatccagtca caagacaaa tctttcctaa tctggataag 3600
 ttctgtgcc tgaagaact gtctgtggat ctggagggca atataaatgt ttttctagtc 3660
 attcctgaag aatttccaaa cttccacat atggagaaat tattgatcca aatttcagct 3720

gagtatgac cttccaaact agtaaaatta attcaaaact cttcaaaact ccatgcttc 3780
 catctgaagt gtaacttctt ttcggatttt gggctctctca tgactatgct tgtttcctgt 3840
 aagaaactca cagaaattaa gttttcggat tcattttttc aagccgtccc atttgttgcc 3900
 agtttgccaa attttatttc tctgaagata ttaaactcttg aaggccagca atttcctgat 3960
 gaggaacat cagaaaaatt tgcctacatt ttaggttctc ttagtaacct ggaagaattg 4020
 atccttccta ctggggatgg aatttatcga gtggccaaac tgatcatcca gcagtgtcag 4080
 cagcttcatt gtctccgagt cctctcattt ttcaagactt tgaatgatga cagcgtggtg 4140
 gaaattgcc aagtagcaat cagtggaggt ttccagaaac ttgagaacct aaagctttca 4200
 atcaatcaca agattacaga ggaaggatac agaaatttct ttcaagcact ggacaacatg 4260
 ccaaaactgc aggagtgg aatctccagg catttcacag agtgtatcaa agctcaggcc 4320
 acaacagtca agtctttgag tcaatgtgtg ttacgactac caaggctcat tagactgaac 4380
 atgttaagtt ggctcttgg aagcagatgat attgcattgc ttaatgtcat gaaagaaaga 4440
 catcctcaat ctaagtactt aactattctc cagaaatgga tactgccgtt ctctccaatc 4500
 attcagaaat aaaagattca gctaaaaact gctgaatcaa taatttgtct tggggcatat 4560
 tgaggatgta aaaaaagttg ttgattaatg ctaaaaacca aattatccaa aattatttta 4620
 ttaaatttg catacaaaag aaaatgtgta aggcttgcta aaaaacaaaa caaaacaaaa 4680
 cacagtctg catactcacc accaagctca agaaataaat catcaccaat acctttgagg 4740
 tccttgagta atccacccca gctaaaggca aaccttcaa tcaagtttat acagcaaacc 4800
 ctccattgtc catggtcaac agggaagggg ttggggacag gtctgccaat ctatctaaaa 4860
 gccacaatat ggaagaagta ttcaatttat ataataaatg gctaacttaa cggttgaatc 4920
 actttcatal atggatgaaa cgggtttaac acaggatcca catgaatctt ctgtgggcca 4980
 agagatgtt ctaaatcctt gtagaacctg tttctatat tgaactagct ttggtacagt 5040
 agagttaact tactttccat ttatccactg ccaatataaa gaggaacag gggttaggga 5100
 aaaatgactt cattccagag gcttctcaga gttcaacata tgctataatt tagaattttc 5160
 ttatgaatcc actctacttg ggtagaaaat attttatctc tagtgattgc atattatttc 5220
 catatcatag tatttcatag tatttatatt gatatgagt tctatatcaa tgcagtgtc 5280
 cagaatttcg ttccctaccag ttaagtagtt ttctgaacgg ccagaagacc attcgaat 5340
 catgatacta ctataagttg gtaaacaccc atacttttat cctcattttt attctcacta 5400
 agaaaaagt caactccct ccccttgccc aagtatgaaa tatagggaca gtatgtatgg 5460
 tgtgtctca tttgtttaga aaaccactta tgactgggtg cgggtgctca cacctgtaat 5520
 cccagcactt tgggaggctg aggcggggcga atcatttgag gtgaggaatt cgagaccagc 5580
 ctggccagca tgggtgaaacc ccactctctac taaaaatata aaaattagcc aggtgtggtg 5640
 gcacatgcct gtagtccag ccactagggc ggctgagacg caagacttgc ttgaaccgg 5700
 gaggcagagg ttgcagtga ccaagatggc gccactgcat tccagcctgg gcaacagagc 5760
 aagacctgt ctgtctcaaa acaaaaaaca aaaccactta tattgctagc tacattaaga 5820
 atttctgaat atgttactga gcttgcttgt ggtaaccatt tataatatca gaaagtatat 5880
 gtacaccaa acatgttgaa catccatgtt gtacaactga aatataaata attttgtcaa 5940
 ttatacctaa ataaaactgg aaaaaaattt ctggaagttt atatctaaaa atgttaatag 6000
 tgcgtacctc taggaagtgg gcctggaagc cattcttact ttccagtctc tccattctg 6060
 tactgttttt tgttttactt tcgtgcctgc attatttttc tttttaaacc aaaaataaat 6120

ctagtttagc act

6133

<210> 79

<211> 4028

<212> DNA

<213> Homo sapiens

<400> 79

gaattccggc tcgtgtgctg cgagctggcg gccgggccgg agtgctgggg ctttgaactc 60
cgagaggagg tggaccagaa cttttggaac tagtgccggc ggctctccac cccccagtat 120
aaaagaacgt gtggatcact ttgctgagta catccaagat ttgaagaact gaaataaatc 180
agctttaaac ctgcttttta aaaatatctg ggttgaatt tgcccctgac aaataataaa 240
atgatgagtg atgcaagtga catgttggtt gcagcgttgg agcagatgga tggatcata 300
gcaggttcta aggccttggg atattccaat gggatttttg attgccaatc tcccacctct 360
ccattcatgg gaagtgtgag agctctgcac cttgtggaag acctgcgtgg attgtagag 420
atgatggaaa cagatgagaa agaaggcttg agatgccaga tcccagattc aacagcagaa 480
acgcttgttg aatggcttca gagtcaaatg acaaatggac acctaccagg gaacggagat 540
gtgtatcaag aaaggctggc acgtttagaa aatgataaag aatccctcgt tcttcaggta 600
agtgtgttaa cagaccaggt ggaggctcag ggagagaaga ttcgagattt ggagtttgt 660
cttgaagagc acagagagaa gttgaatgcc acagaagaaa tgctgcagca ggagcttcta 720
agtaggacat ccttagaacc tcagaagttg gatctgatgg ctgaaatata taacttgaag 780
ttgaaactga cagctgtaga gaaggacaga ttggattatg aagataagtt cagagacaca 840
gaggggttga ttcaggagat caatgatttg aggttaaaag ttagtgaaat ggacagtga 900
agacttcagt atgaaaaaaa gcttaaatca accaaagatg aactggcatc tttaaaagaa 960
caactagaag aaaaggaatc tgaagtaaaa aggcctacaag aaaaattggt ttgcaagatg 1020
aaaggagaag gggttgaaat tgttgataga gatgaaaatt ttaaaaagaa gctcaaagaa 1080
aaaaacatcg aagtacaaaa aatgaaaaaa gctgtggagt ccttgatggc agcaaatgaa 1140
gaaaaggatc ggaataatga agatcttcga cagtgcctga acaggatcaa gaaaatgcaa 1200
gacacggttg tactggccca aggtaaaaaa ggcaaagatg gagaatatga agagctgctc 1260
aattccagtt ccatctcttc tttgctggat gcacagggtt tcagtgtatc ggagaaaagt 1320
ccatcaccca ctccagtaat gggatctccc agttgtgacc catttaacac aagtgttccc 1380
gaagagttcc atactacat cttgcaagtt tccatccctt cattattgcc agcaactgta 1440
agcatggaaa cttctgaaaa atcaaagttg actcctaagc cagagacttc atttgaagaa 1500
aatgatggaa acataatcct tgggtccact gttgataccc aactgcgtga taaactttta 1560
acttcaagtc tgcagaagtc cagcagcctg ggcaatctga agaaagagac atctgatggg 1620
gaaaaggaaa ctattcagaa gacttcagag gacagagctc cggcagaaag caggccattt 1680
gggacccttc ctcccaggcc cccaggggcag gacacctcca tggatgacaa ccccttcggc 1740
actcgaagg tcatagcttc ctttggccgg ggctttttta aaatcaaaag taacaagaga 1800
acagcaagtg caccaaactt agatcgtaaa cgaagtgccg gtgcacccac cctagctgaa 1860
acagaaaaag agacagcagc gcacctagat ctggctggtg cttcttctcg gccaaaagat 1920
tcacagagga acagtccctt ccagataccg cctccatctc cagattccaa aaagaaatcc 1980
agaggtatca tgaactctt tggaaaactt aggagaagtc aatcaactac attcaacca 2040
gatgacatgt ctgagcctga attcaaaaga ggagggacaa gggcaaccgc ggggccccga 2100

ttaggttggt ctcgagactt gggacagtct aacagtgact tggatatgcc atttgccaag 2160
 tggaccaagg agcaggtttg caattggctg atggaacagg gcttgggctc gtacctgaat 2220
 tctggcaagc actggattgc atctggccaa acgcttttgc aggcttctca acaagatcta 2280
 gagaaggaac ttggaatcaa gcattcactt catcgaaaga aactccagct agcactccaa 2340
 gccctgggat ctgaagaaga aaccaatcat ggaagctgg atttcaactg ggtcactaga 2400
 tggttggatg acattggcct ccctcaatat aagaccagc ttgatgaagg acgggttgat 2460
 ggtcgaatgc tacattacat gactgttgat gacttactgt ctctgaaggc tgaagtgtg 2520
 ctacaccatc tcagtatcaa aagggccatc caggctctga ggatcaataa ctttgaacca 2580
 aactgtctac gggagcgcc atctgatgag aataccatcg ccccatcaga agttcagaag 2640
 tggactaacc atcgagtgat ggagtggctg cgctccgtgg acttggcaga atatgcgccc 2700
 aatctcagag gcagtgggtt ccatggggg ctcatggttc tagagcctcg ttttaacgta 2760
 gaaacaatgg ctcaattatt gaacatccca ccaataaga ctttgcgtcg aagacatttg 2820
 gccactcatt tcaaccttct gattggggct gaggcacagc accagaagcg agatgccatg 2880
 gagctgcccg attatgtact tctaacagct actgccaag tgaagccaaa gaaacttgcc 2940
 ttagcaatt ttgggaattt gagaaagaag aaacaggaag atggtgaaga atatgtttgt 3000
 ccaatggaat tgggacaggc atcaggaagt gcatctaaga aaggatttaa acctggtttg 3060
 gatatgcgcc tgtatgagga agatgatttg gaccggtag agcagatgga agattcagaa 3120
 gggacagtga gacagatagg tgcatctctt gaaggcatca acaatctgac gcacatgta 3180
 aaagaagatg acatgtttta agattttgct gcccggtccc ccagtgccag cattacagat 3240
 gaagactcaa acgtttgacc gtagcacctg gatgaacatt aggagtgcct agtctttttt 3300
 ctacttgctt ttccaaacac tcacagtata tacaacaggc agcggattgt ctattgtttg 3360
 ttgttctaac ttctgctgct gagaagtta aacagaaagc aggagtaatg tgccgattct 3420
 gaagttgcca caaaaaataa gacactgggtg aatgagagta taattgtttt tcttctattt 3480
 aatgtaaaaa tctgtgatat attatattta aagtgttgca ttttaagatga gtattttacc 3540
 agagtgttcc cattcatatc cgcggtatgg aggatttgag gaacagtaac caggatgtga 3600
 atgattttgt tacatcagtg ttactgttag ccacctaatg aggacattat atgatttcag 3660
 aatcaatatg tggaaacttct ttaagcattc agtgtgccc ctaaatgcca gccacacctc 3720
 cacttgcttc ttattgtctt atttttatat atttttctaa atatatgtat atatacagta 3780
 catagaaaat agaactttta tttgtgacc taaggacgat ggtgaaaaga tcacgttttc 3840
 aaaacaatct ggtgatcaga atgttcatat accagctggg ttctgaagag gtcagaatga 3900
 tctttctcca tactgacttt taacaatgtt gatcattgag gctaaattaa tatatatgaa 3960
 atattccttt ttgatgacac cacaaaattg ttgaacagtt taagaatttc aaccttaac 4020
 ttggatcc 4028

<210> 80
 <211> 9588
 <212> DNA
 <213> Homo sapiens

<400> 80
 ccgaccaaca ccaacaccca gctccgacgc agctcctctg cgcccttgcc gccctccgag 60
 ccacagcttt cctcccgtc ctgcccccg cccgtcgccg tctccgcgt cgcagcgcc 120
 tcgggagggc ccaggtagcg agcagcgacc tcgagagcct tccgaactcc cgcccggttc 180


```

ccccgccgtc cgcctatcct tggccccctc cgctttctcc gcgccggccc gcctcgctta 240
tgccctggcg ctgagccgct ctcccgattg cccgccgaca tgagctgcaa cggaggctcc 300
caccgcgga tcaacactct gggccgcatg atccgcgccg agtctggccc ggacctgcgc 360
tacgaggtag ccagcgccgg cgggggcacc agcaggatgt actattctcg gcgcggcggtg 420
atcaccgacc agaactcgga cggctactgt caaacccgca cgatgtccag gcaccagaac 480
cagaacacca tccaggagct gctgcagaac tgctccgact gcttgatgag agcagagctc 540
atcgtgcagc ctgaattgaa gtatggagat ggaatacaac tgactcggag tcgagaattg 600
gatgagtgtt ttgccaggc caatgaccaa atggaaatcc tcgacagctt gatcagagag 660
atcgggcaga tgggccagcc ctgtgatgct taccagaaaa ggcttcttca gctccaagag 720
caaatgcgag ccttttataa agccatcagt gtccctcgag tccgcagggc cagctccaag 780
gggtggtgag gctacacttg tcagagtggc tctggctggg atgagttcac caaacatgctc 840
accagtgaat gtttgggggtg gatgaggcag caaaggcgcg agatggacat ggtggcctgg 900
gggtgtgacc tggcctcagt ggagcagcac attaacagcc accggggcat ccacaactcc 960
atcggcgact atcgctggca gctggacaaa atcaaagccg acctgcgca gaaatctgctg 1020
atctaccagt tggaggagga gtatgaaaac ctgctgaaag cgtcctttga gaggatggat 1080
cacctgcgac agctgcagaa catcattcag gccacgtcca gggagatcat gtggatcaat 1140
gactgcgagg aggaggagct gctgtacgac tggagcgaca agaaccacaa catcgctcag 1200
aaacaggagg ccttctccat acgcatgagt caactggaag ttaaagaaaa agagctcaat 1260
aagctgaac aagaaagtga ccaacttgct ctcaatcagc atccagcttc agacaaaatt 1320
gaggcctata tggacactct gcagacgagc tggagttgga ttcttcagat caccaagtgc 1380
attgatgttc atctgaaaga aaatgctgcc tactttcagt tttttgaaga ggcgcagtct 1440
actgaagcat acctgaagg gctccaggac tccatcagga agaagtaccc ctgcgacaag 1500
aacatgcccc tgcagcacct gctggaacag atcaaggagc tggagaaaga acgagagaaa 1560
atccttgaat acaagcgtca ggtgcagaac ttggtaaaca agtctaagaa gattgtacag 1620
ctgaagcctc gtaaccaga ctacagaagc aataaaccca ttattctcag agctctctgt 1680
gactacaac aagatcagaa aatcgtgcat aagggggatg agtgatcct gaaggacaac 1740
aacgagcgca gcaagtggta cgtgacgggc ccgggaggcg ttgacatgct tgttccctct 1800
gtggggctga tcctccctcc tccgaacca ctggccgtgg acctctcttg caagattgag 1860
cagtactagc aagccatctt ggctctgtgg aaccagctct acatcaacat gaagagcctg 1920
gtgtcctggc actactgcat gattgacata gagaagatca gggccatgac aatcgccaag 1980
ctgaaaaaa tgcggcagga agattacatg aagacgatag ccgacctga gttacattac 2040
caagagttca tcagaaatag ccaaggctca gagatgtttg gagatgatga caagcggaaa 2100
atacagtctc agttcaccga tggccagaag cattaccaga ccctggatcat tcagctccct 2160
ggctatcccc agcaccagac agtgaccaca actgaaatca ctcatcatgg aacctgcaa 2220
gatgtcaacc ataataaagt aattgaaacc aacagagaaa atgacaagca agaaacatgg 2280
atgctgatgg agctgcagaa gattcgcagg cagatagagc actgcgaggg caggatgact 2340
ctcaaaaacc tccctctagc agaccagggg tcttctcacc acatcacagt gaaaattaac 2400
gagcttaaga gtgtgcagaa tgattcacia gcaattgctg aggttctcaa ccagcttaaa 2460
gatatgcttg ccaacttcag aggttctgaa aagtactgct atttacagaa tgaagtattt 2520

```

ggactatttc agaaactgga aaatatcaat ggtgttaccg atgtgttacc aaatagutta 2580
tgcacagtaa gggcactgct ccaggctatt ctccaaacag aagacatggt aaagggttat 2640
gaagccaggc tcaactgagga ggaactgtc tgcctggacc tggataaagt ggaagcttac 2700
cgctgtggac tgaagaaaat aaaaaatgac ttgaacttga agaagtcggt gttggccact 2760
atgaagacag aactacagaa agcccagcag atccactctc agacttcaca gcagtatcca 2820
ctttatgac tggacttggg caagtccggt gaaaaagtca cacagctgac agaccgctgg 2880
caaaggatag ataacagat cgactttaga ttatgggacc tggagaaaca aatcaagcaa 2940
ttgaggaatt atcgtgataa ctatcaggct ttctgcaagt ggctctatga tcgtaaacgc 3000
cgccaggatt ccttagaatc catgaaattt ggagattcca acacagtcac gcggtttttg 3060
aatgagcaga agaacttgca cagtgaataa tctggcaaac gagacaaac agagggaagta 3120
caaaaaattg ctgaactttg cgccaattca attaaggatt atgagctcca gctggcctca 3180
tacacctcag gactggaaac tctgctgaac atacctatca agaggacat gattcagtc 3240
ccttctggg tgattctgca agaggctgca gatgttcacg ctccgtacat tgaactactt 3300
acaagatctg gagactatta caggttctta agtgagatgc tgaagagttt ggaagatctg 3360
aagctgaaaa ataccaagat cgaagttttg gaagaggagc tcagactggc ccgagatgcc 3420
aactcggaat actgtaataa gaacaaattc ctggatcaga acctgcagaa ataccaggca 3480
gagtgttccc agttcaaacg gaagcttgcg agcctggagg agctgaagag acaggctgag 3540
ctggatggga agtcggctaa gcaaaatcta gacaagtgc acggccaaat aaaagaactc 3600
aatgagaaga tcacccgact gacttatgag attgaagatg aaaagagaag aagaaaatct 3660
gtggaagaca gatttgacca acagaagaat gactatgacc aactgcagaa agcaaggcaa 3720
tgtgaaaagg agaaccttg ttggcagaaa ttagagtctg agaaagccat caaggagaag 3780
gagtacgaga ttgaaaggt gaggttcta ctgcaggaag aaggcaccg gaagagagaa 3840
tatgaaaatg agctggcaaa ggtaagaac cactataatg aggagatgag taatttaagg 3900
aacaagtatg aaacagagat taacattacg aagaccacca tcaaggagat atccatgcaa 3960
aaagaggatg attccaaaaa tcttagaaac cagcttgata gactttcaag ggaaaatcga 4020
gatctgaagg atgaaattgt caggctcaat gacagcatct tgcaggccac tgagcagcga 4080
aggcgagctg aagaaaacgc ccttcagcaa aaggcctgtg gctctgagat aatgcagaag 4140
aagcagcatc tggagataga actgaagcag gtcatgcagc agcgtctga ggacaatgcc 4200
cggcacaagc agtccctgga ggaggctgcc aagaccattc aggacaaaaa taaggagatc 4260
gagagactca aagctgagtt tcaggaggag gccaaagcgc gctgggaata tgaatatgaa 4320
ctgagtaagg taagaaacaa ttatgatgag gagatcatta gcttaaaaaa tcagtttgag 4380
accgagatca acatcaccaa gaccaccatc caccagctca ccatgcagaa ggaagaggat 4440
accagtggct accgggctca gatagacaat ctaccccgag aaaacaggag cttatctgaa 4500
gaaataaaga ggctgaagaa cactctaacc cagaccacag agaatctcag gaggttgga 4560
gaagacatcc aacagcaaaa ggccactggc tctgaggtgt ctgagaggaa acagcagctg 4620
gaggttgagc tgagacaagt cactcagatg cgaacagagg agagcgtaag atataagcaa 4680
tctcttgatg atgctgcaa aaccatccag gataaaaaca aggagataga aagggttaaaa 4740
caactgatcg acaagaaac aaatgaccgg aaatgcctgg aagatgaaaa cgcgagatta 4800
caaagggtcc agtatgacct gcagaaagca aacagtagtg cgacggagac aataaacaaa 4860
ctgaagggttc aggagcaaga actgacacgc ctgaggatcg actatgaaag ggtttcccag 4920

gagaggactg tgaaggacca ggatatcacg cggttccaga actctctgaa agagctgcag 4980
 ctgcagaagc agaaggtgga agaggagctg aatcggtga agaggaccgc gtcagaagac 5040
 tcctgcaaga ggaagaagct ggaggaagag ctggaaggca tgaggaggtc gctgaaggag 5100
 caagccatca aaatcaccaa cctgaccacg cagctggagc aggcattccat tgttaagaag 5160
 aggagtgagg atgacctccg gcagcagagg gacgtgctgg atggccacct gagggaaaag 5220
 cagaggaccc aggaagagct gaggaggctc tcttctgagg tcgaggccct gaggcggcag 5280
 ttactccagg aacaggaaag tgtcaacaa gctcacttga ggaatgagca tttccagaag 5340
 gcgatagaag ataaaagcag aagcttaaat gaaagcaaaa tagaaattga gaggctgcag 5400
 tctctcacag agaacctgac caaggagcac ttgatgttag aagaagaact gcggaacctg 5460
 aggctggagt acgatgacct gaggagagga cgaagcgaag cggacagtga taaaaatgca 5520
 accatcttgg aactaaggag ccagctgcag atcagcaaca accggaccct ggaactgcag 5580
 gggctgatta atgatttaca gagagagagg gaaaatttga gacaggaaat tgagaaattc 5640
 caaaagcagg ctttagaggc atctaatagg attcaggaat caaagaatca gtgtactcag 5700
 gtggtacagg aaagagagag ccttctggtg aaaatcaaag tcctggagca agacaaggca 5760
 aggctgcaga ggctggagga tgagctgaat cgtgcaaat caactctaga ggcagaaacc 5820
 aggggtgaac agcgcctgga gtgtgagaaa cagcaaattc agaatgacct gaatcagtgg 5880
 aagactcaat attcccga aagaggaggc attaggaaga tagaatcgga aagagaaaag 5940
 agtgagagag agaagaacag tcttaggagt gagatcgaaa gactccaagc agagatcaag 6000
 agaattgaag agagggtcag gcgtaagctg gaggattcta ccaggagagc acagtcacag 6060
 ttagaaacag aacgctcccg atatcagagg gagattgata aactcagaca gcgcccata 6120
 gggccccatc gagagaccca gactgagtgt gaggggaccg ttgacacctc caagctggtg 6180
 tttgatgggc tgaggaagaa ggtgacagca atgcagctct atgagtgtca gctgatcgac 6240
 aaaacaacct tggacaaact attgaagggg aagaagtcag tggaagaagt tgcttctgaa 6300
 atccagccat tccttcgggg tgcaggatct atcgctggag catctgcttc tcctaaggaa 6360
 aaatactctt tggtagaggc caagagaaag aaattaatca gcccagaatc cacagtcag 6420
 cttctggagg ccagggcagc tacagggtgtg ataattgatc cccatcgga tgagaagctg 6480
 actgtcgaca gtgccatagc tcggggacctc attgacttcg atgaccgtca gcagatatat 6540
 gcagcagaaa aagctatcac tggttttgat gatccatttt caggcaagac agtatctgtt 6600
 tcagaagcca tcaagaaaaa tttgattgat agagaaaccg gaatgcgcct gctggaagcc 6660
 cagattgctt cagggggtgt agtagaccct gtgaacagtg tctttttgcc aaaagatgtc 6720
 gccttgcccc gggggctgat tgatagagat ttgtatcgat ccctgaatga tccccgagat 6780
 agtcagaaaa actttgtgga tccagtcacc aaaaagaagg tcagttacgt gcagctgaag 6840
 gaacgggtgca gaatcgaacc acatactggt ctgctcttgc tttcagtaca gaagagaagc 6900
 atgtccttcc aaggaatcag acaacctgtg accgtcactg agctagtaga ttctggtata 6960
 ttgagaccgt cactgtcaa tgaactggaa tctggtcaga tttcttatga cgaggttggt 7020
 gagagaatta aggacttctc ccagggttca agctgcatag caggcatata caatgagacc 7080
 aaaaaacaga agcttgcat ttatgaggcc atgaaaattg gcttagtccg acctggtact 7140
 gctctggagt tgctggaagc ccaagcagct actggcttta tagtgatcc tgttagcaac 7200
 ttgaggttac cagtggagga agcctacaag agaggctctg tgggcattga gttcaagag 7260

aagctcctgt ctgcagaacg agctgtcact gggataaaly atccctgaac aygaacacac 7320
 atctctttgt tccaagccat gaataaggaa ctcacgaaa agggccacgg tattcgctta 7380
 ttagaagcac agatcgcaac cggggggatc attgacccaa aggagagcca tcgtttacca 7440
 gttgacatag catataagag gggctatttc aatgaggaac tcagttagat tctctcagat 7500
 ccaagtgatg ataccaaagg attttttgac cccaacactg aagaaaatct tacctatctg 7560
 caactaaaag aaagatgcat taaggatgag gaaacagggc tctgtcttct gcctctgaaa 7620
 gaaaagaaga aacagggtca gacatcacia aagaataccc tcaggaagcg tagagtggtc 7680
 atagttgacc cagaacccaa taaagaaatg tctgttcagg aggcctacaa gaagggccta 7740
 attgattatg aaaccttcaa agaactgtgt gagcaggaat gtgaatggga agaaataacc 7800
 atcacgggat cagatggctc caccagggtg gtcctggtag atagaaagac aggcagtcag 7860
 tatgatattc aagatgctat tgacaagggc cttgttgaca ggaagttctt tgatcagtac 7920
 cgtaccggca gcctcagcct cactcaattt gctgacatga tctccttgaa aaatgggtgc 7980
 ggcaccagca gcagcatggg cagtgggtgc agcgatgatg tttttagcag ctcccacat 8040
 gaatcagtaa gtaagatttc caccatatcc agcgtcagga atttaacat aaggagcagc 8100
 tctttttcag acaccctgga agaatcgagc cccattgcag ccactcttga cacagaaaac 8160
 ctggagaaaa tctccattac agaaggtata gagcggggca tcgttgacag catcacgggt 8220
 cagaggcttc tggaggctca ggctgcaca ggtggcatca tccaccaac cacgggccag 8280
 aagctgtcac ttcaggacgc agtctccag ggtgtgattg accaagacat ggccaccagc 8340
 gtgaagcctg ctcagaaagc cttcataggc ttcgagggtg tgaagggaaa gaagaagatg 8400
 tcagcagcag aggcagtga agaaaaatgg ctcccgtatg aggcctggcca gcgcttctg 8460
 gagttccagt acctcacggg aggtcttgtt gaccgggaag tgcattggag gataagcacc 8520
 gaagaagcca tccggaagg gttcatagat ggccgcgccg cacagaggct gcaagacacc 8580
 agcagctatg ccaaaatcct gacctgcccc aaaaccaa ataaaaatc ctataaggat 8640
 gccataaatc gctccatggt agaagatc actgggctgc gccttctgga agccgcctcc 8700
 gtgtcgtcca agggcttacc cagcccttac aacatgtctt cggctccggg gtcccgtcc 8760
 ggctcccgt cgggatctcg ctccggatct cgctccgggt cccgcagtg gtcccggaga 8820
 ggaagcttg acgccacagg gaattcttcc tactcttatt cctactcatt tagcagtagt 8880
 tctattgggc actagtagtc agttgggagt ggttgctata ccttgacttc atttatatga 8940
 atttccactt tattaaataa tagaaaagaa aatcccgggt cttgcagtag agtgatagga 9000
 cattctatgc ttacagaaaa tatagccatg attgaaatca aatagtaaag gctgttctgg 9060
 ctttttatct tcttagctca tcttaaataa gcagtacact tggatgcagt gcgtctgaag 9120
 tgctaatacag ttgtaacaat agcacaatc gaacttagga tttgtttctt ctcttctgtg 9180
 tttcgatttt tgatcaattc ttttaatttg gaagcctata atacagtttt ctattcttgg 9240
 agataaaaat taaatggatc actgatattt tagtcattct gcttctcacc taaatatttc 9300
 catattctgt attaggagaa aattaccctc ccagcaccag cccccctc aaaccccaa 9360
 cccaaaacca agcatttttg aatgagctc ctttagtttc agagtgtgga ttgtataacc 9420
 catatactct tcgatgtact tgtttggtt ggtattaatt tgactgtgca tgacagcggc 9480
 aatcttttct ttggtaaaag tttctgttt attttgcttgc tcatattcga tgtacttta 9540
 ggtgtcttta tgaagtttgc tattctggca ataaactttt agactttt 9588

<210> 81
 <211> 1311
 <212> DNA
 <213> Homo sapiens

<400> 81
 agtccgggag attctcgctc tgctgcttta gtttcggagt gtttggcgac ggggcagcgc 60
 gagatgtgga ggctcatgct gaggtttaat gcattcaaaa ggactaatac catactgcac 120
 catttgagaa tgtccaagca cacagatgca gcagaagagg tgctattgga aaaaaaaggt 180
 tgcgcgggag tcataacact aaacagacca aagttcctca atgcactgac tcttaatatg 240
 attcggcaga tttatccaca gctaaagaag tggaacaag atcctgaaac tttcgtgac 300
 attataaagg gagcaggagg aaaggctttc tgtgccgggg gtgatatcag agtgcctcgc 360
 gaagctgaaa aggcaaaaaca gaagatagct ccagttttct tcagagaaga atatatgctg 420
 aataatgctg ttggttcttg ccagaaacct tatgttcac ttattcatgg aattacaatg 480
 ggtgggggag ttggtctctc agtccatggg caatttcgag tggctacaga aaagtgtctt 540
 tttgctatgc cagaaactgc aataggactg ttcctgatg tgggtggagg ttatttcttt 600
 gccacgactc caaggaagaaac ttggttactt ccttgatta acggattcag actaaaagga 660
 agagatgtgt acagagcagg aattgctaca cactttgtag attctgaaaa gttggccatg 720
 ttagaggaag atttgttagc cttgaaatct ccttcaaaag aaaatattgc atctgtctta 780
 gaaaattacc atacagagtc taagattgat cgagacaagt cttttatact tgaggaacac 840
 atggacaaaa taaacagttg tttttcagcc aatactgtgg aagaaattat tgaaaactta 900
 cagcaagatg gttcatcttt tgccctagag caattgaagg taattaataa aatgtctcca 960
 acatctctaa agatcacact aaggcaactc atggaggggt cttcaaagac cttgcaagaa 1020
 gtactaacta tggagtatcg gctaagtcga gcttgatga gaggtcatga ctttcatgaa 1080
 ggcgttagag ctgttttaat tgataaagac cagagtccaa aatggaaacc agctgatcta 1140
 aaagaagtta ctgaggaaga tttgaataat cactttaagt ctttgggaag cagtgaattg 1200
 aaattttgag gtgacaggct ttttaaggat atttttagc atgggttggc aatctacagc 1260
 atgtgggcca aatccagcct gctgcctgtt tttatatacc ctgtaagcaa g 1311

<210> 82
 <211> 4368
 <212> DNA
 <213> Homo sapiens

<400> 82
 cgaaatgaga gcaaaaaggg agagagcagg aaagcgagca caggcgagta cagtatacaa 60
 agtgttttga gtttctgact ggcgtgccgg aaagatcatg ttagcacacc cagaaactcc 120
 acacgatgca gaccccagag gtaccagcag aaagggtccc tcgtagacgg agtatctcag 180
 ggaccagtac atcagagaaa cccaactcca tggacactgc aaatacctca cccttcaaag 240
 taccaggatt cttcagcaag cgcctgaaag gctccatcaa gaggaccaa agccagtcaa 300
 agcttgacag aaacacgagc tttcggcttc catcccttcg cagtacagat gacaggcttc 360
 gtgggctgcc taaactaaaa gagtacggtt cccatgaatc cttgctgagc ccatgcagca 420
 cagtggaatg tctggtctt ggtagagggg aacctgtatc agtgaaacca cttcatagta 480
 gcaccttg acaagacttc tgctttgagg ttacctactt aagtggaggt aaatgcttca 540
 gctgtaattc tgcttctgag agagacaagt ggatggaaaa ccttcgagg acagttcaac 600
 ctaataagga caattgcagg cgagctgaaa atgttcttcg tttatggatc attgaagcca 660

```

aggaccttgc ccctaaaaag aaatatttct gcgaactgtg ccttgatgat acccctcttg 720
ctcgtacaac cagcaagacc aaagcagaca atattttctg gggcgaacat tttgaattct 780
tcagccttcc acctcttcat agtatcacag ttcacattta caaggatgtg gaaaaaaaga 840
aaaaaaagga caagaataat tatgtagggc tagtcaacat cccactgcc agtgtgactg 900
gtcgccaatt tgtagaaaag tggatatccag tgagtacacc tacaccaac aaaggaaaga 960
caggaggacc ttctattcgg attaaatcac gtttccaaac tatcaccatt ctgcctatgg 1020
agcaatacaa agaatttgca gaatttgta ccagcaacta caccatgctg tgttctgtcc 1080
ttgagccagt aattagtgtg agaaataaag aggagtggc ttgtgcctta gtgcacattc 1140
ttcaaagtac tggcagagcc aaggattttc tgactgactt ggtgatgtct gaggtggatc 1200
gttgtggaga gcatgatgtc ttgatcttca gagagaacac tattgccacc aaatccattg 1260
aggaataacct caagttgggt ggacaacagt atcttcatga cgcactggg gagtttatca 1320
aagctttgta tgagtccgat gagaactgtg aagtggatcc cagcaaatgt tcatctagt 1380
aactgataga ccatacagac aacctgaaa tgtgctgtga gctggctttc tgcaagatca 1440
tcaactctta ctgtgttttc cctcgtgagt tgaagaagt gttgcatca tggaaagcagc 1500
agtcctgaa ccgtggcaag caagacatca gcgagaggct catcagtgcc tcattatttc 1560
tccgttttct gtgtccagcc attatgtctc ccagtcttt caaccttatg caggagtatc 1620
ctgatgaccg cacatctcgg actctaactc ttattgcaa ggtcattcag aacctggcca 1680
actttgcaa gtttggaac aaagaggaat acatggcatt catgaatgat tttttagaac 1740
atgaatggg tggaatgaag cgctttcttt tggagatctc taatccagac accatctcaa 1800
acacccagg ctttgatggg tacattgatc tgggccgaga gctttcagtt ttgcattcct 1860
tactgtggga agtagtttcc caacttgata aggtgaaaa ttccttccta caggcgaccg 1920
tggcaaaatt ggggcctctc cctcgtgttc ttgctgatat taccaagtca ttgactaatc 1980
ctacgccaat acaacagcaa ctgagacgct tcaactgaaca taactccagt ccaaatgtca 2040
gtggaagcct ctctctggg ctgcagaaaa tatttgaaga cccactgac agtgatttgc 2100
ataaactaaa atctccaagc caggacaaca cagacagcta cttcagaggg aaaacattat 2160
tgctggttca gcaagcctcc tctcagagca tgacttattc tgaaaaggat gaaagggaaa 2220
gtagccttcc taatggctcg agcgtctccc tcatggacct ccaggacact catgctgtc 2280
aagtggagca tgcatctgtc atgcttgatg tgcctatacg cttgaccgga agccagcttt 2340
ccataacca ggtggccagc atcaaacagc tgcgggaaac ccagagcact ccccaaagt 2400
cacccaagt gagaaggccc ctgcaccag ccttgaacca gccagggtgc cttcagccct 2460
tgtcgttcca gaaccctgtc tatcacctca ataaccaat tccagcaatg ccaaaggcct 2520
ctatagattc cagtttgag aacctaaaga ctgccagttc cagaagccaa agtaacagt 2580
aagacttcaa gctcagtga cccagcaata gcagcatgga agatttcact aaacgtagca 2640
ctcagagtga ggacttctcc aggcggcaca cgggtgccaga tagacacata cctcttgctt 2700
tgccacgaca aaatagtact gggcaggccc agatccgaaa agtggaccag ggtgggttag 2760
gtgcccagc caaagcccca ccacccctgc cacacagtgc ttctttacgt agcaccggga 2820
gcatgtcagt ggtgtccgca gccctggtg ccgaacctgt gcagaatggg agccgggtccc 2880
ggcagcagtc ctcttctc agagagagcc ctgttcccaa agttagagca atccagagac 2940
aacagacaca gcaggttcag tcacctgtg actctgccac aatgtccca gtagagagga 3000
cagcagcctg ggttctgaac aatgggcagt atgaagagga tgtggaagaa actgagcaaa 3060

```

atctagatga agccaagcat gctgagaagt atgaacaaga aattactaaa ctgaaggagc 3120
 gcctgagagt ttccagccgg cgactggagg aatatgaacg ccgcttgctg gtgcaggagc 3180
 agcagatgca gaagctgctg ctggaatata aggcccgact ggaggacagc gaggagcggc 3240
 tccgaagaca gcaggaagaa aaagatagcc agatgaaaag catcatcagc aggctaattg 3300
 ctgtggaaga ggaactgaag aaggatcatg ctgagatgca agcagttatt gatgcaaagc 3360
 agaaaataat tgatgcacag gaaaaacgga tcgtgtccct ggattcagcc aacaccagac 3420
 tgatgagcgc gctgacccaa gtgaaggagc ggtacagcat gcaggccgc aatggcatct 3480
 cccccaccaa cccaccaaag ctttccatca cggagaatgg tgaattcaaa aacagcagct 3540
 gctgacgggc tttgtctgtg gaaggagaca gaaggaaatt gaccactct cctatctcca 3600
 gacctttacc tagcccctcc aggtttacag aatgttgcta cttcacaatg gcgatgtggt 3660
 gagaaactcc tgaatgaaga aaggaacctt gtctttcagg gcataaggcg gcgacttcca 3720
 aggtcaatgc ttttccccca catctctatg tacataggga acttagttct gggccatgta 3780
 cagaaaatat cactgtaata taccaaaagg aagttaataa ttagattac ctttttgatt 3840
 attgctatgt ttattattgt tttcctcttg ttgaaagcac tgcagttgtt acaggaagta 3900
 aagtaggaat gttgtgtgag cgagacatga gcctgtagtt cagtaggtag agaccaagca 3960
 tctatctgat agaacacatg gagtgcaata ggacattgtg agaaggattt ttcagggtt 4020
 catctactag tttaaaaacc ccactctggc cctcttgctc tttcagaaaa catgcaaata 4080
 ccaagatcca taaaaacaa taattttatc cactgatcaa ccaagactgg tcttggttg 4140
 acagctaatac tgatttggg attcactgtt tcagaggaca cagacaaaag ctgttgcatc 4200
 aaaactggac tttaggagta atttctattg aactcctgtc aatatgttta tttcctctgt 4260
 ctacagcaga tgggagctct ctcttttaga caggggcttt ttgtttttaa cccaattgt 4320
 aataaagggt gttcttttct ctcttttaga aaaaaaaaaa aaaaaaaaaa 4368

<210> 83
 <211> 1355
 <212> DNA
 <213> Homo sapiens

<400> 83
 cagtggctgg taggcagtgg ctgggaggca gcggcccaat tagtgtcgtg cggcccgtgg 60
 cgaggcgagg tccggggagc gagcgagcaa gcaaggcggg aggggtggcc ggagctgcgg 120
 cggctggcac aggaggagga gcccgggcgg gcgaggggag gccggagagc gccagggcct 180
 gagctgccgg agcggcgccct gtgagttagt gcagaaagca ggcgcccgcg cgctagccgt 240
 ggcaggagca gcccgcacgc cgcgctctct ccctgggcga cctgcagttt gcaatatgac 300
 tttggaggaa ttctcggtg gagagcagaa gaccgaaagg atggataagg tgggggatgc 360
 cctggaggaa gtgctcagca aagccctgag tcagcgacg atcactgtcg ggggtgtacga 420
 agcggccaag ctgctcaacg tcgacccgga taactgtgtg ttgtgcctgc tggcggcgga 480
 cgaggacgac gacagagatg tggtctgca gatccacttc accctgatcc aggcgttttg 540
 ctgcgagaac gacatcaaca tcctgcgcgt cagcaaccg gcccggtgg cgagctcct 600
 gctcttgag accgacgtg gcccgcggc gagcgagggc gccgagcagc ccccgacct 660
 gcaactgcgt ctggtgacga atccacattc atctcaatg aaggatcctg ccttaagtca 720
 acttatttgt ttttgcggg aaagtcgcta catggatcaa tgggttccag tgattaatct 780
 ccctgaacg tgatggatc tgaatgaaa taactgaacc aaattgcact gaagtttttg 840

aaataccttt gtagttactc aagcagttac tccctacact gatgcaagga ttacagaaac 900
 tgatgccaaag gggctgagtg agttcaacta catgttcttg gggcccgag atagatgact 960
 ttgcagatgg aaagaggtga aaatgaagaa ggaagctgtg ttgaaacaga aaaataagtc 1020
 aaaaggaaca aaaattacaa agaaccatgc aggaaggaaa actatgtatt aatttagaat 1080
 ggttgagtta cattaaaata aaccaaataat gttaaagttt aagtgtgcag ccatagtttg 1140
 ggtatttttg gtttatatgc cctcaagtaa aagaaaagcc gaaagggtta atcatatttg 1200
 aaaaccatat tttattgtat tttgatgaga tattaaattc tcaaagtttt attataaatt 1260
 ctactaagtt attttatgac atgaaaagtt atttatgcta taaatttttt gaaacacaat 1320
 acctacaata aactggtatg aataattgca tcatt 1355

<210> 84
 <211> 2746
 <212> DNA
 <213> Homo sapiens

<400> 84
 gaattcctat cctgagcatg gctaaactct gagctaatag tatcattata gaaagatgag 60
 gaaacggagg cacagacaga ttgagtcctt gccacggcc tcgtggctca tacgtggagg 120
 agtcagaatt ggaactagag actgatcgaa tgaatgacac tcgggtcacc aggacacctt 180
 cctatctcca ctcttacatc tgtttcttag caatcatctc ccaactccta cctcctcttt 240
 tcaggttcct cttggtgaca tctgttataa ctcaccctt ctctcccttt ccgatggtcc 300
 tacctccata tccccctgt tacttatttc caacttcttc cctagtttcc atcttgattc 360
 acccttctct cctctggcca gcggatcgcg ggctcccagc tctcctccag gctgcagtat 420
 tttgggcagg cactgagcgg gggtaagac ctcaccagg atggactggg ggacctggct 480
 gtggggggccc ggggcccagg gctcctgctc aggtgagagc agactttctc agaggctccc 540
 catgtgttcc taggttcaga tgggggtgcc caccacgtg gtgctccac cagcgacggc 600
 tgtcctcagc tcgggtgtct gccgcagac cagacctgtg ctctgggtgg gggtagcat 660
 gcagttcata cctgccgaga tccccaggtc tgcgtttgag tgcgggagc aggtggtctc 720
 tgagcagacc ctggtacagt ccaacatctg cctttacatt gacaaacgtt ctaagaacct 780
 gcttgggagc cgtgagtcct cctccctcca acccaggaca cctgacctc tggagtcccc 840
 catccaggc cctgtctcc caccctgctc attgtccac caaggagtgc ctgtctcaac 900
 gccgtccctg cgaccgccta caggtgacct ccaaagctct gtgaccttg acctggccct 960
 cgaccctggc cgcttgagtc cccgtgccac cttccaggaa acaagaacc ggagtctgag 1020
 ccgagtccga gtcctcgggc tgaaggcaca ctgtgaaaac ttcaacctgc tgctccggg 1080
 gcgtctgggc atgaacgtg gtggcgccg cgctggggct ggcagaaggc agggcaggga 1140
 gagaacaggc tgtgttcgg cctccctgtg gctcagccca gcacaggacc agccatgcag 1200
 gacgtgttta ctgcacgta gccagtga gtgagcga gcaacaagt gatgagatcg 1260
 tctgcaattt ccagggccac acgattggat ttcaggaaag agaattgggc aacctgagag 1320
 agctctgggc ttacctctg gcttttcagg cattcactga cagggttacc gagctgctcc 1380
 tggagacagc ctgacctgg ccatgggcat aggtggccaa aacagtcatt gctgatcggg 1440
 aggtctgggg gggggaggaa aaaaacaaag acaacaagg ggagaggaca gagagggtgt 1500
 caggagggca tcctgaaggc ggtgacgctg agcaggctct ggagggaagt aagcagagcg 1560
 ggagctgggc agaggcagga taagaactgc ggatgaggcc gagcgagct cttaccctcc 1620


```

ccttacccctc gctccccgcg acgcccgtcc cccagagctg cgtggaggac tctgtgaccc 1680
ccattacctt gcgtctgaac ttacgctgg tgggaagcc cctccttgcc ttcagaaacc 1740
tgcgccctat gctggccgcc gatgctcaga gatacttcac ggcctccgtg agtcctggca 1800
ctgggtctcc cagagagggg gcacagcgtg gggcctgggt ctcgagaaa acccccgtt 1860
gccttccac gcagctaccc tttgagaaga actgtggagc cgaccatata tggcaggaca 1920
atctcggcat ctccctcagc ttcccagggt gagcgccca ccttagatgc cctactgcc 1980
cagcctcctt cctggaatct gggactcctg cctctgctct ccctaacatt gtctcatcct 2040
atagtcaaaa cccaggtgtc ttggctgggc acagtggctc actcctgtaa tccagcactt 2100
tgggaggccg aggtgggagg acttttgagg ccaggagtta gggttacgac ctgggcaaca 2160
gagcgacacc catttccaca aaaacaaaac aacaacaaca acaacaacaa caacaacaac 2220
aacaacatca cttagtgtg gtagagcatg cctatagtcc cagctacttg ggaggctgaa 2280
gcttaaggct tgcttgagct ctggagttgg aggtctgcag tgagccataa tcacaccact 2340
gcactccagc ctgggtgaaa gagcaggact ctgtctctta aaaaaaaga agaagaagaa 2400
gaagaagaag aagaaccag ggtccgtcc cctgtctatc tcccaaatcc cccccaccc 2460
cattttatcc cagaccattt ctagcctcag tcacagaatc atcttctcct ttccttcacc 2520
tgataccag ctgaagtcc ctgctggtgg ggagtaacct ggagctgaa gcagaagtga 2580
tggtgtgaa tgacgggaa gactcctacg gaaccacat cacttctcc cccccgag 2640
gactgtcta ccgctacgtg gcagagggcc aggtgcacct ctgggaagg aggaggaggc 2700
agggctgggc gttagcgtag attcccgctg gggttcagaa cccggg 2746

```

```

<210> 85
<211> 2551
<212> DNA
<213> Homo sapiens

```

```

<400> 85
gcaagagtga cacacaggtg ttcaaagacg cttctgggga gtgagggaag cggtttacga 60
gtgacttggc tgagacctca ggggcgggca ctggcacgga acacaccctg aggccagccc 120
tggtgcccc ggcggagctg cctctctcc cgcgggttg tggaccgct cagtacggag 180
ttggggaagc tctttcactt cggaggattg ctcaacaacc atgtgggca tctggaccct 240
cctacctctg gttcttacgt ctgttgctag attatcgcc aaaagtgtta atgcccagt 300
gactgacatc aactccaagg gattggaatt gaggaagact gttactacag ttgagactca 360
gaacttgaa ggcctgcac atgatggcca attctgcat aagccctgtc ctccaggtga 420
aaggaaagct agggactgca cagtcaatgg ggatgaacca gactgcgtgc cctgccaaga 480
agggaaggag tacacagaca aagccattt ttcttccaaa tgcagaagat gtagattgtg 540
tgatgaagga catggcttag aagtggaaat aaactgcacc cggaccaga ataccaagt 600
cagatgtaaa ccaactttt ttgttaactc tactgtatgt gaacactgtg acccttgac 660
caaatgtgaa catggaatca tcaaggaatg cacactcacc agcaacacca agtgcaaaga 720
ggaaggatcc agatctaact tgggtgggt ttgtcttctt cttttgcaa ttcactaat 780
tgtttgggtg aagagaaagg aagtacagaa aacatgcaga aagcacagaa aggaaaacca 840
aggttctcat gaatctcaa ccttaaatcc tgaacagtg gcaataaatt tatctgatgt 900
tgacttgagt aaatatatca ccactattgc tggagtcag acactaagtc aagttaaagg 960
ctttgttcca aagaatggtg tcaatgaagc caaaatagat gagatcaaga atgacaatgt 1020

```

```

ccaagacaca gcagaacaga aagttcaact gcttcgtaat tggcatcaac ttcattgaaa 1080
gaaagaagcg tatgacacat tgattaaaga tctcaaaaaa gccaatcttt gtactcttgc 1140
agagaaaatt cagactatca tcctcaagga cattactagt gactcagaaa attcaaaactt 1200
cagaaatgaa atccaaagct tggcttagag tgaaaaacaa caaattcagt tctgagtata 1260
tgcaattagt gtttgaagag attcttaata gctggctgta aatactgctt ggttttttac 1320
tgggtacatt ttatcattta ttagcgctga agagccaaca tttttgtaga tttttaatat 1380
ctcatgattc tgcctccaag gatgtttaaa atctagttgg gaaaacaaac ttcattcaaga 1440
gtaaatgcag tggcatgcta agtaccctaa taggagtgtg tgcagaggat gaaagattaa 1500
gattatgctc tggcatctaa catatgattc tgtagtatga atgtaatcag tgtatgttag 1560
tacaagtgc tatccacagg ctaacccccc tctatgaatc aatagaagaa gctatgacct 1620
tttgctgaaa tatcagttac tgaacaggca ggccactttg cctctaaatt acctctgata 1680
attctagaga tttaccata tttctaaact ttgtttataa ctctgagaag atcatattta 1740
tgtaaagtat atgtatttga gtgcagaatt taaataaggc tctacctcaa agacctttgc 1800
acagtttatt ggtgtcatat tatacaatat ttcaattgtg aattcacata gaaaacatta 1860
aattataatg ttgactatt atatattgtg atgcatttta ctggctcaaa actacctact 1920
tctttctcag gcacaaaag cattttgagc aggagagtat tactagagct ttgccacctc 1980
tccatttttg ccttggtgct catcttaatg gcctaattga ccccaaaaca tggaaatata 2040
acaaaaaat acttaatagt ccacaaaag gcaagactgc ccttagaat tctagcctgg 2100
tttgagata ctaactgctc tcagagaaag tagctttgtg acatgtcatg aacctatgtt 2160
tgcaatcaaa gatgataaaa tagattctta tttttcccc acccccgaaa atgttcaata 2220
atgtcccatg taaaacctgc tacaatggc agcttataca tagcaatggt aaaatcatca 2280
tctggattta ggaattgctc ttgtcatacc cccaagtttc taagatttaa gattctcctt 2340
actactatcc tacgtttaaa tatctttgaa agtttgtatt aaatgtgaat ttaagaaat 2400
aatatttata tttctgtaa tgtaactgt gaagatagtt ataaactgaa gcagatacct 2460
ggaaccacct aaagaacttc catttatgga ggattttttt gcccttctgt tttggaatta 2520
taaaatatag gtaaaagtac gtaattaaat a 2551

```

```

<210> 86
<211> 6005
<212> DNA
<213> Homo sapiens

```

```

<400> 86
gactggctgc agccgcagtc ttggtggagg aggtgggtgac caccaccgct cctccacctg 60
catccggctg cgggactgcg gcggccgctg ttgcctgca gacctgcac cccgggacgc 120
ggctcatctg tcattagcac cggcactaag ctcccaccgc tcagcgactt ggtccgccc 180
aagctccgcc gcaggctttg tccgctagcg ctccgctgag tctgggcggg cgggaaacct 240
gggctagggc gaggcggggc ccctggacat gcctttctcc acgtccgcct cctcgacctt 300
attgtaagcg gagaaactta gtgtgcgagg caggcagggg acgtcccat tttgatgtcc 360
cgtaccctcc acccccttcg gatcgaggta gtaaagaggc tcctgtagga aactgactgc 420
ctctatgatt gcggcctctt gggggatttt gcgtttagcc cgaaagtgtg ctttgccaaa 480
agacgcacgg gtaggaaggc cgaagaggaa accctgtatt ccgtcgcgct gggctctccg 540
agtccgtgcg caaagcggcc tacgagtcct ggctccgcac ctgcagagga caagagccaa 600

```

tgcttaaaaa	agaacagcgg	aggaaccggc	tggcgcggcc	agctggaacg	ctggatcgca	660
gtgcgcccag	ggaaggccgg	gggcgcccgc	cgcccttagc	cctcagtggc	cctctcccac	720
gccggcccgc	gcgtgcctct	gcctacaaga	cctggggcgt	cctggccaga	tctggatggc	780
aggtccctcc	gccacccccg	gcccggttcc	gggggcgtgg	cttggcgcg	gggcgggttt	840
aagtcaccgc	gggtgtctga	ccactctgac	aggtctccaa	atttctccca	gtcgcctggc	900
gcccgcggtg	cgtttcagag	ctccagggtg	gcacgcggcg	gcgcttcctt	agatccagag	960
gcgtctctgt	cgacttccac	gcggcctcgg	gcctcccttc	tctccaaac	cttcgcctca	1020
tccgccaagc	ttcggttctc	agcctcagat	atccgcaccg	gcggcttctc	tctgttctcg	1080
gagctcttgg	ctttggagcc	ctcaccactt	tttcttccc	ccgcctctcc	tgatcctcct	1140
agctccgagc	caaatggact	ccaaagaacg	aaataaagg	gatgagaact	gtgtgctg	1200
acccttcgaa	agcacagctg	aaagcgttga	cctcgtctta	tagatcaggc	tgggaccctg	1260
gggcgagagt	ccccacaccc	cctccgggag	ggatgcttct	ggccagagcc	agcgtg	1320
tgtcagtcct	tgtctccgaa	ctaggaaaga	gcctaggagg	gagcctcagc	atacccttc	1380
ctccaaatta	actatttgg	gaattgttag	cgccgaggt	accacctctc	caaccctgtc	1440
gcggggcg	cgccacctc	accgtgaccc	cctcctctc	cttcttggc	accgccccca	1500
gctccgcccc	tgtccccat	cccggcgcaa	tggagtctc	cgaaggcg	tgattccagc	1560
cacatctgct	aacttcgcac	ccatcgctgc	cgccgggtcac	cgccggccag	gccccctgca	1620
gccgcggagc	agtgggcg	caaagcccag	tgcagcagcc	aggaccggc	cgacgcgag	1680
cagaagcagc	gcgcccaggc	gcttaggcgt	ctcttgaga	gcaaaggctg	cgccaaaacg	1740
ctgagcctag	aatcaaccaa	ggagcctgag	cccaggaagg	ggctgcgtg	ctcacagcgc	1800
tgcggctcct	gaggacaaat	agccactgcc	gctgcgtacc	caagctgcgc	cggtgcg	1860
gagagcagca	cgcaaggacg	ccgaggtccg	ccgcgatctt	ccaggtgcc	tttgccccctg	1920
ggcacagtat	gacccgacct	acagggagcc	ctagcgcagg	gctcctgcaa	cggtcagcc	1980
taggataaaa	aggatccttg	ccaagctcct	accaggccgc	ctttgagtct	ttaggaaccc	2040
ctcctccggc	tgcctcccca	aggttctggg	cctccttccc	tgcggcccag	agccatggag	2100
ctctccgatg	tgcgtgcctt	tacaggcagc	gaggaaactct	acaccatcca	cccgcgccc	2160
ccggccggcg	acggcaggag	cgctcccg	ccgcagcg	tgtgtggca	gacggcggtg	2220
cgacacatca	cggagcagcg	cttcattcac	gggcaccggg	gaggcagcg	cagcgggagt	2280
ggaggctcgg	gcaaagcctc	ggaccctgcg	ggcggcggcc	ccaaccacca	cgcccgag	2340
ctgtcaggcg	actcggcgct	gcccccttac	tgcctggg	cgggagagcg	agcgcacagc	2400
acctgcggca	ccaagtctt	cccggaacgc	agcgggagcg	gcagtgccag	cggcagcgga	2460
ggcggggggc	acctgggctt	cctgcacctt	gactgtgccc	ctagcaactc	ggatttcttt	2520
cttaattggg	gctatagcta	ccgaggggtc	atttcccca	ccctgcgcaa	ctccttcaaa	2580
tctcgggatt	tggaaacgct	ctaccagcgc	tatttcttgg	gccaaaggcg	caaatcgga	2640
gtggtgatga	acgtgctgga	cgtgctgacc	aaactcactc	tcttggctct	acacttgagc	2700
ctggcctcgg	ccccatgga	cccgtcaag	ggcatcctgc	tgggttctt	caccggcatt	2760
gaggtagtga	tctgcgccct	ggtggtggtc	aggaaggaca	ccacctccca	cacgtacctg	2820
cagtacagcg	gcgtggtcac	ctgggtggcc	atgaccaccc	agatcctggc	agcaggcctc	2880
ggctacgggc	tcttgggcga	cggcataggc	tacgtgctct	tcacgtctt	cgccacctac	2940

agtatgctgc cgctgccgct cacctgggcc atcctggccg gcctgggcac ctgctgctg 3000
cagggtcatcc tccaagtggt cataccccg ctggcgggtca tttccatcaa ccaggttgtg 3060
gcccaggcag tgctattcat gtgtatgaac acagctggaa tcttcatcag ttacctgtca 3120
gaccggggccc agcggcaagc tttcctggag actcggaggt gtgtggaggc caggctgcgc 3180
ctggagacag agaaccaaa acaggagcgg ctgctgcttt ctgtgctccc ccggtttgtt 3240
gtcctggaaa tgatcaacga catgaccaat gtggaagatg agcacctgca gcaccagttc 3300
catcggtatc acatccatcg ctatgagaac gtcagtattc tttttgcaga tgttaaagga 3360
tttaccaacc tctccacgac cttgtctgct caggagctgg tcaggatgct caacgagctc 3420
tttgccagat ttgatcgact ggccccatgag catcactgcc ttcgtattaa aatcctgggg 3480
gactgctact actgctgtc tggacttctt gagccccgcc aggaccatgc ccactgctgt 3540
gttgaaatgg gtctcagcat gatcaaaacc atcaggtatg tgcggtcaag gacaaaacac 3600
gatgttgaca tgaggattgg aatccactcc ggctcgggtc tgtcgggtgt tttgggacta 3660
cggaagtggc agtttgatgt ctggtcttgg gatgtggata ttgcaaaaa actcgaatct 3720
ggaggaatcc ccgggaggat tcacatttcc aaagccacgc tggactgtct caacggtgac 3780
tataacgtgg aagagggcca tggtaaagag aggaatgaat tcctgaggaa gcataatc 3840
gaaacttact taattaagca gcctgaggac agtctgctgt ccttgctga agatatcgtc 3900
aaggagtcat tgagctctc agaccggaga aacagtggg ccacattcac tgaaggatcc 3960
tggagccctg aactgccctt tgataatc gtggggaac agaatactct ggctgcccta 4020
acaagaaatt caataaatct gcttccaaac catcttgac aagctttgca tgtccagtct 4080
gggctgagg aaattaacaa gagaatagaa cataccatcg acttgcgag tggcgataaa 4140
ttgagaagag agcatatcaa gccatttca ctgatgttta aagactccag cctggagcac 4200
aagtattctc aaatgaggga tgaagtgtc aagtcaaac tggctctgtc atttatcgtt 4260
cttctattta tcacggcaat acaagtttg cttccttctt caagagtgtt gccaatgacc 4320
atccagttct ccattctgat tatgctgcac tcggctctgg tcctcatcac cacagcagag 4380
gattataaat gtttgccct catcctccg aaaaacttgc gttggattaa tgagacctat 4440
ttggcccgga acgtcatcat ctttgcatcc attttgatta atttcctggg tgccatctta 4500
aatacctgt ggtgtgatt tgacaagtc ataccctga agaacctgac tttcaattcc 4560
tcagctgtgt ttacagatat ctgctctac ccagagtact ttgtcttcac gggggtgtt 4620
gccatggtga cctgtgcagt tttcctccg ctgaactccg tcctgaagct ggcagtgtc 4680
ctgatcatga ttgccatcta tgccctgctc actgagaccg tctacgcagg cctctttctg 4740
cgttatgaca acctcaacca cagtggagaa gatttcctgg ggaccaagga ggtatcactg 4800
ctactgatgg ccattgtcct cctggctgtg ttctaccatg gacagcagct ggagtacaca 4860
gcccgcctgg acttccttg gcgagtacag gccaaagg agatcaatga gatgaaggag 4920
ctgagggaa acaatgagaa catgctccg aatatcttac ccagccatgt gggccgccat 4980
ttcctagaga aggaccgaga caatgaggag ctgtattctc aatcctatga tgcgtgtggg 5040
gtgatgtttg cctccatccc aggatttgcg gacttttact ctcagactga aatgaataac 5100
caggagtggt aatgcctgc cttgctcaat gagatcattg ctgacttcga tgagtgtctt 5160
gggtgaagacc gatttcaaga cattgaaaag attaaagaca ttggcagcac ctacatggcc 5220
gtgtcaggcc tgtcacctga aaaacagcaa tgtgaagaca agtggggaca tttgtgtgct 5280
ctggctgact tctcactgc cctgacagaa agcatacagg agatcaacaa gcattcattc 5340

aacaattttg aactccggat tggcatcagc cacggctcag tggtagctgg cgttatcggc 5400
 gctaagaaac cacagtatga catttggggc aaaactgtga acctggcaag ccgaatggac 5460
 agcacggggg ttagtgccg gatccaagtc ccagaggaga cctatctcat cctgaaggac 5520
 cagggccttg cctttgatta ccgaggggag atctatgtga agggatcag tgaacaggaa 5580
 ggaaaaatca aaacgtactt tcttctggga agagtccaac ccaaccatt catcttgccc 5640
 ccaagaagac tgcctgggca gtactccctg gccgcggttgc tcctgggact tgtccagtcc 5700
 ctcaataggc aaaggcagaa gcagctactc aatgagaaca acaacacagg aatcatcaag 5760
 ggtcattaca accggcggac tttgtgtgca ccagcggca cagagcctgg agcccaggct 5820
 gaaggcaccg acaaatctga tttgccataa aagcattttc tttctgtttt tttttttttt 5880
 tgtatttctt ttatatataa aataaatata ctaataaaaa ggtttaattt tttttagaac 5940
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaacccc aaaaaaaaaa 6000
 aaaaaa 6005

<210> 87
 <211> 488
 <212> DNA
 <213> Homo sapiens

<400> 87
 tggcgcggac aggatgggca agtgtcgtgg acttcgtact gctaggaagc tccgtagtca 60
 ccgacgagac cagaagtggc atgataaaca gtataagaaa gctcatttgg gcacagccct 120
 aaaggccaac ccttttgagg gtgcttctca tgcaaaagga atcgtgctgg aaaaagtagg 180
 agttgaagcc aaacagccaa attctgccat taggaagtgt gtaagggtcc agctgatcaa 240
 gaatggcaag aaaatcacag cctttgtacc caatgacggt tgcttgaact ttattgagga 300
 aaatgatgaa gttctggttg ctggatttgg tcgcaaaggt catgctgttg gtgatattcc 360
 tggagtcgcg ttttaagggtg tcaaagtagc caatgtttct cttttggccc tatacaagg 420
 caagaaggaa agaccaagat cataaatatt aatggtgaaa acactgtagt aataaatatt 480
 catatgcc 488

<210> 88
 <211> 1398
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1398)
 <223> n=A,T,C, or G

<400> 88
 ctgcgcggcc tttctccgct ggcaacggcg ccgctccccg ctctcctcc ccagccatgg 60
 cgttcacgtt cgcggccttc tgctacatgc tggcgtgct gctcactgcc gcgctcatct 120
 tcttcgcat tttgcacatt atagcatttg atgagctgaa gactgattac aagaatccta 180
 tagaccagtg taataccctg aatcccttg tactcccaga gtacctcacc cagcctttct 240
 tctgtgtcat gtttcttgg gcagcagagt ggcttacct gggctcact atgcccctct 300
 tggcatatca tttttggagg tatatgagta gaccagtgat gaggggccca ggactctatg 360
 accctacaac catcatgaat gcagatattc tagcatattg tcagaaggaa ggatggtgca 420
 aattagcttt ttatcttcta gcattttttt actacctata tggcatgac tatgttttgg 480

```

tgagctctta gaacaacaca cagaagaatt ggtccagcca aglycatyca aaaagccacc 540
aaatgaaggg attctatcca gcaagatcct gtccaagagt agcctgtgga atctgatcag 600
ttacttttaa aaatgactcc ttatttttta aatgtttcca catttttgct tgtggaaaga 660
ctgttttcca tatgtttatac tcagataaag attttaaatg gtattacgta taaattaata 720
taaaatgatt acctctgggtg ttgacagggt tgaacttgca cttcttaagg aacagccata 780
atcctctgaa tgatgcatta attactgact gtccctagtag attggaagct tttgtttata 840
ggaacttgta gggctcattt tggtttcatt gaaacagtat ctaattataa attagctgta 900
gatatcaggt gcttctgatg aagtgaataa gtatatctga ctagtgggaa acttcatggg 960
tttctctatc tgcctatgctg atgattatat atggatacat ttacaaaaat aaaaaaaaaa 1020
gcgggaattt tccctctgct tgaatattat ccctgtatat tgcattgaatg agagatttcc 1080
catatttcca tcagagtaat aaatataactt gctttaattt nntaagcata agtaaacatg 1140
atataaaat atatgctgaa ttacttgta agaatgcatt taaagctatt ttaaatgtgt 1200
ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg ttctaactctg 1260
gtggtaaaag tattcttaag aatttgcagg tactacagat tttcaaaact gaatgagaga 1320
aaattgtata accatcctgc tgttccttta gtgcaatata ataaaactnt gaaattaaga 1380
aaaaaaaaa aaaaaaaaaa 1398

```

```

<210> 89
<211> 4848
<212> DNA
<213> Homo sapiens

```

```

<400> 89
gccggccgaa gcgtggcggc cacagactgt gggtagccggg tccgagggac tcgcgctttt 60
ctctccgtgc catggcgcca gcgaaagcca cgaacgtggt gcggtgcta ctaggctcca 120
cagcgctgtg gctttcgcag ctccggtccg ggacggctgc cgcgtccaag tcggtgactg 180
cccacttggc cgcgaagtgg cccgagaccc cgctgctgct ggaggcaagt gaatttatgg 240
cagaagaaag taatgaaaaa ttttggcagt ttttggaaac tgtgcaagaa ttagcaattt 300
ataagcaaac agaatcagat tattcttatt acaacttaat cctgaagaaa gctggacagt 360
ttctagacaa ttacacatc aaccttttaa agtttgcttt ctctataagg gcatactccc 420
cagctattca gatgtttcag cagattgcag ctgatgagcc accaccagat ggttgtaatg 480
catttgtygt tattcataag aagcacacct gtaaaattaa tgagattaaa aagctgctga 540
agaaagctgc ttcaaggact agaccttata tatttaagag agatcacaaa ttctctacaa 600
acaaagagaa cttaccagtg gtgattctct atgccgaaat ggttactaga acatttagtg 660
catttcacaa agtattgtct gaaaaagctc aaaatgagga aattctgtat gttcttcgcc 720
attatattca gaaaccaagc tcacggaaaa tgtacttata tgggtatggt gtggagctag 780
caattaagag tacagaatac aaagcactgg atgataccca agttaaaact gtgactaata 840
ctactgtaga ggatgagact gaaacaaatg aagttcaagg atttctcttt gggaaactaa 900
aagaaatata ttcagatctt agagataatc tgacagcatt ccataaatac ctgattgaga 960
gtaacaaaca aatgatgcct ttgaaagtct gggaaactaca agatcttagt tttcaagcag 1020
cttctcaaat aatgtccact ccagtttatg atgccattaa attaataaaa gacatttcac 1080
agaacttccc cataaaagcc agatctctaa ccagaattgc tgtaaatcaa catatgagag 1140
aagaaataaa ggaaatacaa aaggatcttc aagttagatt taaaattcag ccaggcgatg 1200

```

ctctgtctatt tataaatggc cttcgtgttg atatggatgt ttatgacgct tttagtattt 1260
 tggatatgct gaaattagaa ggaataatga tgaatggcct tcgcaatctt gggatcaatg 1320
 ggggaagatat gagcaaat ttaaaattaa attcacacat ttgggaatat acttatgtat 1380
 tagatattcg acattcttct ataatgtgga ttaatgactt agaaaatgat gatttgtata 1440
 ttacatggcc tacaagtgc cagaaacttc tgaagccagt atttcctgga agtgtagcctt 1500
 ccataaggcg caattttcat aatttggttc tgtttattga tccggcccaa gaatatacct 1560
 tggattttat aaaacttgct gatgttttct attctcacga agttcctctt agaattgggt 1620
 ttgtgttcat tcttaataca gatgatgaag ttgatggagc aaatgatgct ggagtgtgctc 1680
 tctggcgagc tttcaactat attgcagaag aatttgatat atcagaagca tttatttcta 1740
 tagtacacat gtacaaaaa gtgaagaagg atcaaaatat actcactgtg gacaatgtga 1800
 agagtgttct ccaaaatata tttcctcatg ctaatatattg ggatattttg ggaattcatt 1860
 ctaaatatga tgaagaaaga aaggctggag caagctttta taagatgact ggcctgggtc 1920
 ctttgcctca agctctttat aatggtgaac cctttaaaca tgaagagatg aatattaaag 1980
 aactaaaaat ggctgttctt caaagaatga tggatgcac tgtatattta caaagagaag 2040
 ttttttggg cacattaaat gatcgacga atgcaattga ttttctaag gataggaata 2100
 atgttgtagc ccgtataaat actttgat tgcgtactaa ccagcagtag ctcaatttaa 2160
 tatctacac agtaactgct gatgttgaag atttctctac tttcttttct ttggattcac 2220
 aagataagag tgctgtaatt gcaaagaaca tgtattattt aaccaagac gatgagagta 2280
 taatttctgc agtcactctc tggattattg cagattttga taagccttct gggagaaaac 2340
 ttctttttaa tgcattaaag cacatgaaa caagtgttca tagtcggttg gggattattt 2400
 ataactctac atcaaaaata aatgaagaga acacagctat ttctagaggg attttggcag 2460
 cttttcttac acagaagaac atgtttttga gaagctttct tgggcaactg gcaaaggaag 2520
 aaattgtcac aactatttac tctggagata aaattaaaac attccttatt gaggggatgg 2580
 ataagaatgc ttttgagaaa aaatataata ctgttgaggt gaatattttt cgaactcacc 2640
 agttgttctg tcaagatgta cttaaattac gtcctggaga aatgggtatt gtcagcaatg 2700
 ggagattctt aggaccttta gatgaagatt tttatgcaga agatttttac ttgttgaaa 2760
 agataacatt tagtaattta ggagagaaaa ttaaggcat tgtgaaaat atgggaatca 2820
 acgcaataa catgagtgc tttattatga aagttgatgc ccttatgtcc tctgtgccta 2880
 agcgtgcac tcgatatgat gtcacatttc ttagggagaa tcacagtgtt ataaagacga 2940
 atcctcaaga gaatgatatg ttcttcaatg tcattgctat tgtgatcta ttggcaagag 3000
 aagcacagaa aatggcacag ttgttggttg tacttgcaa gattatcaac ctgaagataa 3060
 agttgttcat gaactgtagg ggcaggcttt cagaagcccc ttagaaagc tttaccgtt 3120
 ttgttctgga accagaactg atgtcagggg ctaatgacgt ttcttctctt ggaccagtgg 3180
 caaaattttt ggatattcct gaatcaccct tcctaactct caacatgatt actccagaag 3240
 gctggttggt tgaacagtg cacagcaact gtgacctga taatattcac ttaaaggata 3300
 ctgagaaaac cgctacagca ggatatgaac tagaatactt actactggaa ggacaatgct 3360
 ttgataaagt gacagaacag cctcctcggg gtctgcagtt cacactaggc acaaaaaata 3420
 aacctgtgt ggttgataga atagtgtg cacatcatgg gtattttcaa ttaaaagcaa 3480
 acccaggtgc ttggatactg aggttacacc aaggaaaatc tgaagatatt tatcaaatag 3540
 ttgggcatga aggaactgac tctcaagcag acctagaaga tatcattgtt gtattaaaca 3600

gcttcaaaag caagatactc aaagtaaaag tgaaaaaaga aacagacaaa attaaggaag 3660
 atatccttac cgaatgaagat gaaaaaacaa aaggactgtg ggattccatt aaaagtttca 3720
 cagtaagctt gcataaagaa aacaaaaagg aaaaagatgt cctaaacatt ttttcagttg 3780
 cttctgggtca tttatatgaa cgttttttaa gaattatgat gctttctggt ttgcgtaaca 3840
 ccaaaacacc agtgaaattc tgggtgctaa aaaattatct ctcaccgaca tttaaagaag 3900
 taattcctca catggctaaa gagtatggat tccgatatga actagttaa tatagggtggc 3960
 cccgttggtc tcgtcaacag actgaaagac agaggattat ttgggggttac aaaattcttt 4020
 tccttgatgt tcttttccca ctgacagtgg acaaatcat tttgttgat gctgaccaga 4080
 ttgtgagaca tgatctaaaa gaacttcgag atttcgatct ggatggagct ccttatgggt 4140
 atactccatt ttgtgatagc cgcagggaaa tggatggata tcgtttcttg aaaacaggat 4200
 actgggcatc acatctttta agacggaaat accatatcag tgctttatat gtagtggatc 4260
 tcaagaagtt caggagaatt ggagcaggtg acaggctcag gagccagtat caagctctca 4320
 gtcaagatcc aaacagctct tcaaacctag atcaggatct cccaataat atgatttacc 4380
 aagtcgcat taagtctctt cctcaagact ggctgtggtg tgaacactgg tgtgatgatg 4440
 aatccaaaca aagagccaaa acaattgatc tgtgcaataa tcccaaaaca aaagaatcca 4500
 aactaaaagc tgctgccaga attgtcccag aatgggtgga gtatgatgct gagataagac 4560
 aactattaga tcactttgaa aacaagaagc aagatacaat ttgacacat gatgaactct 4620
 agcactggtg tatatgagaa ggaaggcgaa agcatgacag gaaacctgcc gcctgctggg 4680
 gaagtctgga gccctgctg agacgatttg gaagtctgt taagatcagt gacatatctt 4740
 ttaattttaa aaaattgtaa ttatttaaaa cagttattta atgtattgaa tgagtttaag 4800
 ttatataata atgaccatt gagtatttaa aaaaaaaaaa aaaaaaaaaa 4848

<210> 90
 <211> 3614
 <212> DNA
 <213> Homo sapiens

<400> 90
 gtccgcaaaa acctgcgcgg atagggaaga acagcacccc ggcgccgatt gccgtaccaa 60
 acaagcctaa cgtccgctgg gccccggacg ccgcgcggaa aagatgaatt tacaaccaat 120
 tttctggatt ggactgatca gttcagtttg ctgtgtgttt gctcaaacag atgaaaatag 180
 atgtttaaaa gcaaatgcc aatcatgttg agaattgata caagcagggc caaattgttg 240
 gtgggtgcaca aattcaacat ttttacagga aggaatgcct acttctgcac gatgtgatga 300
 tttagaagcc ttaaaaaaga agggttgccc tccagatgac atagaaaatc ccagaggctc 360
 caaagatata aagaaaaata aaaatgtaac caaccgtagc aaaggaacag cagagaagct 420
 caagccagag gatattcatc agatccaacc acagcagttg gttttgcgat taagatcagg 480
 ggagccacag acattttacat taaaattcaa gagagctgaa gactatccca ttgacctcta 540
 ctaccttatg gacctgtctt attcaatgaa agacgatttg gagaatgtaa aaagtcttg 600
 aacagatctg atgaatgaaa tgaggaggat tacttcggac ttcagaattg gatttggtc 660
 atttgtgaa aagactgtga tgccttacat tagcacaaca ccagctaagc tcaggaaccc 720
 ttgcacaagt gaacagaact gcaccacccc atttagctac aaaaatgtgc tcagtcttac 780
 taataaagga gaagtattta atgaacttgt tggaaaacag cgcatatctg gaaatttgg 840
 ttctccagaa ggtgggtttcg atgccatcat gcaagttgca gttgtggat cactgattgg 900


```

ctggaggaat gttacacggc tgctgggtgtt ttccacagat gccgggtttc actttgctgg 960
agatgggaaa cttggtggca ttgttttacc aaatgatgga caatgtcacc tggaaaataa 1020
tatgtacaca atgagccatt attatgatta tccttctatt gctcaccttg tccagaaact 1080
gagtgaaaat aatattcaga caatttttgc agttactgaa gaatttcagc ctgtttacaa 1140
ggagctgaaa aacttgatcc ctaagtcagc agtaggaaca ttatctgcaa attctagcaa 1200
tgtaattcag ttgatcattg atgcatacaa ttccctttcc tcagaagtca ttttggaana 1260
cggcaaattg tcagaaggag taacaataag ttacaaatct tactgcaaga acgggggtgaa 1320
tggaacaggg gaaaatggaa gaaaatgttc caatatttcc attggagatg aggttcaatt 1380
tgaaattagc ataacttcaa ataagtgtcc aaaaaaggat tctgacagct ttaaaattag 1440
gcctctgggc tttacggagg aagtagaggt tattcttcag tacatctgtg aatgtgaatg 1500
ccaaagcgaa ggcacccctg aaagtcccaa gtgtcatgaa ggaaatggga catttgagtg 1560
tggcgcgtgc aggtgcaatg aagggcgtgt tggtagacat tgtgaatgca gcacagatga 1620
agttaacagt gaagacatgg atgcttactg caggaaagaa aacagttcag aaatctgcag 1680
taacaatgga gagtgcgtct gcggacagtg tgtttgtagg aagagggata atacaaatga 1740
aattttattct ggcaaattct gcgagtgtga taatttcaac tgtgatagat ccaatggctt 1800
aattttgtga ggaatgggtg tttgcaagtg tcgtgtgtgt gagtgcacac ccaactacac 1860
tggcagtgca tgtactgtt ctttgatac tagtacttgt gaagccagca acggacagat 1920
ctgcaatggc cggggcatct gcgagtgtgg tgtctgtaag tgtacagatc cgaagtttca 1980
agggcaaacg tgtgagatgt gtcagacctg ccttggtgtc tgtgctgagc ataaagaatg 2040
tgttcagtgc agagccttca ataaaggaga aaagaaagac acatgcacac aggaatgttc 2100
ctattttaac attaccaagg tagaaagtcg ggacaaatta cccagcccg tccaacctga 2160
tcctgtgtcc cattgtaagg agaaggatgt tgacgactgt tggttctatt ttacgtattc 2220
agtgaatggg aacaacgagg tcatggttca tgttggtggag aatccagagt gtccactgg 2280
tccagacatc attccaattg tagctgggtg ggttgctgga attgttctta ttggccttgc 2340
attactgctg atatggaagc ttttaatgat aattcatgac agaagggagt ttgctaaatt 2400
tgaaaaggag aaaatgaatg ccaaatggga cacgggtgaa aatcctattt ataagagtgc 2460
cgtaacaact gtggtcaatc cgaagtatga gggaaaatga gtactgccg tgcaaatccc 2520
acaacactga atgcaaagta gcaatttcca tagtcacagt taggtagctt tagggcaata 2580
ttgccatggt tttactcatg tgcaggtttt gaaaatgtac aatatgtata atttttaaaa 2640
tgttttatta ttttgaaaat aatgttgtaa ttcattgccag ggactgacaa aagacttgag 2700
acaggatggt tattcttgtc agctaaggtc acattgtgcc tttttgacct tttcttctg 2760
gactattgaa atcaagctta ttgattaag tgatatttct atagcgattg aaagggaat 2820
agttaaagta atgagcatga tgagagtttc tgtaaatcat gtattaaaac tgatttttag 2880
ctttacatat gtcagtttgc agttatgcag aatccaaagt aaatgtcctg ctactagtt 2940
aaggattgtt ttaaatctgt tattttgcta tttgcctgtt agacatgact gatgacatat 3000
ctgaaagaca agtatgttga gagtgtctgg tgtaaaatac gtttgaaata gttgatctac 3060
aaaggccatg gggaaaattc agagagttag gaaggaaaaa ccaatagctt taaaacctgt 3120
gtgccatttt aagagtact taatgtttgg taacttttat gccttcactt taaaaattca 3180
agccttagat aaaagaaccg agcaattttc tgctaaaaag tccttgattt agcactattt 3240

```

acatacaggc catacttttac aaagtatttg ctgaatgggg accttttgag ttgaatttat 3300
 tttattattt ttattttggt taatgtctgg tgctttctat cacctcttct aatcttttaa 3360
 tgtatttggt tgcaattttg gggtaagact tttttatgag tactttttct ttgaagtttt 3420
 agcggtaaat ttgccttttt aatgaacatg tgaagttata ctgtggctat gcaacagctc 3480
 tcacctacgc gagtcttact ttgagttagt gccataacag accactgtat gtttacttct 3540
 caccatttga gttgcccatac ttgtttcaca ctagtccatc tcttgtttta agtgccttta 3600
 gttttaacag ttca 3614

<210> 91
 <211> 1093
 <212> DNA
 <213> Homo sapiens

<400> 91
 ctgcaaggcg gcggcaggag aggttggtgt gctagtttct ctaagccatc cagtgccatc 60
 ctgctcgtcg cagcgacacc gctctcgccg ccgccatgac tgagcagatg acccttcgtg 120
 gcacctcaa gggccacaac ggctgggtaa ccagatcgc tactaccccg cagttcccgg 180
 acatgatcct ctccgcctct cgagataaga ccatcatcat gtggaaactg accagggatg 240
 agaccaacta tggaattcca cagcgtgctc tgcggggtea ctcccacttt gttagtgtg 300
 tggttatctc ctcatgtggc cagtttgccc tctcaggctc ctgggatgga accctgcgcc 360
 tctgggatct cacaacgggc accaccacga ggcgatttgt gggccatacc aaggatgtgc 420
 tgagtgtggc ctctctctct gacaaccggc agattgtctc tggatctcga gataaaacca 480
 tcaagctatg gaataccctg ggtgtgtgca aatacactgt ccaggatgag agccactcag 540
 agtgggtgtc ttgtgtccgc ttctcgccca acagcagcaa ccctatcacc gtctctgtg 600
 gctgggacaa gctgtgcaag gtatggaacc tggctaactg caagctgaag accaaccaca 660
 ttggccacac aggctatctg aacacgggtg ctgtctctcc agatggatcc ctctgtgctt 720
 ctggaggcaa ggttgccag gccatgttat gggatctcaa cgaaggcaaa cacctttaca 780
 cgctagatgg tggggacatc atcaacgccc tgtgcttcag ccctaaccgc tactggctgt 840
 gtgctgccac agggcccagc atcaagatct gggatttaga gggaaagatc attgtagatg 900
 aactgaagca agaagttatc agtaccagca gcaaggcaga accaccccag tgcacttccc 960
 tggcctggtc tgctgatggc cagactctgt ttgctggcta cacggacaac ctggtgcgag 1020
 tgtggcaggt gaccattggc acacgctaga agtttatggc agagctttac aaataaaaaa 1080
 aaaatggctt ttc 1093

<210> 92
 <211> 1860
 <212> DNA
 <213> Homo sapiens

<400> 92
 ggcgaggggc ctacgtctcg gcccggaac aaggcccgc tcggccctc gggaccagag 60
 cccacccga tcggaagcgg atcctttacc agggccatag gccagtgact aggccgggcc 120
 tggacctccc atcgggggcg gactaggacg agggcccggg gagggccctg gcctaccaga 180
 cccttttctc agggcgacag ccgccaggaa gatgcaacgt gccctgccag gcgcccgcca 240
 gcacttgggg gccattctgg ccagcgccag cgtgggtggt aaggctctgt gtgcggcggt 300
 actattctc tacctgtctc ccttcgccgt ggacacaggc tgctggcggt tcacccggg 360
 ctacctctt cctcccaact tctggatctg gaccctggcc acccatgggc tgatggagca 420

```

gcatgtgtgg gacgtggcca tcagcctgac aacggtggtg gtggccgggc gtttgcctgga 480
gccccctctgg ggggccttgg agctgctcat cttcttctca gtggtgaatg tgtctgtagg 540
gctgctgggg gccttcgcct acctcctcac ctacatggct tccttcaacc tggctctacct 600
gttcactgtc cgtatccacg gcgccttggg ctccctaggt ggcgtcctgg tggcactcaa 660
gcaaaccatg ggggactgtg tggctcctgc agtgccccag gtgcgcgtca gtgtgatgcc 720
catgctgctg ctggcgctgc tgcctcctgct gcggctcgcc aactgctcc agagccccggc 780
gctggcttcc tatggcttcg ggctgctctc cagttgggta tatcttcgct tctaccagcg 840
ccatagccga ggccgagggg acatggctga ccactttgct ttcgccactt tcttcctga 900
gacccctgag cctgtggtgg gtttgcctgg gaacttggtg cacagcctcc tgggaaggt 960
aaagatatgc cagaagacgg tgaagcgcta cgatgtgggt gccccatcct ccataccat 1020
cagcctgcca ggcacagacc ctcaagacgc cgagcggaaga aggcaactgg ccctgaaggc 1080
actcaatgag cggtgaaga gagtgaaga ccagtcctac tggccagca tggatgatga 1140
tgaagaggag tctggggcca aggtggacag cccctgccc tcagacaaag ctcccacacc 1200
cccagggaag ggggtgccc cagaatccag tctaatacc ttcgaggcag ctccccgac 1260
gctgtaactc cagaccacct tgagtgtggc acctcccctc ccaagcccc cggtgacatc 1320
ctctcagcta ctccagggca cctgactgct ctgaggagag ggaagaaggc ctgctggggc 1380
tttccatggc cttctgtgtt ttctcgcaa cactaccag gactcttctt acctggttcc 1440
aactccagac aacctatg ccaggcccg agcctctgag gcacggcca gtccaggccc 1500
tcacttgagg taagaatgta catcagctgg cagcccaag caagtggctg cagggaact 1560
gatgccacag ctccctgggc ggccctcaca tctgaaactg gttgccgaga gccctgagcc 1620
aaggcaagga tttgcaaaa atgttctggg ggcccagcaa atgcaggagc cgacctggg 1680
ctgcacatcc ctgccatcc ccagaaagac tgttctgtc aggtttgtt tccctctgct 1740
gtggcggtga ctgcttctg accagaacag ctccagctcc caggtatttt ctacaggacc 1800
acttgagtgg gcagccaagc ccaggctcgc agtatcaata aagcagttct ctgaggaatg 1860

```

<210> 93
<211> 2402
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(2402)
<223> n=A,T,C, or G

```

<400> 93
ggagaggtgc gggccgaatc cgagccgagc gagaggaatc cggcagtaga gagcggaactc 60
cagccggcgg accctgcagc cctcgcctgg gacagcgcg cgctgggcag gcgccaaga 120
gagcatcgag cagcggaacc cgcgaagccg gcccgagcc gcgaccgag cagcctgccg 180
ctctcccgcc gccggtccg gcagcatgag gcgcgcggcg ctctggctct ggctgtgcgc 240
gctggcgctg agcctgcagc tggccctgcc gcaaattgtg gctactaatt tgccccctga 300
agatcaagat ggctctgggg atgactctga caacttctcc ggctcagggt caggtgcttt 360
gcaagatata acctgtcac agcagacccc ctccacttgg aaggacacgc agctcctgac 420
ggctattccc acgtctccag aaccaccgg cctggaggct acagctgcct ccacctcac 480
cctgcgggct ggagaggggc ccaaggagg agaggctgta gtcctgccag aagtggagcc 540

```

```

tggcctcacc gcccgaggc aggaggccac ccccgaccc agggagacca cacagctccc 600
gaccactcat caggcctcaa cgaccacagc caccacggcc caggagcccg ccacctccca 660
ccccacagg gacatgcagc ctggccacca tgagacctca acccctgcag gaccagcca 720
agctgacctt cacactcccc acacagagga tggaggctct tctgccaccg agagggctgc 780
tgaggatgga gcctccagtc agctcccagc agcagagggc tctggggagc aggacttcac 840
ctttgaaacc tcgggggaga atacggctgt agtggccgtg gacgctgacc gccggaacca 900
gtccccagtg gatcaggggg ccacgggggc ctcacagggc ctctgggaca ggaaagaggt 960
gctgggaggg gtcattgccg .gaggcctcgt ggggctcatc tttgctgtgt gcctgtggg 1020
tttcatgtg taccgcatga agaagaagga cgaaggcagc tactccttgg aggagccgaa 1080
acaagccaac ggcggggcct accagaagcc caccaaacag gaggaattct atgcctgacg 1140
cgggagccat gcgccccctc cgccctgcca ctactaggc cccacttgc ctcttccttg 1200
aagaactgca ggccttgcc tccctgcca ccaggccacc tcccagcat tccagcccct 1260
ctggctgctc ctgccacgg agtcgtgggt gtgctgggag ctccactctg cttctctgac 1320
ttctgcctgg agacttaggg caccaggggt ttctgcata ggaccttcc accacagcca 1380
gcacctggca tcgcaccatt ctgactcgggt ttctccaaac tgaagcagcc tctccccagg 1440
tccagctctg gaggggaggg ggatccgact gctttggacc taaatggcct catgtggctg 1500
gaagatctgc ggggtgggct tggggctcac acacctgtag cacttactgg taggaccaag 1560
catcttgggg ggggtggccg tgagtggcag ggacaggagt cactttgttt cgtggggagg 1620
tctaacttag atatcgactt gtttttgac atgtttcctc tagttctttg ttcatagcc 1680
agtagacctt gttacttctg aggttaagta agtaagtga ttcggtatcc ccccatcttg 1740
cttcccta atctatgtcg gagacagcat cagggttaag aagacttttt tttttttttt 1800
ttaaactagg agaaccaaat ctggaagcca aaatgtaggc ttagtttgtg tgttgtctct 1860
tgagtttgtc gctcatgtgt gcaacagggt atggactatc tgtctggtgg ccccgtttct 1920
ggtggtctgt tggcaggctg gccagtcag gctgccgtg ggcgcggcc tctttcaagc 1980
agtcgtgcct gtgtccatgc gctcagggcc atgctgaggc ctgggcccgt gccacgttg 2040
agaagcccgt gtgagaagtg aatgctggga ctcagccttc agacagagag gactgtaggg 2100
agggcggcag gggcctggag atcctcctgc agaccacncc cgtcctgcct gtgcgccgtc 2160
tccaggggct gcttctcctt ggaaattgac gaggggtgtc ttgggcagag ctggctctga 2220
gcgcctccat ccaagccag gttctccgtt agctcctgtg gccccacctt gggccctggg 2280
ctggaatcag gaatattttc caaagagtga tagtcttttg cttttggcaa aactctactt 2340
aatccaatgg gtttttcctt gtacagtaga ttttccaaat gtaataaact ttaataataa 2400
gt 2402

```

```

<210> 94
<211> 7389
<212> DNA
<213> Homo sapiens

```

```

<400> 94
gtttctctct ctggctcgaa gcggcggtaa tggcggtagg tgggtgtgg cgcggcgggc 60
ggctgctgtg agggacgatg agtgctcctc tcgtgccgaa cggggccagc ctggaagatt 120
gtcactgtaa cctctctctg ctggctgact tgacaggaat taagtggaaa aaatatgtat 180
ggcaaggccc aacttctgcc cctattctgt ttcctgtgac agaagaagac cccattttga 240

```

gcagtttttag tcgctgcctt aaggcagatg tacttggtgt ttggcggcga gatcaaagac 300
 ctggaagaag agaattgtgg atattttggt ggggtgaaga cccagttttg ctgaccttat 360
 tcaccatgac ttatcagaag aagaagatgg aatgtgggag aatggacttt cctatgaatg 420
 ccgtactctg cttttccaaa gcagttcaca atctattgga acggtgttta atgaacagga 480
 attttgtacg tattggcaag tggtttgtaa agccttatga aaaagatgaa aaacctataa 540
 ataaaagtga acacttgctc tgctccttca ctttttctt gcatggagac agcaatgttt 600
 gtaccagtgt ggaattaac caacatcaac ctgtatacct tctcagtga gagcatatca 660
 cccttgctca acagtctaag agccatttc aagttatctt atgccattt ggactaaatg 720
 gcactctcac aggacaggca ttcaagatgt ctgattcagc tacaaaaaa ttaattggtg 780
 aatggaaca gttctatcct atctcatggt gcttgaagga gatgtctgaa gaaaaacagg 840
 aagatatgga ttgggaagat gattcttttag ctgcagtaga agttcttgtt gctggtgtcc 900
 gaatgatcta ccagcatgc tttgttctag tccctcagtc agacattcct actcctagcc 960
 ctgtgggac cactcactgt tcacttctt gcttgggtgt ccaccaagtg cctgcttcca 1020
 caagagatcc tgctatgtct tcggttacgc ttaccaccac tacgtctcct gaggaagtcc 1080
 aaacagtga tctcagtct gtccagaagt gggtaaaatt ttcttcagta tctgatggct 1140
 tcaactccga tagtactagc caccatggtg gaaaaatacc cagaaaatta gcaaatcatg 1200
 tggtagtag agtttgga caatgcaata tgaacagagc acagaacaag aagaagtatt 1260
 ctgcttcac aggtggtcta tgcgaagaag cgacagctgc taaagtggca tcctgggatt 1320
 ttgttgaagc cacacaaaga acaaatgca gttgtttgag gcacaaaaat ctcaagtcaa 1380
 gaaatgttg acaacaagga caggcaccat ctttaggtca gcaacaacaa atacttcta 1440
 agcacaagac caatgagaag caagaaaaga gtgaagagcc acagaaacgc cccttgactc 1500
 cttttcacca tcgtgtgtct gttagtgtat atgttggcat ggacgcagat tcagccagcc 1560
 aaagacttgt gatctctgct ccagacagtc aagtgagatt ttcaaatac cgaactaatg 1620
 atgtagcaa gactcctcag atgcatggca ccgaaatggc aaattcacct caaccacccc 1680
 cacttagtcc tcacccttgt gatgtggtg atgaaggagt gactaaaaca ctttcaactc 1740
 ctcagagtca acatttttat caaatgcaa caccagatcc cttggttct tctaaaccaa 1800
 tggaagatag gatagacagt ttgtcccagt ctttcccacc tcaatatcag gaagctgtag 1860
 aacctacagt atatgttggt acagcagtaa acttgaaga agatgaagcc aatatagcct 1920
 ggaagtatta caagtccca aagaaaaag atgtagagtt ttaccacct caacttcaa 1980
 gtgataaatt caaggatgat ccagttggac cttttggaca ggaagtgt acatcagtta 2040
 cagagttaat ggtgcaatgt aagaacctt taaaagtct tgatgaatta gtgcagcaat 2100
 atcaaattaa aaaccagtgt ctttcagcaa tagcatctga tgcagaacaa gaacctaaaa 2160
 ttgatccata tgcatttgtt gaaggagatg aggaattcct tttcctgat aaaaaagata 2220
 gacaaaatag tgagagagaa gctggaaaa aacacaaggt agaagatggg acatctagtg 2280
 taacagtgt atcacatgaa gaagatgcta tgtcattatt tagtccctct atcaagcaag 2340
 atgtccacg ccctactagt catgccgct cccatcaac aagtttgatt tatgactcag 2400
 acctggctgt ctcttatact gaccttgata atctcttcaa ttctgatgaa gatgaactaa 2460
 cacctggatc taaaagatca gcaaatggat cagatgataa agccagctgc aaggaatcaa 2520
 agacagga tctggaccg ttatcttgca taagcactgc agatcttcat aaaatgtatc 2580

ctacaccacc atcattggaa caacatatta tgggattttc cccaatgaat atgaataata 2640
aagaatatgg tagtatggat acaacacctg gaggaactgt tctagaagga aatagttcta 2700
gtataggagc gcagttcaaa attgaggttg atgagggatt ctgtagcccc aaaccttctg 2760
aaattaaaga tttttcttat gtctataagc ctgaaaattg tcaaattcta gtgggatgtt 2820
ccatgtttgc acctctaaaa actctacca gccaatatct gccccttctc aaattgccag 2880
aagagtgtat ttaccgtcag agttggactg ttggaaaatt ggaattgctt tcttcagggc 2940
cttcaatgcc attcatcaaa gaggtgatg gaagtaatat ggatcaagaa tatggcactg 3000
cttatacacc tcaaactcat acttcttggt ggatgcctcc tagcagtga cctcctagta 3060
acagcggagc aggaattctt ccttctccat ccacccctcg gtttccaact ccaaggactc 3120
caaggactcc tcggactcct cgtggagctg gtggacctgc tagtgctcaa ggttcagtca 3180
aatatgaaa ttcagacttg tattcaccag cttctacccc atctacatgc agaccctta 3240
attctgttga acctgcaact gtcccttcca tccctgaagc acacagtctt tatgtaaac 3300
tcacctttc agaatcagtt atgaattgt ttaaagactg taactctgat agttgttgca 3360
tctgtgtttg caacatgaac atcaaggtg ccgatgttg agtttacatt ccagatccaa 3420
cgcaggaagc acaatatagg tgtacctgtg gcttcagtgc tgcacatgaac agaaaatttg 3480
gaaacaattc aggattatct cttgaagatg aactagatat cataggacgc aatacagact 3540
gtggcaaaga agcagaaaaa cgttttgaag ctctcagggc tacctctgct gaacatgtta 3600
atggaggact aaaggaatct gaaaaattat ctgatgatt gatattattg ctacaagatc 3660
agtgcactaa tttattttca ccctttggag cagcagacca agatcctttt cctaaaagt 3720
gtgtaattag caattgggta cgtgttgaag agcgtgactg ttgcaatgac tgctacctg 3780
cattagaaca tgggcgtcag ttcattggata acatgtcagg aggaaaagtt gatgaagcac 3840
tttgtaaaag ttcattgctta caccctgggt ccaaaagaaa cgatgtgagt atgcagtgt 3900
cacaggatat acttcgaatg ctctctctc ttcagccagt tcttcaggat gccattcaga 3960
aaaaaagaac agtaagacct tgggtgttcc aggtctctc cacttgga caatttcata 4020
aaatggcttg ccgaggctct tatggaactg atgaatcccc agaaccactg ccaatcccca 4080
catttttgtt gggttatgat tatgattatc tgggtgcttc tccatttgct cttccttatt 4140
gggagagact tatgctggaa ccctatggat ctcaaagaga tatagcctat gttgtactgt 4200
gtccagaaaa tgaagccttg ttaaatggag caaaaagctt ttttagagat cttactgcaa 4260
tatatgagtc ctgtcgatta ggtcaacata gacctgttc tcgactgtta acagatggga 4320
tcatgagagt tggatctact gcatcaaaga aactatcaga aaagttggtg gcagaatggt 4380
tttctcaggc agctgatggt aacaatgaag cattttctaa actcaagctt tatgcacaag 4440
tctgcagata tgacctaggt ccttatcttg ctccctgcc attggacagc tctctacttt 4500
cccagccaaa tttagttgcc cctacaagtc agtctttgat tactccacct cagatgacaa 4560
atactggaaa tgctaatact ccatctgcc ccttagcatc tgcagcagc agcactatga 4620
cagtgaactc aggtgttgcc atatctactt cagttgccac agctaattca actttgacca 4680
cagcttcaac ttcattctca tcactctcca acttgaatag tggagtatca tcaataaac 4740
taccttcgtt tccacctttt ggcagtatga acagtaatgc tgcaggatcc atgtctacac 4800
aagcaaatc agttcagagt ggtcagctag gagggcaaca gacatcagct ctacagacag 4860
ctgggatttc tggagaatca tcttcaactc ccactcagcc gcactcctgat gtgtctgaaa 4920
gcacgatgga tcgggataaa gtgggaatcc ccacagatgg tgattcacat gcagtcacgt 4980

atccacctgc aattgttggt tatataattg atcctttttac atacgaaaat acagacgaga 5040
 gcactaactc ttctagtgtg tggacattgg ggctacttcg atgctttcta gaaatgggtcc 5100
 agactcttcc tcctcatatc aagagtactg tttctgtaca gattattcct tgtcagtacc 5160
 tgttgcaacc tgtgaagcat gaagatagag aaatctatcc ccagcattta aaatccctgg 5220
 ctttttcggc ctttaccagc tgtcggaggc cacttccaac atcaaccaat gtgaaaacat 5280
 tgactggctt tgggtccaggt ttagccatgg aaactgccct tagaagtcct gatagaccag 5340
 agtgtattcg actttatgca cctcctttta ttctggctcc agtgaaggac aaacagacag 5400
 agctaggaga aacatttgga gaagctggac agaaatataa tgttcttttt gtgggatact 5460
 gtttatcaca tgatcaaagg tggattcttg catcttgac agatctatat ggagaacttt 5520
 tagaaaactg tatcataac atcgatgttc caaatagggc tcgtcggaaa aaaagtctg 5580
 ctgaaaaatt tgggtctacag aaactttggg agtgggtgctt aggacttgta caaatgagtt 5640
 cattgccatg gagagttgta attggctgct taggaaggat tggatcatga gaattgaaag 5700
 attggagctg tttgctgagt cgtcgaaact tgcagtctct aagtaaaagg ctcaaagaca 5760
 tgtgtagaat gtgtggtata tctgctgcag actcccctag cattctcagt gcttgcttgg 5820
 tggcaatgga gccgcaaggc tcttttggtt ttatgccaga ttctgtgtca actggttctg 5880
 tatttggaag aagcacgact ctaaatatgc agacatctca gctaaatacc ccacaggata 5940
 catcatgtac tcataactt gtgtttccta cttctgcttc tgtgcaagta gcttcagcta 6000
 cttataccac tgaaaatttg gatttagctt tcaatcccaa caatgatgga gcagatggaa 6060
 tgggtatctt tgatttggtt gacacaggag atgatcttga ccctgatatc attaatatcc 6120
 ttctgcttc tccaactggt tctcctgtac attctccagg atctcattac ccccatggag 6180
 gtgatgctgg caagggctcag agtactgac ggctactatc aacagaacct catgaggaag 6240
 tacctaatat tcttcagcaa ccattggccc ttggttactt tgtatcaact gccaaagcag 6300
 gtccattacc tgactgggtc tggtcagcat gtccctcaagc acaatatcag tgtccccttt 6360
 ttcttaaggc ctctttgcac ctccacgtgc cttcagtgca atctgacgag ctgcttcaca 6420
 gtaaacactc ccaccactt gactcaaatc agacttcaga tgcctcagg tttgttttgg 6480
 aacagtacaa tgcactctcc tggctaacct gtgaccctgc aaccaggac agacgctcat 6540
 gtctcccaat tcattttgtg gtgctgaatc agttatataa ctttattatg aatatgctgt 6600
 gatcttcatt tgatggaact gtgcaagaaa agaacaagga aaaatggatg tttcgctgca 6660
 ggattaagtt acaattatct tctcagtga ggtcatttgt gatgggtctt aattcttatt 6720
 acttcaacaa atattgtttt gacttggggg gaggggctat aaccctgcta ttttctattg 6780
 actctattga actctttagg atgatgactg atcatacaaa acgtattata acattttcgt 6840
 agcaaaaatta accttttttt ttccagtcag cagtatttgt gaaaagtaat gagccatagt 6900
 acccagtcac gttaaatgaa tattaagaagc atggagagga aacatgagga acaatgaatt 6960
 tcaacatatg gcttcagaac atgaagatgt tcttgatgg attatagtat ctagtattca 7020
 aaaatgcctg catctcttct cttatttatt gtaagttttt aaatgtataa attgtcttat 7080
 atttcttaac ctcttttata aaaattttcc tagaaggttt atactgcctt cttgctttaa 7140
 agcaattggt ctaaaatata tgtaatcgtc ttaattaaaa agttgcagta ggggttgctt 7200
 tagagtatta tttttttgta aggggggtggg tgggacagta aatttgatt gtctcgatgt 7260
 acagtttaac ggggtagag ggggaataat gtccatacca ttgtgtgtgg aggatttaca 7320

gctaagctgt agttgcagag tacatgtaca gtaatgaagt tcaactgtgt tataaattga 7380
 aaaggtacc 7389

<210> 95
 <211> 1911
 <212> DNA
 <213> Homo sapiens

<400> 95
 gaattcccct gtgttagacg gtacaggtgg aagaagactg ctgtgtgcag gaggaatttg 60
 cagtgcagact tcaaggaaga gaataagctc gccacataaa gaggaacaa agagcaaccc 120
 agagttcaga cccaggaagc ggccgggagg gcaggagcga atcgggccgc cgcgccatg 180
 gagctgagag tcgggaacag gtaccggctg ggccggaaga tcggcagcgg ctcccttcgga 240
 gacatctatc tcggtagcga cattgtctga ggagaagagg ttgccatcaa gcttgaatgt 300
 gtcaaaacca aacaccctca gctccacatt gagagcaaaa tctacaagat gatgcaggga 360
 ggagtgggca tccccacat cagatggtgt ggggcagagg gggactacaa cgtcatggtg 420
 atggagctgc tggggccaag cctggaggac ctcttcaact tctgctccag gaaattcagc 480
 ctcaaaaccg tctgtctgct tgctgaccaa atgatcagtc gcatcgaata cattcattca 540
 aagaacttca tccaccgga tgtgaagcca gacaacttc tcatggcctt ggggaagaag 600
 ggcaacctgg tgtacatcat cgacttcggg ctggccaaga agtaccgga tgcacgcacc 660
 caccagcaca tccccatcg tgagaacaag aacctcacgg ggacggcgcg gtacgcctcc 720
 atcaacacgc accttggaat tgaacaatcc cgaagagatg acttgagtc tctgggctac 780
 gtgctaattg acttcaacct gggtctcttc cctggcagg ggctgaaggc tgccaccaag 840
 agacagaaat acgaaaggat tagcgagaag aaaatgtcca cccccattga agtgttgtgt 900
 aaaggctacc ctccgaatt tgccacatac ctgaatttct gccgttcctt gcgttttgac 960
 gacaagcctg actactcgta cctgcggcag cttttccgga atctgttcca tcgccagggc 1020
 ttctctatg actacgtgtt cgactggaac atgcttaaat ttggtgccag ccgggccgcc 1080
 gatgacgccg agcgggagcg cagggaaccg gaggagcggc tgagacactc gcggaacccg 1140
 gctaccgcg gcctcccttc cacagactcc ggccggctgc gggggacgca ggaagtggct 1200
 cccccacac cctcaccac tacctcacac acggctaaca cctccccccg gcccgctctc 1260
 ggcattggaga gagaacgga agtgagtatg cggctgcacc gcggggcccc cgtcaacatc 1320
 tcctcgtccg acctcacagg ccgacaagat acctctcgca tgtccacctc acagattcct 1380
 ggtcgggtgg ctccagtggt tcttcagtct gtcgtgcacc gatgagaact ctcccttattg 1440
 ctgtgaaggc cagacaatgc atggctgac tactctgtta ccaatggctt tacctagtga 1500
 cagctcccc ggtctaggat cgaatgtta acaccgggag ctctccaggc cactcaccca 1560
 gcgacgctcg tgggggaaac atactaaacg gacagactcc aagagctgcc accgctgggg 1620
 ctgcaactgc gccccccacg tgaactcggg tgaacgggg ctgggaagaa aagcagagag 1680
 agaattgcag agaactcagac tctttttcca ggccctcagc tccctccagt ggtggccgcc 1740
 ctgtactccc tgacgattcc actgtaacta ccaatcttct acttggttaa gacagttttg 1800
 tatcattttg ctaaaaaatta ttggcttaaa tctgtgtaaa gaaaatctgt ctttttattg 1860
 tttctgtct gtttttgag tcttcaaaaa aaaatgttga ctaaggaatt c 1911

<210> 96
 <211> 705
 <212> DNA

<213> Homo sapiens

<400> 96

cgccgagtga cagagacgct caggctgtgt tctcaggatg accgagtgga agacagcagc 60
accagcggtg gcagagaccc cagacatcaa gctctttggg aagtggagca ccgatgatgt 120
gcagatcaat gacatttccc tgcaggatta cattgcagtg aaggagaagt atgccaagta 180
cctccctcac agtgcagggc ggtatgccgc aaacgcttcc cgcaaagctc agtgtcccat 240
tgtggagcgc ctactaact ccatgatgat gcacggccgc aacaacggca agaagctcat 300
gactgtgcgc atcgtcaagc atgccttcga gatcatacac ctgctcacgg gcgagaaccc 360
tctgcaggtc ctggtgaacg ccatcatcaa cagtgtctcc cgggaggact ccacacgcat 420
tgggcgcgcc gggactgtga gacgacaggc tgtggatgtg tccccctgc gccgtgtgaa 480
ccaggccatc tggctgctgt gcacaggcgc tcgtgaggct gccttcggga acattaagac 540
cattgtgtag tgcttgagc atgagctcat caatgtgcc aagggtcctc cgaactccta 600
tgccattaag aagaaggacg agctggagcg tgtggccaag tccaaccgct gattttccag 660
ctgctgcccc ataaacctgt ctgccctttg ggatcccagc caaaa 705

<210> 97

<211> 4485

<212> DNA

<213> Homo sapiens

<400> 97

cgccggcgcc gcggaagcgg cgccggcgcc gccggggcag ccagtgcgc attgtctgcg 60
gcgccggcgcc ccttcggggt ctacgcggta ggcggcgccg tgatcctggc gcagctgctg 120
cgccgctgcc gcgggggctt cctggagcca ggtcccccac catgagcagc cgtccagcag 180
gcaggctccg gtggagaagc aatggagaat aaaagcctgg agagctccca gacagacctg 240
aagctggtgg cccacccccg cgccaagagc aagggtgtga agtatttcgg ctccgacacc 300
aacgccgagg gatgcacct gcagtgaag aaaatctact gccgcacctg catggcccag 360
atgcctact ccggaaacac ctccaacctg tcctaccacc tggagaagaa ccccccgag 420
gaattctgcg agttctgcaa gagcaacacg gagcagatgc gtgaagcctt cgccaccgcc 480
ttctccaagc tgaagcccg gtcgtcccag cagcccgggc aggacgcgct ggccgtcaag 540
gcgggccacg gctacgacag caagaagcag caggagctga cggccgccgt gctgggctc 600
atctgcgagg ggtgtatccc agcctccatc gtggacgagc ccacctcaa ggtgctgctg 660
aagacggccg acccccggta tgagctgccc agccggaagt acatctctac caaggccatc 720
cctgagaagt acggggccgt ccgggaggtg atcctgaag agctggccga ggccacctg 780
tgtggcatct ccaccgacat gtggaggagt gagaatcaga accgcgccta cgtcacgctg 840
gccgcccact tcctgggctt gggcgcccc aactgcctgt ccatgggctc ccgctgcctg 900
aagaccttcg aggtgcccga agagaacacg gcggagacca tcacgcgagt gctctatgag 960
gtcttcatcg agtggggcat cagcgccaag gtcttcgggg ccaccaccaa ctatggcaag 1020
gacatcgtga aggcgtgctc cctgctggac gtcgagtgac acatgccctg cctgggccac 1080
accttcaatg ccggcatcca gcaggccttc cagctcccga agctgggggc gctgctgtcg 1140
cgctgccgca aactggtgga gtacttccag cagtctgccg tggccatgta catgctctat 1200
gagaagcaga agcagcagaa cgtggcccac tgcagctggt tgagcaaccg cgtctcctg 1260
tgggggagca cgctggccat gctgcagcgc ctcaaggagc agcagttcgt catcgccggg 1320
gtcttggtgg aggacagcaa caaccaccac ctcatgctgg aggccagcga gtggggccac 1380

atcgaggggc tgggtggagct cctgcagccc ttcaagcagg tggccgagat gctgtcggcc 1440
tccaggtacc ccaccatcag catggtgaag ccgctgctgc acatgctcct gaacaccacg 1500
ctcaacatca aggagaccga ctccaaggag ctccagcatgg ccaaggaggt catcgccaag 1560
gagctttcca agacctacca ggagacgccc gagatcgaca tgtttctcaa cgtggccacc 1620
ttcctggacc cccgctacaa gaggtgccc ttcctctccg ccttcgagcg gcagcaggtg 1680
gagaatcgcg tggtggaaga ggccaagggc ctgctggaca aggtcaaaga cggcggctac 1740
cggccggtcg aggacaagat cttcccgtg cccgaggagc ctcccgtcaa gaagctcatg 1800
cggacatcca cggccgccc cgccagcgtc atcaacaaca tgctggccga gatcttctgc 1860
cagacaggcg gcgtggagga ccaggaagag tggcatgccc aggtggtgga ggagctgagc 1920
aacttcaagt ccagaaagt gcttggcctc aacgaagacc ccctcaagtg gtggtcagac 1980
cgcttggccc tcttcccct gctgccaag gtgctgcaga agtactggtg cgtgacggcc 2040
acgcgcgtcg cccctgagcg tctcttcgga tccgcccga acgtggtcag cgccaagagg 2100
aaccggcttg ctcccgcga cgtggacgag caggtgttct tgtatgagaa cgcccggagt 2160
ggggcagagg cggaaccga ggaccaggac gagggggagt ggggcctgga ccaggagcag 2220
gtgttctcct tgggggatg cgtcagcggc ggttctttg gcattagga cagcagcttc 2280
ctgtagcgag gaagcgtgtt gtcttacaag tcatccccgc agcagcccat tggatgcttt 2340
gctgtaata cttaccgggt cagcttggtt ttgaacctca gagaccatcc actgtctttg 2400
acacctagaa ggtggaaaaa ggaaagagat tcgagaagt agagaggggc gggggcggtg 2460
gctcctgtct ataatcgag cactttggga ggccgaggtg ggcagatcag ctgaggtcag 2520
gagatcgaga ccagcctggc caacatggcg aaaccccgtc tctactaaaa atacaaaaat 2580
tagccaggac tgatggcatg tgcctgtaat cccagcttct ggaggctgag gccagagaat 2640
cgctgaacc tgggaggtg aggttgagc aagctgagat cgctgcactc cagcctgggc 2700
gacaagagcg agactctctc aaaaagaaaa aagaagacac aagagaggtg gctttgagt 2760
ggttctcttt cctcccctat tcccggggcc cggacgactt ctgcttggga actgccaacg 2820
cttctgcttg ggaattgcgt gcagcagagc ctgaggagc tgttccttcc ttcacagata 2880
cttaagacct ccaccatgct tgattcgagt tctccctggg agggtttaga agaaacgcag 2940
gaacattctg ggtggcgtcg aaggagcctt tcccgatcat catgtgtgac ttctgcgagg 3000
tccagatcac tgaattcatg ttacattct cgtgcaagca gggacctctt gcttctgaga 3060
aatggggaag agacctttta gccaaaatgc ccttcttaaa aagagagacc ttttttttta 3120
atgttcggtt aaaaatgtga cagatgagta gaaaaatgca gaccttaac aaaaagcaaa 3180
cagaaaaaaa agtgtggaat gtgttgatt ttcgacaggt tgctgccaga gagcctgctt 3240
cctgctgcct gccgaaattt cactttgcgg agttggctct taaaactggg cggtgccgg 3300
gcgtggtggc tcacgctgag gtcaggagtt cgagaccagc ctggccaacc aacatggtga 3360
aacctcgtgt ctactaaaa tacaagaac tagccagatg cggtggcacc cgcctgtaat 3420
cccagctact cgggaggctg aggcggaaga ttcgcttgag cccaggaggt ggagggtgca 3480
gtgagccaag actacgccac tgcactccag cctggaggcc agagtggagac tccgtctcaa 3540
aacaaaacaa aagtgggtg ctactggtc cggaggttat gtcttcggtg tctcagccct 3600
aaaagtccag ttccccgtg cggccagctt ttccacataa ggtgtttttg atttgattac 3660
cggaaaggac tcttgattct tctcttttaa actgaatacc ataggggaaa tgaattttaa 3720

aatattgccc cccgaggggt tttccgtggc tggattcctg cgagttgctt tcagtcattc 3780
 agggaaacag aaagacgttt tccaacatgt agaactgctt tttaactgga ggaaaaatac 3840
 ttcaggaggc ttagcatatt gcttggtatc tacgtgcagc gggttctctg cctccgtgaa 3900
 gacaagctgg gctggggagg acggtgtcta ggagggatga cccactcag ctccaggcag 3960
 tgttctgccg agacccaag aactcggggt gtcagagggc aaaggaacta cctgcctttc 4020
 acggctgctg acttctcagg gctgcaagca gcacagaatg ttatccttac gtcctgagcc 4080
 ggtttaagtc tgtggaaaag gaagcacggg agaaatccac gtaacctttg cttctttttt 4140
 aagggaagcg gttccgcgt gaacttgaa cctcagctc cgggtgttct cggcagaagg 4200
 gcagctggaa gggacacagt ggggcaggct ttggggttgc tccctgttct gccccaggc 4260
 cggggacgca gggcagccca cgcctccgtg ggctccattc tgtagcattg ccagcgttct 4320
 cttcacgtct ctaacaatcc ttgtcttttc ctactcacg tggaaatgtg aactgtcccg 4380
 gctctgtctt cttttttatt ttaagccat cgttcccctc ctgaacggtt gcccttatt 4440
 taatgctgta aagttggact gttgttcaat aaaccagagc aatgc 4485

<210> 98
 <211> 2709
 <212> DNA
 <213> Homo sapiens

<400> 98
 gggaaatagca gaataggagc aagccagcac tagtcagcta actaagtgc tcaaccaagg 60
 ccttttttcc ttgttatctt tgcagatact tcattttctt agcgtttctg gagattacaa 120
 catcctgcgg tccggttctt gggaacttta ctgatttata tccccctca cacaaataag 180
 cattgattcc tgcatttctg aagatctcaa gatctggact actgttgaaa aaatttccag 240
 tgaggctcac ttatgtctgt aaagatggga aaaaaatata agaacattgt tctactaaaa 300
 ggattagagg tcataatga ttatcatttt agaatggta agtccttact gagcaacgat 360
 ttaaaactta atttaaaat gagagaagag tatgacaaaa ttcagattgc tgacttgatg 420
 gaagaaaagt tccgaggatga tgctgggttg ggcaactaa taaaaatttt cgaagatata 480
 ccaacgcttg aagacctggc tgaaactctt aaaaaagaaa agttaaagt aaaaggacca 540
 gccctatcaa gaaaggaggaa gaagggaagt catgctactt cacctgcacc ctccacaagc 600
 agcactgtca aaactgaagg agcagaggca actcctggag ctcaaaaaag aaaaaatca 660
 accaaagaaa aggctggacc caaaggaggt aaggtgtccg aggaacagac tcagcctccc 720
 tctcctgcag gagccgcat gtccacagcc atgggccgtt cccatctcc caagacctca 780
 ttgtcagctc caccacaagc ttcttcaact gagaaccoga aaacagtgc caaatgtcag 840
 gtaactccca gaagaaatgt tctccaaaaa cggccagtga tagtgaagg actgagtaca 900
 acaaagccat ttgaatatga gacccagaa atggagaaaa aaataatgtt tcatgctaca 960
 gtggctacac agacacagtt cttccatgtg aaggttttaa acaccagctt gaaggagaaa 1020
 ttcaatggaa agaaaatcat catcatatca gattatttgg aatatgatag tctcctagag 1080
 gtcaatgaag aatctactgt atctgaagct ggtcctaacc aaacgtttga ggttccaaat 1140
 aaaatcatca acagagcaaa ggaaactctg aagattgata ttcttcacaa acaagcttca 1200
 ggaaatattg tatatgggt atttatgcta cataagaaaa cagtaaatca gaagaccaca 1260
 atctacgaaa ttcaggatga tagaggaaaa atggatgtag tggggacagg acaatgtcac 1320
 aatatccct gtgaagaagg agataagctc cagcttttct gcttctgact tagaaaaaag 1380

```

aaccagatgt caaaactgat ttcagaaatg catagtttta tccagataaa gaaaaaaaca 1440
aaccgcgagaa acaatgaccc caagagcatg aagctacccc aggaaacagcg tcagcttcca 1500
tacccttcag aggccagcac aaccttcctt gagagccatc ttcggactcc tcagatgcca 1560
ccaacaactc catccagcag tttcttcacc aagaaaagtg aagacacaat ctccaaaatg 1620
aatgacttca tgaggatgca gatactgaag gaagggagtc attttccagg accgttcatg 1680
accagcatag gccagctga gagccatccc cacactcctc agatgcctcc atcaaacacca 1740
agcagcagtt tcttaaccac gttgaaacca agactgaaga ctgaacctga agaagtttcc 1800
atagaagaca gtgcccagag tgacctcaaa gaagtgatgg tgctgaacgc aacagaatca 1860
tttgatatag agcccaaaga gcagaagaaa atgtttcatg ccacagtggc aactgagaat 1920
gaagtcttcc gagtgaaggt ttttaatat gacctaaagg agaagttcac cccaaagaag 1980
atcattgccca tagcaaatga tgtttgccgc aatgggttcc tggaggata tcctttcaca 2040
cttggtgctg atgtgaatgc tgaccgaaac atggagatcc caaaaggatt gattagaagt 2100
gccagcgtaa ctcttaaat caatcagctt tgctcacaaa ctaaaggag tttgtgaat 2160
ggggtgtttg aggtacataa gaaaaatgta aggggtgaat tcacttatta tgaatacaa 2220
gataatacag ggaagatgga agtggtggtg catggacgac tgaacacaat caactgtgag 2280
gaaggagata aactgaaact caccagcttt gaattggcac cgaagagtg gaataccggg 2340
gagttgagat ctgtaattca tagtcacatc aaggtcatca agaccaggaa aaacaagaaa 2400
gacatactca atcctgattc aagtatggaa acttcaccag actttttctt ctaaaatctg 2460
gatgtcattg acgataatgt ttatggagat aaggtctaag tccctaaaaa aatgtacata 2520
tacctggttg aaatacaaca ctatacatc acaccacat atatactagc tgtaaatcct 2580
atggaatggg ggtattggga gtgctttttt aatttttcat agttttttt taataaaatg 2640
gcataatttg catctacaac ttctataata agaaaaaata aataaacatt atcttttttg 2700
tgaaaaaaa 2709

```

```

<210> 99
<211> 417
<212> DNA
<213> Homo sapiens

```

```

<400> 99
aaaaaccttg tagagagagt aaaaatttta acaccaacct cggccgcgac cacgctggcc 60
gccccggcag gtaccgcaag ggaaagatga aaaattataa ccaagcataa tatagcaagg 120
actaaccctt ataccctctg cataatgaat taactagaaa taactttgca aggagagcca 180
aagctaagac ccccgaaacc agacgagcta cctaagaaca gctaaaagag cacaccgctc 240
tatgtagcaa aatagtggga agatttatag gttagggcga caaacctacc gagcctggtg 300
atagctggtt gtccaagaga atcttagttc aactttaaat ttgccacag aacctctaa 360
atcccttgtt aaatttaact gttagtccaa agaggacag ctctttggac actagga 417

```

```

<210> 100
<211> 893
<212> DNA
<213> Homo sapiens

```

```

<400> 100
gggtttcgcc tccgcctgtg gatgctgcgc ctctccgaac gcaacatgaa ggtgctcctt 60
gccgcgccc tcacgcggg gtccgtcttc ttctgctgc tgccgggacc ttctgcggcc 120
gatgagaaga agaaggggcc caaagtcacc gtcaagggtg attttgacct acgaattgga 180

```

gatgaagatg taggccgggt gatctttggt ctcttcggaa agactgttcc aaaaacagtg 240
 gataattttg tggccttagc tacaggagag aaaggatttg gctacaaaaa cagcaaattc 300
 catcgtgtaa tcaaggactt catgatccag ggcggagact tcaccagggg agatggcaca 360
 ggaggaaaga gcatctacgg tgagcgcttc cccgatgaga acttcaaact gaagcactac 420
 gggcctggct gggtagcat ggccaacgca ggcaaagaca ccaacggctc ccagttcttc 480
 atcacgacag tcaagacagc ctggctagat ggcaagcatg tgggttttg caaagtctta 540
 gagggcatgg aggtggtgcy gaaggtggag agcaccaaga cagacagccg ggataaaccc 600
 ctgaaggatg tgatcatcgc agactgcggc aagatcgagg tggagaagcc ctttgccatc 660
 gccaggagt agggcacagg gacatcttctc tttagtgac cgtctgtgca ggcctgtag 720
 tccgccacag ggctctgagc tgcactggcc ccggtgctgg catctggtgg agcggaccca 780
 ctccccac attccacagg cccatggact cacttttgta acaaaactct accaacactg 840
 accaataaaa aaaaatgtgg gttttttttt tttttaatat aaaaaaaccc ccc 893

<210> 101
 <211> 2360
 <212> DNA
 <213> Homo sapiens

<400> 101
 gctacgagg ccacgctgct ggctggcctg acctaggcgc gcggggtcgg gcggccgcgc 60
 gggcgggctg agtgagcaag acaagacact caagaagagc gagctgcgcc tgggtcccg 120
 ccaggcttgc acgcagaggc gggcggcaga cgggtcccgg cggaatctcc tgagctccgc 180
 cggccagctc tggtgccagc gcccagtggc cggcgcttcg aaagtgactg gtgcctcgcc 240
 gcctcctctc ggtgcgggac catgaagctg ctgccgtcgg tgggtctgaa gctctttctg 300
 gctgcagttc tctcggaact ggtgactggc gagagcctgg agcggcttcg gagagggcta 360
 gctgctggaa ccagcaaccc ggaccctccc actgtatcca cggaccagct gctacccta 420
 ggaggcgcc gggaccgaa agtccgtgac ttgcaagagg cagatctgga ccttttgaga 480
 gtcactttat cctccaagcc acaagcactg gccacaccaa acaaggagga gcacgggaaa 540
 agaaagaaga aaggcaagg gctagggaag aagagggacc catgtcttcg gaaatacaag 600
 gactttctga tccatggaga atgcaaatat gtgaaggagc tccgggctcc ctctgcac 660
 tgccaccggt gttaccatgg agagaggtgt catgggctga gcctcccagt ggaaaatcgc 720
 ttatatacct atgaccacac aaccatcctg gccgtggtgg ctgtggtgct gtcactgtc 780
 tgtctgctgg tcatcgtggg gcttctcatg ttaggtacc ataggagagg aggttatgat 840
 gtggaaaatg aagagaaagt gaagttgggc atgactaatt cccactgaga gagacttg 900
 ctcaaggaat cggctgggga ctgctacctc tgagaagaca caagtgatt tcagactgca 960
 gaggggaaag acttccatct agtcacaaag actccttcgt cccagttgc cgtctaggat 1020
 tggcctccc ataattgctt tgccaaaata ccagagcctt caagtgccaa acagagtatg 1080
 tccgatgta tctgggtaag aagaaagcaa aagcaaggga cctcatgcc cttctgattc 1140
 cctccacca aacccactt cccctcataa gtttgttaa acacttatct tctggattag 1200
 aatgccggtt aaattccata tgctccagga tctttgactg aaaaaaaaaa agaagaagaa 1260
 gaaggagagc aagaaggaaa gatttgtaaa ctggaagaaa gcaacaaaga ttgagaagcc 1320
 atgtactcaa gtaccaccaa gggatctgcc attgggaccc tccagtgtg gatttgatga 1380
 gttaactgtg aaataccaca agcctgagaa ctgaattttg gacttctac ccagatggaa 1440

```

aaataacaac tatttttgtt gttgttgttt gtaaatgcct cttaaattat atattttatt 1500
tattctatgt atgttaattt atttagtttt taacaatcta acaataatat ttcaagtgcc 1560
tagactgtta ctttggaat ttcttgccc tccactcctc atccccacaa tctggcttag 1620
tgccaccacac ctttgccaca aagctaggat ggttctgtga cccatctgta gtaatttatt 1680
gtctgtctac atttctgcag atcttccgtg gtcagagtgc cactgcggga gctctgtatg 1740
gtcaggatgt aggggttaac ttggtcagag ccactctatg agttggactt cagtcttgcc 1800
taggcgattt tgtctacat ttgtgtttt aaagcccaag gtgctgatgt caaagtgtaa 1860
cagatatcag tgtctccccg tgtcctctcc ctgccaagtc tcagaagagg ttgggcttcc 1920
atgcctgtag ctttcttgtt cctcaccacc catggcccca ggccacagcg tgggaactca 1980
ctttcccttg tgtcaagaca tttctctaac tcttgccatt cttctggtgc tactccatgc 2040
aggggtcagt gcagcagagg acagtctgga gaaggatta gcaaagcaaa aggcctgagaa 2100
ggaacaggga acattggagc tgaactgtct tggtaactga ttacctgcca attgctaccg 2160
agaaggttg aggtggggaa ggctttgtat aatcccaccc acctcaccaa aacgatgaag 2220
gtatgctgtc atgggtcctt ctggaagttt ctggtgccat ttctgaactg ttacaacttg 2280
tatttccaaa cctggttcat atttatactt tgcaatccaa ataaagataa cccttattcc 2340
ataaaaaaaa aaaaaaaaaa 2360

```

```

<210> 102
<211> 1090
<212> DNA
<213> Homo sapiens

```

```

<400> 102
gctccgggag acttccggca gggcgggagc ggggtcttgg cgaacggtct tcggaagcgg 60
cggcggcgcg atgaccacgc tacgggcctt tacctgcgac gacctgttcc gttcaacaa 120
cattaacttg gatccactta cagaaactta tgggattcct ttctacctac aatacctcgc 180
ccactggcca gattatttca ttgttgaga ggcacctggt ggagaattaa tgggttatat 240
tatgggtaaa gcagaaggct cagtagctag ggaagaatgg cacgggcacg tcacagctct 300
gtctgttgcc ccagaatttc gacgccttgg tttggctgct aaacttatgg agttactaga 360
ggagatttca gaaagaaagg gtggattttt tgtggatctc tttgtaagag tatctaacca 420
agttgcagtt aacatgtaca agcagttggg ctacagtgtg tataggacgg tcatagagta 480
ctattcgccc agcaacgggg agcctgatga ggacgcttat gatatgagga aagcactttc 540
cagggatact gagaagaaat ccatcatacc attacctcat cctgtgaggc ctgaagacat 600
tgaataaccc tgggcagtgg ttcttaggca gatactctag atgctttatg gacaatatta 660
ttttcatttg atgattcttg agctctatta ggagaaaagt aatcatttta ggtcttaaag 720
acttcaagaa aatacagggt atcaatttat tttaaatctc attgtttcca gttagcaata 780
tcatacctat taaagctgtt cattgttaaca aaattcaatc aaaaaggcag ctaggtcaga 840
aggaaacata ccactctcat ggttcatagt attcactgta tgtatgctag ggaaaagact 900
tgctccagtc tctcctcag ttctgtgctt gagaaccact gctgcatata tttgttttta 960
aattttgtat tgaactgtta attgaagctt taaaagcata tatgaaatgt ataatctaa 1020
gatgtataat acattattga ctctaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1080
aaaaaaaaaa 1090

```

<210> 103
 <211> 832
 <212> DNA
 <213> Homo sapiens

<400> 103
 cgccgctgca gctggggcca tttagggga gcccatggg cctgaaaggc atctgtcagg 60
 cgccctgcc cggtggcaa cagtagttct agggagagac accatgggcc ctgagcgtat 120
 cttcccaat cagactgagg aactgggaca tcagggccct tcagaaggca ctggggattg 180
 gagcagtgag gagcctgagg aagagcagga ggaacgggg tcggggccag ctgggtactc 240
 ctaccagccc ctgaaccaag atcctgaaca agaggagggt gaactggcac cagtggggga 300
 tggagatgta gttgtgaca tccaggatcg aatccaggcc ctggggcttc atttgccaga 360
 cccaccatta gagagtgaag atgaagatga ggaggagct acagcgtga acaaccacag 420
 ctctattccc atggaccag aacatgtaga gctggtgaaa aggacaatgg ctggagtaag 480
 cctgctgag ccaggggttc ctgctgggc tcgggagata tctgatgcc agtgggaaga 540
 tgtgtacag aaagccctcc aagcccgga gccatccct gcctggaagt gaccacagt 600
 agagctgcct tatattccta cattccaggc cagaaccagc acaggactga acacatccct 660
 ggttgaatg tccatttcca tctcccctg ctcccttcc acatcaaggc acatcagact 720
 tctcagagac ccactttatt cagttctgta catatggga catcggtcca agcccaacca 780
 ccttagcatg tatcactctg tggagaataa agcacctatg tactgagcca aa 832

<210> 104
 <211> 1490
 <212> DNA
 <213> Homo sapiens

<400> 104
 ggggcagcgc agggcagacg gcggcaggag aagcaagatg aatgcaggct cagatcctgt 60
 ggtcatcgtc tcggcggcgc ggaccatcat aggttccttc aatggtgcct tagctgctgt 120
 tcctgtccag gacctgggct ccactgtcat caaagaagtc ttgaagagg ccactgtggc 180
 tccggaagat gtgtctgagg tcacttttg acatgtctt gcagcaggct gtgggcagaa 240
 tcctgttaga caagccagtg tgggtgcagg aattccctac tctgttccag catggagctg 300
 ccagatgac tgtgggtcag gcctaaaagc tgtgtgcct gcagtccagt caataggat 360
 aggagactcc agcattgtg ttgcaggagg catggaaaat atgagcaagg ctccctactt 420
 ggcttacttg agaacaggag taaagatagg tgagatgcca ctgactgaca gtatactctg 480
 tgatggtctt acagatgcat ttcacaactg tcatatgggt attacagctg aaaatgtagc 540
 cacaaaatgg caagtgaagta gagaagatca ggacaagggt gcagttctgt ccagaaacag 600
 gacagagaat gcacagaaag ctggccattt tgacaaagag attgtaccag ttttgggtgc 660
 aactagaaaa ggtcttattg aagttaaac agatgagttt cctcgccatg ggagcaacat 720
 agaagccatg tccaagctaa agccttactt tcttactgat ggaacgggaa cagtcacccc 780
 agccaatgct tcaggaataa atgatggtgc tgcagctgtt gctcttatga agaagtcaga 840
 agctgataaa cgtgggctta cacccttagc acggatagtt tcctggtccc aagtgggtgt 900
 ggagccttcc attatgggaa taggaccaat tccagccata aagcaagctg ttacaaaagc 960
 aggttgggtca ctggaagatg ttgacatatt tgaaatcaat gaagcctttg cagctgtctc 1020
 tgctgcaata gttaaagaac ttggattaaa cccagagaag gtcaatattg aaggaggggc 1080
 tatagccttg ggccaccctc ttggagcacc tggctgtcga attcttgtga ccctgttaca 1140

cacactggag agaatgggca gaagtcgtgg tgttcagacc ctgtgcattg ggggtgggat 1200
 ggggaatagca atgtgtgttc agagagaatg acaatgtgtg ttcagagaga atgaattgct 1260
 taaactttga acaacctcaa tttcttttta aactaataaa gtactagggt gcaatatgtg 1320
 aaatcagagg accaaagtac agatggaaac catttcctac atcacaaaaa cccaagttta 1380
 cagcttgtac tttactttaa tgtgtaatac tcaactcacg gtacaagaca attgcattta 1440
 acattgttat aaataaaagg aacatcagat caatcattaa aaaaaaaaaa 1490

<210> 105
 <211> 2019
 <212> DNA
 <213> Homo sapiens

<400> 105
 acgtgtatcg ctgccgtcaa gatggagggg cctttgtccg tgttcggtga ccgcagcact 60
 ggggaaacga tccgctccca aaacgttatg gctgcagctt cgattgccaa tattgtaaaa 120
 agttctcttg gtccagtttg cttggataaa atgttggtgg atgatattgg tgatgtaacc 180
 attactaacg atggtgcaac catcctgaag ttactggagg tagaacatcc tgcagctaaa 240
 gttctttgtg agctggctga tctgcaagac aaagaagttg gagatggaac tacttcagtg 300
 gttattattg cagcagaact cctaaaaaat gcagatgaat tagtcaaaca gaaaattcat 360
 cccacatcag ttattagtgg ctatcgactt gcttgcaagg aagcagtgcg ttatatcaat 420
 gaaaacctaa ttgttaacac agatgaactg ggaagagatt gcctgattaa tgcgtctaag 480
 acatccatgt ctccaaaat cattgggata aatgggtgatt tctttgctaa catggtagta 540
 gatgctgtac ttgctattaa atacacagac ataagaggcc agccacgcta tccagtcaac 600
 tctgttaata ttttgaaagc ccatgggaga agtcaaatgg agagtatgct catcagtggc 660
 tatgcactca actgtgtggt gggatcccag ggcatgccca agagaatcgt aaatgcaaaa 720
 attgcttgcc ttgacttcag cctgcaaaaa acaaaaatga agcttggtgt acaggtggtc 780
 attacagacc ctgaaaaact ggaccaaatt agacagagag aatcagatat caccaaggag 840
 agaattcaga agatcctggc aactgggtgc aatgttattc taacctactg tggaattgat 900
 gatatgtgtc tgaagtattt tgtggaggct ggtgctatgg cagttagaag agttttaaaa 960
 agggacctta aacgcattgc caaagcttct ggagcaacta ttctgtcaac cctggccaat 1020
 ttggaagggtg aagaaacttt tgaagctgca atgttgggac aggcagaaga agtggtagag 1080
 gagagaattt gtgatgatga gctgatctta atcaaaaata ctaaggctcg tacgtctgca 1140
 tcgattatct tacgtggggc aaatgatttc atgtgtgatg agatggagcg ctctttacat 1200
 gatgcacttt gtgtagtgaa gagagttttg gagtcaaat ctgtggttcc cgttgggggt 1260
 gctgtagaag cagccctttc catatacctt gaaaactatg caaccagcat ggggtctcgg 1320
 gaacagcttg cgattgcaga gtttgcaaga tcacttcttg ttattcccaa tacactagca 1380
 gttaatgctg cccaggactc cacagatctg gttgcaaat taagagcttt tcataatgag 1440
 gcccagggtta acccagaacg taaaaatcta aaatggattg gtcttgattt gagcaatggt 1500
 aaacctcgag acaacaaaca agcaggggtg tttgaaccaa ccatagttaa agttaagagt 1560
 ttgaaatttg caacagaagc tgcaatcacc attcttcgaa ttgatgatct tattaattaa 1620
 catccagaaa tccttcggat taaacatgga agttatgaag atgctgttca ctctggagcc 1680
 cttaatgatt gatctgatgt tccttttatt tataacaatg ttaaatgcaa tgtcttgtag 1740
 cttgagttga gtattacaca ttaaagtaaa gtacaagctg taaactggg tttttgtgat 1800

gtaggaaatg gtttccatct gtactttggt cctctgattt cagatattgc aacctagtac 1860
 ttattagtt taaaaagaaa ttgaggttgt tcaaagttta agcaattcat tctctctgaa 1920
 cacacattgc tattcccatc ccaccccaaa tgcacagggc tgcaacacca cgacttctgc 1980
 ccattctctc cagtgtgtgt aacaggggtca caagaattc 2019

<210> 106
 <211> 891
 <212> DNA
 <213> Homo sapiens

<400> 106
 ttttttttct tctctctctc cgccgcccga gatgccgaaa ggaaagaagg ccaagggaaa 60
 gaaggtggct ccggcccccag ctgtcgtgaa gaagcaggag gctaagaaag tggatgaatcc 120
 cctgtttgag aaaaggccta agaatttttg cattggacag gacatccagc ccaaaagaga 180
 cctcaccgcg tttgtgaaat ggccccgcta tatcaggttg cagcggcaga gagccatcct 240
 ctataagcgg ctgaaagtgc ctctgcgat taaccagttc acccaggccc tggaccgcca 300
 aacagctact cagctgctta agctggccca caagtacaga ccagagacaa agcaagagaa 360
 gaagcagaga ctgttgcccc ggcccgagaa gaaggctgct ggcaaagggg acgtcccaac 420
 gaagagacca cctgtccttc gagcaggagt taacaccgtc accaccttgg tggagaacaa 480
 gaaagctcag ctggtggtga ttgcacacga cgtggatccc atcgagctgg ttgtcttctt 540
 gcctgccttg tgcgttaaaa tgggggtccc ttactgcatt atcaagggaa aggcaagact 600
 gggacgtcta gtccacagga agacctgcac cactgtcgcc ttcacacagg tgaactcgga 660
 agacaaaggc gctttggcta agctggtgga agctatcagg accaattaca atgacagata 720
 cgatgagatc cgccgtcact ggggtggcaa tgtcctgggt cctaagtctg tggctcgtat 780
 cgccaagctc gaaaaggcaa aggctaaga acttgccact aaactgggtt aaatgtacac 840
 tgttgagttt tctgtacata aaaataattg aaataatata aattttcctt c 891

<210> 107
 <211> 830
 <212> DNA
 <213> Homo sapiens

<400> 107
 ccccccgag cgccgctccg gctgcaccgc gctcgtccg agtttcaggc tcgtgctaag 60
 cttagcgcgt cgtcgtctcc cttcagtcgc catcatgatt atctaccggg acctcatcag 120
 ccacgatgag atgttctccg acatctacaa gatccgggag atcgcgagcg ggttgtgcct 180
 ggaggtggag ggaagatgg tcagtaggac agaaggtaac attgatgact cgctcattgg 240
 tggaaatgcc tccgtgaag gccccgagg cgaaggtacc gaaagcacag taatcactgg 300
 tgtcgatatt gtcagtgaac atcacctgca ggaacaagt ttcacaaaag aagcctacaa 360
 gaagtacatc aaagattaca tgaaatcaat caaagggaaa cttgaagaac agagaccaga 420
 aagagtaaaa ccttttatga caggggctgc agaacaaatc aagcacatcc ttgctaattt 480
 caaaaactac cagttcttta ttggtgaaaa catgaatcca gatggcatgg ttgctctatt 540
 ggactaccgt gaggatggtg tgaccccata tatgattttc ttaaggatg gtttagaaat 600
 ggaaaaatgt taacaaatgt ggcaattatt ttggtatctat cacctgtcat cataactggc 660
 ttctgcttgt catccacaca acaccaggac ttaagacaaa tgggactgat gtcacttga 720
 gctcttcatt tattttgact gtgatttatt tggagtggag gcattgtttt taagaaaaac 780
 atgtcatgta ggttgcttaa aaataaatg catttaaact catttgagag 830

<210> 108
 <211> 394
 <212> PRT
 <213> Homo sapiens
 <400> 108
 Met Ser Arg Glu Met Gln Asp Val Asp Leu Ala Glu Val Lys Pro Leu
 1 5 10 15
 Val Glu Lys Gly Glu Thr Ile Thr Gly Leu Leu Gln Glu Phe Asp Val
 20 25 30
 Gln Glu Gln Asp Ile Glu Thr Leu His Gly Ser Val His Val Thr Leu
 35 40 45
 Cys Gly Thr Pro Lys Gly Asn Arg Pro Val Ile Leu Thr Tyr His Asp
 50 55 60
 Ile Gly Met Asn His Lys Thr Cys Tyr Asn Pro Leu Phe Asn Tyr Glu
 65 70 75 80
 Asp Met Gln Glu Ile Thr Gln His Phe Ala Val Cys His Val Asp Ala
 85 90 95
 Pro Gly Gln Gln Asp Gly Ala Ala Ser Phe Pro Ala Gly Tyr Met Tyr
 100 105 110
 Pro Ser Met Asp Gln Leu Ala Glu Met Leu Pro Gly Val Leu Gln Gln
 115 120 125
 Phe Gly Leu Lys Ser Ile Ile Gly Met Gly Thr Gly Ala Gly Ala Tyr
 130 135 140
 Thr Leu Thr Arg Phe Ala Leu Asn Asn Pro Glu Met Val Glu Gly Leu
 145 150 155 160
 Val Leu Ile Asn Val Asn Pro Cys Ala Glu Gly Trp Met Asp Trp Ala
 165 170 175
 Ala Ser Lys Ile Ser Gly Trp Thr Gln Ala Leu Pro Asp Met Val Val
 180 185 190
 Ser His Leu Phe Gly Lys Glu Glu Met Gln Ser Asn Val Glu Val Val
 195 200 205
 His Thr Tyr Arg Gln His Ile Val Asn Asp Met Asn Pro Gly Asn Leu
 210 215 220
 His Leu Phe Ile Asn Ala Tyr Asn Ser Arg Arg Asp Leu Glu Ile Glu
 225 230 235 240
 Arg Pro Met Pro Gly Thr His Thr Val Thr Leu Gln Cys Pro Ala Leu
 245 250 255
 Leu Val Val Gly Asp Ser Ser Pro Ala Val Asp Ala Val Val Glu Cys
 260 265 270
 Asn Ser Lys Leu Asp Pro Thr Lys Thr Thr Leu Leu Lys Met Ala Asp
 275 280 285

Cys Gly Gly Leu Pro Gln Ile Ser Gln Pro Ala Lys Leu Ala Glu Ala
290 295 300

Phe Lys Tyr Phe Val Gln Gly Met Gly Tyr Met Pro Ser Ala Ser Met
305 310 315 320

Thr Arg Leu Met Arg Ser Arg Thr Ala Ser Gly Ser Ser Val Thr Ser
325 330 335

Leu Asp Gly Thr Arg Ser Arg Ser His Thr Ser Glu Gly Thr Arg Ser
340 345 350

Arg Ser His Thr Ser Glu Gly Thr Arg Ser Arg Ser His Thr Ser Glu
355 360 365

Gly Ala His Leu Asp Ile Thr Pro Asn Ser Gly Ala Ala Gly Asn Ser
370 375 380

Ala Gly Pro Lys Ser Met Glu Val Ser Cys
385 390

<210> 109
<211> 780
<212> PRT
<213> Homo sapiens

<400> 109

Met Thr His Glu Glu His His Ala Ala Lys Thr Leu Gly Ile Gly Lys
1 5 10 15

Ala Ile Ala Val Leu Thr Ser Gly Gly Asp Ala Gln Gly Met Asn Ala
20 25 30

Ala Val Arg Ala Val Val Arg Val Gly Ile Phe Thr Gly Ala Arg Val
35 40 45

Phe Phe Val His Glu Gly Tyr Gln Gly Leu Val Asp Gly Gly Asp His
50 55 60

Ile Lys Glu Ala Thr Trp Glu Ser Val Ser Met Met Leu Gln Leu Gly
65 70 75 80

Gly Thr Val Ile Gly Ser Ala Arg Cys Lys Asp Phe Arg Glu Arg Glu
85 90 95

Gly Arg Leu Arg Ala Ala Tyr Asn Leu Val Lys Arg Gly Ile Thr Asn
100 105 110

Leu Cys Val Ile Gly Gly Asp Gly Ser Leu Thr Gly Ala Asp Thr Phe
115 120 125

Arg Ser Glu Trp Ser Asp Leu Leu Ser Asp Leu Gln Lys Ala Gly Lys
130 135 140

Ile Thr Asp Glu Glu Ala Thr Lys Ser Ser Tyr Leu Asn Ile Val Gly
145 150 155 160

Leu Val Gly Ser Ile Asp Asn Asp Phe Cys Gly Thr Asp Met Thr Ile
165 170 175

Gly Thr Asp Ser Ala Leu His Arg Ile Met Glu Ile Val Asp Ala Ile
 180 185 190
 Thr Thr Thr Ala Gln Ser His Gln Arg Thr Phe Val Leu Glu Val Met
 195 200 205
 Gly Arg His Cys Gly Tyr Leu Ala Leu Val Thr Ser Leu Ser Cys Gly
 210 215 220
 Ala Asp Trp Val Phe Ile Pro Glu Cys Pro Pro Asp Asp Asp Trp Glu
 225 230 235 240
 Glu His Leu Cys Arg Arg Leu Ser Glu Thr Arg Thr Arg Gly Ser Arg
 245 250 255
 Leu Asn Ile Ile Ile Val Ala Glu Gly Ala Ile Asp Lys Asn Gly Lys
 260 265 270
 Pro Ile Thr Ser Glu Asp Ile Lys Asn Leu Val Val Lys Arg Leu Gly
 275 280 285
 Tyr Asp Thr Arg Val Thr Val Leu Gly His Val Gln Arg Gly Gly Thr
 290 295 300
 Pro Ser Ala Phe Asp Arg Ile Leu Gly Ser Arg Met Gly Val Glu Ala
 305 310 315 320
 Val Met Ala Leu Leu Glu Gly Thr Pro Asp Thr Pro Ala Cys Val Val
 325 330 335
 Ser Leu Ser Gly Asn Gln Ala Val Arg Leu Pro Leu Met Glu Cys Val
 340 345 350
 Gln Val Thr Lys Asp Val Thr Lys Ala Met Asp Glu Lys Lys Phe Asp
 355 360 365
 Glu Ala Leu Lys Leu Arg Gly Arg Ser Phe Met Asn Asn Trp Glu Val
 370 375 380
 Tyr Lys Leu Leu Ala His Val Arg Pro Pro Val Ser Lys Ser Gly Ser
 385 390 395 400
 His Thr Val Ala Val Met Asn Val Gly Ala Pro Ala Ala Gly Met Asn
 405 410 415
 Ala Ala Val Arg Ser Thr Val Arg Ile Gly Leu Ile Gln Gly Asn Arg
 420 425 430
 Val Leu Val Val His Asp Gly Phe Glu Gly Leu Ala Lys Gly Gln Ile
 435 440 445
 Glu Glu Ala Gly Trp Ser Tyr Val Gly Gly Trp Thr Gly Gln Gly Gly
 450 455 460
 Ser Lys Leu Gly Thr Lys Arg Thr Leu Pro Lys Lys Ser Phe Glu Gln
 465 470 475 480
 Ile Ser Ala Asn Ile Thr Lys Phe Asn Ile Gln Gly Leu Val Ile Ile

485										490										495									
Gly	Gly	Phe	Glu	Ala	Tyr	Thr	Gly	Gly	Leu	Glu	Leu	Met	Glu	Gly	Arg														
			500					505					510																
Lys	Gln	Phe	Asp	Glu	Leu	Cys	Ile	Pro	Phe	Val	Val	Ile	Pro	Ala	Thr														
		515					520					525																	
Val	Ser	Asn	Asn	Val	Pro	Gly	Ser	Asp	Phe	Ser	Val	Gly	Ala	Asp	Thr														
	530					535					540																		
Ala	Leu	Asn	Thr	Ile	Cys	Thr	Thr	Cys	Asp	Arg	Ile	Lys	Gln	Ser	Ala														
545					550					555					560														
Ala	Gly	Thr	Lys	Arg	Arg	Val	Phe	Ile	Ile	Glu	Thr	Met	Gly	Gly	Tyr														
				565					570					575															
Cys	Gly	Tyr	Leu	Ala	Thr	Met	Ala	Gly	Leu	Ala	Ala	Gly	Ala	Asp	Ala														
			580					585					590																
Ala	Tyr	Ile	Phe	Glu	Glu	Pro	Phe	Thr	Ile	Arg	Asp	Leu	Gln	Ala	Asn														
		595					600					605																	
Val	Glu	His	Leu	Val	Gln	Lys	Met	Lys	Thr	Thr	Val	Lys	Arg	Gly	Leu														
	610					615					620																		
Val	Leu	Arg	Asn	Glu	Lys	Cys	Asn	Glu	Asn	Tyr	Thr	Thr	Asp	Phe	Ile														
625					630					635					640														
Phe	Asn	Leu	Tyr	Ser	Glu	Glu	Gly	Lys	Gly	Ile	Phe	Asp	Ser	Arg	Lys														
				645					650					655															
Asn	Val	Leu	Gly	His	Met	Gln	Gln	Gly	Gly	Ser	Pro	Thr	Pro	Phe	Asp														
			660					665					670																
Arg	Asn	Phe	Ala	Thr	Lys	Met	Gly	Ala	Lys	Ala	Met	Asn	Trp	Met	Ser														
		675					680					685																	
Gly	Lys	Ile	Lys	Glu	Ser	Tyr	Arg	Asn	Gly	Arg	Ile	Phe	Ala	Asn	Thr														
	690					695					700																		
Pro	Asp	Ser	Gly	Cys	Val	Leu																							

```
<210> 110
<211> 1403
<212> PRT
<213> Homo sapiens
```

<400> 110

Met Ala Thr Gln Gln Lys Ala Ser Asp Glu Arg Ile Ser Gln Phe Asp
 1 5 10 15
 His Asn Leu Leu Pro Glu Leu Ser Ala Leu Leu Gly Leu Asp Ala Val
 20 25 30
 Gln Leu Ala Lys Glu Leu Glu Glu Glu Gln Lys Glu Arg Ala Lys
 35 40 45
 Met Gln Lys Gly Tyr Asn Ser Gln Met Arg Ser Glu Ala Lys Arg Leu
 50 55 60
 Lys Thr Phe Val Thr Tyr Glu Pro Tyr Ser Ser Trp Ile Pro Gln Glu
 65 70 75 80
 Met Ala Ala Ala Gly Phe Tyr Phe Thr Gly Val Lys Ser Gly Ile Gln
 85 90 95
 Cys Phe Cys Cys Ser Leu Ile Leu Phe Gly Ala Gly Leu Thr Arg Leu
 100 105 110
 Pro Ile Glu Asp His Lys Arg Phe His Pro Asp Cys Gly Phe Leu Leu
 115 120 125
 Asn Lys Asp Val Gly Asn Ile Ala Lys Tyr Asp Ile Arg Val Lys Asn
 130 135 140
 Leu Lys Ser Arg Leu Arg Gly Gly Lys Met Arg Tyr Gln Glu Glu Glu
 145 150 155 160
 Ala Arg Leu Ala Ser Phe Arg Asn Trp Pro Phe Tyr Val Gln Gly Ile
 165 170 175
 Ser Pro Cys Val Leu Ser Glu Ala Gly Phe Val Phe Thr Gly Lys Gln
 180 185 190
 Asp Thr Val Gln Cys Phe Ser Cys Gly Gly Cys Leu Gly Asn Trp Glu
 195 200 205
 Glu Gly Asp Asp Pro Trp Lys Glu His Ala Lys Trp Phe Pro Lys Cys
 210 215 220
 Glu Phe Leu Arg Ser Lys Lys Ser Ser Glu Glu Ile Thr Gln Tyr Ile
 225 230 235 240
 Gln Ser Tyr Lys Gly Phe Val Asp Ile Thr Gly Glu His Phe Val Asn
 245 250 255
 Ser Trp Val Gln Arg Glu Leu Pro Met Ala Ser Ala Tyr Cys Asn Asp
 260 265 270
 Ser Ile Phe Ala Tyr Glu Glu Leu Arg Leu Asp Ser Phe Lys Asp Trp
 275 280 285
 Pro Arg Glu Ser Ala Val Gly Val Ala Ala Leu Ala Lys Ala Gly Leu
 290 295 300

Phe Tyr Thr Gly Ile Lys Asp Ile Val Gln Cys Phe Ser Cys Gly Gly
 305 310 315 320
 Cys Leu Glu Lys Trp Gln Glu Gly Asp Asp Pro Leu Asp Asp His Thr
 325 330 335
 Arg Cys Phe Pro Asn Cys Pro Phe Leu Gln Asn Met Lys Ser Ser Ala
 340 345 350
 Glu Val Thr Pro Asp Leu Gln Ser Arg Gly Glu Leu Cys Glu Leu Leu
 355 360 365
 Glu Thr Thr Ser Glu Ser Asn Leu Glu Asp Ser Ile Ala Val Gly Pro
 370 375 380
 Ile Val Pro Glu Met Ala Gln Gly Glu Ala Gln Trp Phe Gln Glu Ala
 385 390 395 400
 Lys Asn Leu Asn Glu Gln Leu Arg Ala Ala Tyr Thr Ser Ala Ser Phe
 405 410 415
 Arg His Met Ser Leu Leu Asp Ile Ser Ser Asp Leu Ala Thr Asp His
 420 425 430
 Leu Leu Gly Cys Asp Leu Ser Ile Ala Ser Lys His Ile Ser Lys Pro
 435 440 445
 Val Gln Glu Pro Leu Val Leu Pro Glu Val Phe Gly Asn Leu Asn Ser
 450 455 460
 Val Met Cys Val Glu Gly Glu Ala Gly Ser Gly Lys Thr Val Leu Leu
 465 470 475 480
 Lys Lys Ile Ala Phe Leu Trp Ala Ser Gly Cys Cys Pro Leu Leu Asn
 485 490 495
 Arg Phe Gln Leu Val Phe Tyr Leu Ser Leu Ser Ser Thr Arg Pro Asp
 500 505 510
 Glu Gly Leu Ala Ser Ile Ile Cys Asp Gln Leu Leu Glu Lys Glu Gly
 515 520 525
 Ser Val Thr Glu Met Cys Met Arg Asn Ile Ile Gln Gln Leu Lys Asn
 530 535 540
 Gln Val Leu Phe Leu Leu Asp Asp Tyr Lys Glu Ile Cys Ser Ile Pro
 545 550 555 560
 Gln Val Ile Gly Lys Leu Ile Gln Lys Asn His Leu Ser Arg Thr Cys
 565 570 575
 Leu Leu Ile Ala Val Arg Thr Asn Arg Ala Arg Asp Ile Arg Arg Tyr
 580 585 590
 Leu Glu Thr Ile Leu Glu Ile Lys Ala Phe Pro Phe Tyr Asn Thr Val
 595 600 605
 Cys Ile Leu Arg Lys Leu Phe Ser His Asn Met Thr Arg Leu Arg Lys
 610 615 620

Phe Met Val Tyr Phe Gly Lys Asn Gln Ser Leu Gln Lys Ile Gln Lys
 625 630 635 640
 Thr Pro Leu Phe Val Ala Ala Ile Cys Ala His Trp Phe Gln Tyr Pro
 645 650 655
 Phe Asp Pro Ser Phe Asp Asp Val Ala Val Phe Lys Ser Tyr Met Glu
 660 665 670
 Arg Leu Ser Leu Arg Asn Lys Ala Thr Ala Glu Ile Leu Lys Ala Thr
 675 680 685
 Val Ser Ser Cys Gly Glu Leu Ala Leu Lys Gly Phe Phe Ser Cys Cys
 690 695 700
 Phe Glu Phe Asn Asp Asp Asp Leu Ala Glu Ala Gly Val Asp Glu Asp
 705 710 715 720
 Glu Asp Leu Thr Met Cys Leu Met Ser Lys Phe Thr Ala Gln Arg Leu
 725 730 735
 Arg Pro Phe Tyr Arg Phe Leu Ser Pro Ala Phe Gln Glu Phe Leu Ala
 740 745 750
 Gly Met Arg Leu Ile Glu Leu Leu Asp Ser Asp Arg Gln Glu His Gln
 755 760 765
 Asp Leu Gly Leu Tyr His Leu Lys Gln Ile Asn Ser Pro Met Met Thr
 770 775 780
 Val Ser Ala Tyr Asn Asn Phe Leu Asn Tyr Val Ser Ser Leu Pro Ser
 785 790 795 800
 Thr Lys Ala Gly Pro Lys Ile Val Ser His Leu Leu His Leu Val Asp
 805 810 815
 Asn Lys Glu Ser Leu Glu Asn Ile Ser Glu Asn Asp Asp Tyr Leu Lys
 820 825 830
 His Gln Pro Glu Ile Ser Leu Gln Met Gln Leu Leu Arg Gly Leu Trp
 835 840 845
 Gln Ile Cys Pro Gln Ala Tyr Phe Ser Met Val Ser Glu His Leu Leu
 850 855 860
 Val Leu Ala Leu Lys Thr Ala Tyr Gln Ser Asn Thr Val Ala Ala Cys
 865 870 875 880
 Ser Pro Phe Val Leu Gln Phe Leu Gln Gly Arg Thr Leu Thr Leu Gly
 885 890 895
 Ala Leu Asn Leu Gln Tyr Phe Phe Asp His Pro Glu Ser Leu Ser Leu
 900 905 910
 Leu Arg Ser Ile His Phe Pro Ile Arg Gly Asn Lys Thr Ser Pro Arg
 915 920 925
 Ala His Phe Ser Val Leu Glu Thr Cys Phe Asp Lys Ser Gln Val Pro
 930 935 940

Thr Ile Asp Gln Asp Tyr Ala Ser Ala Phe Glu Pro Met Asn Glu Trp
 945 950 955 960
 Glu Arg Asn Leu Ala Glu Lys Glu Asp Asn Val Lys Ser Tyr Met Asp
 965 970 975
 Met Gln Arg Arg Ala Ser Pro Asp Leu Ser Thr Gly Tyr Trp Lys Leu
 980 985 990
 Ser Pro Lys Gln Tyr Lys Ile Pro Cys Leu Glu Val Asp Val Asn Asp
 995 1000 1005
 Ile Asp Val Val Gly Gln Asp Met Leu Glu Ile Leu Met Thr Val
 1010 1015 1020
 Phe Ser Ala Ser Gln Arg Ile Glu Leu His Leu Asn His Ser Arg
 1025 1030 1035
 Gly Phe Ile Glu Ser Ile Arg Pro Ala Leu Glu Leu Ser Lys Ala
 1040 1045 1050
 Ser Val Thr Lys Cys Ser Ile Ser Lys Leu Glu Leu Ser Ala Ala
 1055 1060 1065
 Glu Gln Glu Leu Leu Leu Thr Leu Pro Ser Leu Glu Ser Leu Glu
 1070 1075 1080
 Val Ser Gly Thr Ile Gln Ser Gln Asp Gln Ile Phe Pro Asn Leu
 1085 1090 1095
 Asp Lys Phe Leu Cys Leu Lys Glu Leu Ser Val Asp Leu Glu Gly
 1100 1105 1110
 Asn Ile Asn Val Phe Ser Val Ile Pro Glu Glu Phe Pro Asn Phe
 1115 1120 1125
 His His Met Glu Lys Leu Leu Ile Gln Ile Ser Ala Glu Tyr Asp
 1130 1135 1140
 Pro Ser Lys Leu Val Lys Leu Ile Gln Asn Ser Pro Asn Leu His
 1145 1150 1155
 Val Phe His Leu Lys Cys Asn Phe Phe Ser Asp Phe Gly Ser Leu
 1160 1165 1170
 Met Thr Met Leu Val Ser Cys Lys Lys Leu Thr Glu Ile Lys Phe
 1175 1180 1185
 Ser Asp Ser Phe Phe Gln Ala Val Pro Phe Val Ala Ser Leu Pro
 1190 1195 1200
 Asn Phe Ile Ser Leu Lys Ile Leu Asn Leu Glu Gly Gln Gln Phe
 1205 1210 1215
 Pro Asp Glu Glu Thr Ser Glu Lys Phe Ala Tyr Ile Leu Gly Ser
 1220 1225 1230
 Leu Ser Asn Leu Glu Glu Leu Ile Leu Pro Thr Gly Asp Gly Ile

1235 1240 1245
 Tyr Arg Val Ala Lys Leu Ile Ile Gln Gln Cys Gln Gln Leu His
 1250 1255 1260
 Cys Leu Arg Val Leu Ser Phe Phe Lys Thr Leu Asn Asp Asp Ser
 1265 1270 1275
 Val Val Glu Ile Ala Lys Val Ala Ile Ser Gly Gly Phe Gln Lys
 1280 1285 1290
 Leu Glu Asn Leu Lys Leu Ser Ile Asn His Lys Ile Thr Glu Glu
 1295 1300 1305
 Gly Tyr Arg Asn Phe Phe Gln Ala Leu Asp Asn Met Pro Asn Leu
 1310 1315 1320
 Gln Glu Leu Asp Ile Ser Arg His Phe Thr Glu Cys Ile Lys Ala
 1325 1330 1335
 Gln Ala Thr Thr Val Lys Ser Leu Ser Gln Cys Val Leu Arg Leu
 1340 1345 1350
 Pro Arg Leu Ile Arg Leu Asn Met Leu Ser Trp Leu Leu Asp Ala
 1355 1360 1365
 Asp Asp Ile Ala Leu Leu Asn Val Met Lys Glu Arg His Pro Gln
 1370 1375 1380
 Ser Lys Tyr Leu Thr Ile Leu Gln Lys Trp Ile Leu Pro Phe Ser
 1385 1390 1395
 Pro Ile Ile Gln Lys
 1400
 <210> 111
 <211> 1005
 <212> PRT
 <213> Homo sapiens
 <400> 111
 Met Met Ser Asp Ala Ser Asp Met Leu Ala Ala Ala Leu Glu Gln Met
 1 5 10 15
 Asp Gly Ile Ile Ala Gly Ser Lys Ala Leu Glu Tyr Ser Asn Gly Ile
 20 25 30
 Phe Asp Cys Gln Ser Pro Thr Ser Pro Phe Met Gly Ser Leu Arg Ala
 35 40 45
 Leu His Leu Val Glu Asp Leu Arg Gly Leu Leu Glu Met Met Glu Thr
 50 55 60
 Asp Glu Lys Glu Gly Leu Arg Cys Gln Ile Pro Asp Ser Thr Ala Glu
 65 70 75 80
 Thr Leu Val Glu Trp Leu Gln Ser Gln Met Thr Asn Gly His Leu Pro
 85 90 95
 Gly Asn Gly Asp Val Tyr Gln Glu Arg Leu Ala Arg Leu Glu Asn Asp

100	105	110
Lys Glu Ser Leu Val Leu Gln Val Ser Val Leu Thr Asp Gln Val Glu 115 120 125		
Ala Gln Gly Glu Lys Ile Arg Asp Leu Glu Phe Cys Leu Glu Glu His 130 135 140		
Arg Glu Lys Leu Asn Ala Thr Glu Glu Met Leu Gln Gln Glu Leu Leu 145 150 155 160		
Ser Arg Thr Ser Leu Glu Thr Gln Lys Leu Asp Leu Met Ala Glu Ile 165 170 175		
Ser Asn Leu Lys Leu Lys Leu Thr Ala Val Glu Lys Asp Arg Leu Asp 180 185 190		
Tyr Glu Asp Lys Phe Arg Asp Thr Glu Gly Leu Ile Gln Glu Ile Asn 195 200 205		
Asp Leu Arg Leu Lys Val Ser Glu Met Asp Ser Glu Arg Leu Gln Tyr 210 215 220		
Glu Lys Lys Leu Lys Ser Thr Lys Asp Glu Leu Ala Ser Leu Lys Glu 225 230 235 240		
Gln Leu Glu Glu Lys Glu Ser Glu Val Lys Arg Leu Gln Glu Lys Leu 245 250 255		
Val Cys Lys Met Lys Gly Glu Gly Val Glu Ile Val Asp Arg Asp Glu 260 265 270		
Asn Phe Lys Lys Lys Leu Lys Glu Lys Asn Ile Glu Val Gln Lys Met 275 280 285		
Lys Lys Ala Val Glu Ser Leu Met Ala Ala Asn Glu Glu Lys Asp Arg 290 295 300		
Lys Ile Glu Asp Leu Arg Gln Cys Leu Asn Arg Tyr Lys Lys Met Gln 305 310 315 320		
Asp Thr Val Val Leu Ala Gln Gly Lys Lys Gly Lys Asp Gly Glu Tyr 325 330 335		
Glu Glu Leu Leu Asn Ser Ser Ser Ile Ser Ser Leu Leu Asp Ala Gln 340 345 350		
Gly Phe Ser Asp Leu Glu Lys Ser Pro Ser Pro Thr Pro Val Met Gly 355 360 365		
Ser Pro Ser Cys Asp Pro Phe Asn Thr Ser Val Pro Glu Glu Phe His 370 375 380		
Thr Thr Ile Leu Gln Val Ser Ile Pro Ser Leu Leu Pro Ala Thr Val 385 390 395 400		
Ser Met Glu Thr Ser Glu Lys Ser Lys Leu Thr Pro Lys Pro Glu Thr 405 410 415		

Ser Phe Glu Glu Asn Asp Gly Asn Ile Ile Leu Gly Ala Thr Val Asp
 420 425 430
 Thr Gln Leu Arg Asp Lys Leu Leu Thr Ser Ser Leu Gln Lys Ser Ser
 435 440 445
 Ser Leu Gly Asn Leu Lys Lys Glu Thr Ser Asp Gly Glu Lys Glu Thr
 450 455 460
 Ile Gln Lys Thr Ser Glu Asp Arg Ala Pro Ala Glu Ser Arg Pro Phe
 465 470 475 480
 Gly Thr Leu Pro Pro Arg Pro Pro Gly Gln Asp Thr Ser Met Asp Asp
 485 490 495
 Asn Pro Phe Gly Thr Arg Lys Val Arg Ser Ser Phe Gly Arg Gly Phe
 500 505 510
 Phe Lys Ile Lys Ser Asn Lys Arg Thr Ala Ser Ala Pro Asn Leu Asp
 515 520 525
 Arg Lys Arg Ser Ala Ser Ala Pro Thr Leu Ala Glu Thr Glu Lys Glu
 530 535 540
 Thr Ala Ala His Leu Asp Leu Ala Gly Ala Ser Ser Arg Pro Lys Asp
 545 550 555 560
 Ser Gln Arg Asn Ser Pro Phe Gln Ile Pro Pro Pro Ser Pro Asp Ser
 565 570 575
 Lys Lys Lys Ser Arg Gly Ile Met Lys Leu Phe Gly Lys Leu Arg Arg
 580 585 590
 Ser Gln Ser Thr Thr Phe Asn Pro Asp Asp Met Ser Glu Pro Glu Phe
 595 600 605
 Lys Arg Gly Gly Thr Arg Ala Thr Ala Gly Pro Arg Leu Gly Trp Ser
 610 615 620
 Arg Asp Leu Gly Gln Ser Asn Ser Asp Leu Asp Met Pro Phe Ala Lys
 625 630 635 640
 Trp Thr Lys Glu Gln Val Cys Asn Trp Leu Met Glu Gln Gly Leu Gly
 645 650 655
 Ser Tyr Leu Asn Ser Gly Lys His Trp Ile Ala Ser Gly Gln Thr Leu
 660 665 670
 Leu Gln Ala Ser Gln Gln Asp Leu Glu Lys Glu Leu Gly Ile Lys His
 675 680 685
 Ser Leu His Arg Lys Lys Leu Gln Leu Ala Leu Gln Ala Leu Gly Ser
 690 695 700
 Glu Glu Glu Thr Asn His Gly Lys Leu Asp Phe Asn Trp Val Thr Arg
 705 710 715 720
 Trp Leu Asp Asp Ile Gly Leu Pro Gln Tyr Lys Thr Gln Phe Asp Glu
 725 730 735

Gly Arg Val Asp Gly Arg Met Leu His Tyr Met Thr Val Asp Asp Leu
740 745 750

Leu Ser Leu Lys Val Val Ser Val Leu His His Leu Ser Ile Lys Arg
755 760 765

Ala Ile Gln Val Leu Arg Ile Asn Asn Phe Glu Pro Asn Cys Leu Arg
770 775 780

Arg Arg Pro Ser Asp Glu Asn Thr Ile Ala Pro Ser Glu Val Gln Lys
785 790 795 800

Trp Thr Asn His Arg Val Met Glu Trp Leu Arg Ser Val Asp Leu Ala
805 810 815

Glu Tyr Ala Pro Asn Leu Arg Gly Ser Gly Val His Gly Gly Leu Met
820 825 830

Val Leu Glu Pro Arg Phe Asn Val Glu Thr Met Ala Gln Leu Leu Asn
835 840 845

Ile Pro Pro Asn Lys Thr Leu Leu Arg Arg His Leu Ala Thr His Phe
850 855 860

Asn Leu Leu Ile Gly Ala Glu Ala Gln His Gln Lys Arg Asp Ala Met
865 870 875 880

Glu Leu Pro Asp Tyr Val Leu Leu Thr Ala Thr Ala Lys Val Lys Pro
885 890 895

Lys Lys Leu Ala Phe Ser Asn Phe Gly Asn Leu Arg Lys Lys Lys Gln
900 905 910

Glu Asp Gly Glu Glu Tyr Val Cys Pro Met Glu Leu Gly Gln Ala Ser
915 920 925

Gly Ser Ala Ser Lys Lys Gly Phe Lys Pro Gly Leu Asp Met Arg Leu
930 935 940

Tyr Glu Glu Asp Asp Leu Asp Arg Leu Glu Gln Met Glu Asp Ser Glu
945 950 955 960

Gly Thr Val Arg Gln Ile Gly Ala Phe Ser Glu Gly Ile Asn Asn Leu
965 970 975

Thr His Met Leu Lys Glu Asp Asp Met Phe Lys Asp Phe Ala Ala Arg
980 985 990

Ser Pro Ser Ala Ser Ile Thr Asp Glu Asp Ser Asn Val
995 1000 1005

<210> 112
<211> 2871
<212> PRT
<213> Homo sapiens

<400> 112

Met Ser Cys Asn Gly Gly Ser His Pro Arg Ile Asn Thr Leu Gly Arg
1 5 10 15

Met Ile Arg Ala Glu Ser Gly Pro Asp Leu Arg Tyr Glu Val Thr Ser
 20 25 30
 Gly Gly Gly Gly Thr Ser Arg Met Tyr Tyr Ser Arg Arg Gly Val Ile
 35 40 45
 Thr Asp Gln Asn Ser Asp Gly Tyr Cys Gln Thr Gly Thr Met Ser Arg
 50 55 60
 His Gln Asn Gln Asn Thr Ile Gln Glu Leu Leu Gln Asn Cys Ser Asp
 65 70 75 80
 Cys Leu Met Arg Ala Glu Leu Ile Val Gln Pro Glu Leu Lys Tyr Gly
 85 90 95
 Asp Gly Ile Gln Leu Thr Arg Ser Arg Glu Leu Asp Glu Cys Phe Ala
 100 105 110
 Gln Ala Asn Asp Gln Met Glu Ile Leu Asp Ser Leu Ile Arg Glu Met
 115 120 125
 Arg Gln Met Gly Gln Pro Cys Asp Ala Tyr Gln Lys Arg Leu Leu Gln
 130 135 140
 Leu Gln Glu Gln Met Arg Ala Leu Tyr Lys Ala Ile Ser Val Pro Arg
 145 150 155 160
 Val Arg Arg Ala Ser Ser Lys Gly Gly Gly Tyr Thr Cys Gln Ser
 165 170 175
 Gly Ser Gly Trp Asp Glu Phe Thr Lys His Val Thr Ser Glu Cys Leu
 180 185 190
 Gly Trp Met Arg Gln Gln Arg Ala Glu Met Asp Met Val Ala Trp Gly
 195 200 205
 Val Asp Leu Ala Ser Val Glu Gln His Ile Asn Ser His Arg Gly Ile
 210 215 220
 His Asn Ser Ile Gly Asp Tyr Arg Trp Gln Leu Asp Lys Ile Lys Ala
 225 230 235 240
 Asp Leu Arg Glu Lys Ser Ala Ile Tyr Gln Leu Glu Glu Glu Tyr Glu
 245 250 255
 Asn Leu Leu Lys Ala Ser Phe Glu Arg Met Asp His Leu Arg Gln Leu
 260 265 270
 Gln Asn Ile Ile Gln Ala Thr Ser Arg Glu Ile Met Trp Ile Asn Asp
 275 280 285
 Cys Glu Glu Glu Glu Leu Leu Tyr Asp Trp Ser Asp Lys Asn Thr Asn
 290 295 300
 Ile Ala Gln Lys Gln Glu Ala Phe Ser Ile Arg Met Ser Gln Leu Glu
 305 310 315 320
 Val Lys Glu Lys Glu Leu Asn Lys Leu Lys Gln Glu Ser Asp Gln Leu
 325 330 335

Val Leu Asn Gln His Pro Ala Ser Asp Lys Ile Glu Ala Tyr Met Asp
 340 345 350
 Thr Leu Gln Thr Gln Trp Ser Trp Ile Leu Gln Ile Thr Lys Cys Ile
 355 360 365
 Asp Val His Leu Lys Glu Asn Ala Ala Tyr Phe Gln Phe Phe Glu Glu
 370 375 380
 Ala Gln Ser Thr Glu Ala Tyr Leu Lys Gly Leu Gln Asp Ser Ile Arg
 385 390 395 400
 Lys Lys Tyr Pro Cys Asp Lys Asn Met Pro Leu Gln His Leu Leu Glu
 405 410 415
 Gln Ile Lys Glu Leu Glu Lys Glu Arg Glu Lys Ile Leu Glu Tyr Lys
 420 425 430
 Arg Gln Val Gln Asn Leu Val Asn Lys Ser Lys Lys Ile Val Gln Leu
 435 440 445
 Lys Pro Arg Asn Pro Asp Tyr Arg Ser Asn Lys Pro Ile Ile Leu Arg
 450 455 460
 Ala Leu Cys Asp Tyr Lys Gln Asp Gln Lys Ile Val His Lys Gly Asp
 465 470 475 480
 Glu Cys Ile Leu Lys Asp Asn Asn Glu Arg Ser Lys Trp Tyr Val Thr
 485 490 495
 Gly Pro Gly Gly Val Asp Met Leu Val Pro Ser Val Gly Leu Ile Ile
 500 505 510
 Pro Pro Pro Asn Pro Leu Ala Val Asp Leu Ser Cys Lys Ile Glu Gln
 515 520 525
 Tyr Tyr Glu Ala Ile Leu Ala Leu Trp Asn Gln Leu Tyr Ile Asn Met
 530 535 540
 Lys Ser Leu Val Ser Trp His Tyr Cys Met Ile Asp Ile Glu Lys Ile
 545 550 555 560
 Arg Ala Met Thr Ile Ala Lys Leu Lys Thr Met Arg Gln Glu Asp Tyr
 565 570 575
 Met Lys Thr Ile Ala Asp Leu Glu Leu His Tyr Gln Glu Phe Ile Arg
 580 585 590
 Asn Ser Gln Gly Ser Glu Met Phe Gly Asp Asp Asp Lys Arg Lys Ile
 595 600 605
 Gln Ser Gln Phe Thr Asp Ala Gln Lys His Tyr Gln Thr Leu Val Ile
 610 615 620
 Gln Leu Pro Gly Tyr Pro Gln His Gln Thr Val Thr Thr Thr Glu Ile
 625 630 635 640
 Thr His His Gly Thr Cys Gln Asp Val Asn His Asn Lys Val Ile Glu

	645		650		655
Thr Asn Arg Glu Asn Asp Lys Gln Glu Thr Trp Met Leu Met Glu Leu	660		665		670
Gln Lys Ile Arg Arg Gln Ile Glu His Cys Glu Gly Arg Met Thr Leu	675		680		685
Lys Asn Leu Pro Leu Ala Asp Gln Gly Ser Ser His His Ile Thr Val	690		695		700
Lys Ile Asn Glu Leu Lys Ser Val Gln Asn Asp Ser Gln Ala Ile Ala	705		710		715
Glu Val Leu Asn Gln Leu Lys Asp Met Leu Ala Asn Phe Arg Gly Ser	725		730		735
Glu Lys Tyr Cys Tyr Leu Gln Asn Glu Val Phe Gly Leu Phe Gln Lys	740		745		750
Leu Glu Asn Ile Asn Gly Val Thr Asp Gly Tyr Leu Asn Ser Leu Cys	755		760		765
Thr Val Arg Ala Leu Leu Gln Ala Ile Leu Gln Thr Glu Asp Met Leu	770		775		780
Lys Val Tyr Glu Ala Arg Leu Thr Glu Glu Glu Thr Val Cys Leu Asp	785		790		795
Leu Asp Lys Val Glu Ala Tyr Arg Cys Gly Leu Lys Lys Ile Lys Asn	805		810		815
Asp Leu Asn Leu Lys Lys Ser Leu Leu Ala Thr Met Lys Thr Glu Leu	820		825		830
Gln Lys Ala Gln Gln Ile His Ser Gln Thr Ser Gln Gln Tyr Pro Leu	835		840		845
Tyr Asp Leu Asp Leu Gly Lys Phe Gly Glu Lys Val Thr Gln Leu Thr	850		855		860
Asp Arg Trp Gln Arg Ile Asp Lys Gln Ile Asp Phe Arg Leu Trp Asp	865		870		875
Leu Glu Lys Gln Ile Lys Gln Leu Arg Asn Tyr Arg Asp Asn Tyr Gln	885		890		895
Ala Phe Cys Lys Trp Leu Tyr Asp Arg Lys Arg Arg Gln Asp Ser Leu	900		905		910
Glu Ser Met Lys Phe Gly Asp Ser Asn Thr Val Met Arg Phe Leu Asn	915		920		925
Glu Gln Lys Asn Leu His Ser Glu Ile Ser Gly Lys Arg Asp Lys Ser	930		935		940
Glu Glu Val Gln Lys Ile Ala Glu Leu Cys Ala Asn Ser Ile Lys Asp	945		950		955
					960

Tyr Glu Leu Gln Leu Ala Ser Tyr Thr Ser Gly Leu Glu Thr Leu Leu
 965 970 975
 Asn Ile Pro Ile Lys Arg Thr Met Ile Gln Ser Pro Ser Gly Val Ile
 980 985 990
 Leu Gln Glu Ala Ala Asp Val His Ala Arg Tyr Ile Glu Leu Leu Thr
 995 1000 1005
 Arg Ser Gly Asp Tyr Tyr Arg Phe Leu Ser Glu Met Leu Lys Ser
 1010 1015 1020
 Leu Glu Asp Leu Lys Leu Lys Asn Thr Lys Ile Glu Val Leu Glu
 1025 1030 1035
 Glu Glu Leu Arg Leu Ala Arg Asp Ala Asn Ser Glu Asn Cys Asn
 1040 1045 1050
 Lys Asn Lys Phe Leu Asp Gln Asn Leu Gln Lys Tyr Gln Ala Glu
 1055 1060 1065
 Cys Ser Gln Phe Lys Ala Lys Leu Ala Ser Leu Glu Glu Leu Lys
 1070 1075 1080
 Arg Gln Ala Glu Leu Asp Gly Lys Ser Ala Lys Gln Asn Leu Asp
 1085 1090 1095
 Lys Cys Tyr Gly Gln Ile Lys Glu Leu Asn Glu Lys Ile Thr Arg
 1100 1105 1110
 Leu Thr Tyr Glu Ile Glu Asp Glu Lys Arg Arg Arg Lys Ser Val
 1115 1120 1125
 Glu Asp Arg Phe Asp Gln Gln Lys Asn Asp Tyr Asp Gln Leu Gln
 1130 1135 1140
 Lys Ala Arg Gln Cys Glu Lys Glu Asn Leu Gly Trp Gln Lys Leu
 1145 1150 1155
 Glu Ser Glu Lys Ala Ile Lys Glu Lys Glu Tyr Glu Ile Glu Arg
 1160 1165 1170
 Leu Arg Val Leu Leu Gln Glu Glu Gly Thr Arg Lys Arg Glu Tyr
 1175 1180 1185
 Glu Asn Glu Leu Ala Lys Val Arg Asn His Tyr Asn Glu Glu Met
 1190 1195 1200
 Ser Asn Leu Arg Asn Lys Tyr Glu Thr Glu Ile Asn Ile Thr Lys
 1205 1210 1215
 Thr Thr Ile Lys Glu Ile Ser Met Gln Lys Glu Asp Asp Ser Lys
 1220 1225 1230
 Asn Leu Arg Asn Gln Leu Asp Arg Leu Ser Arg Glu Asn Arg Asp
 1235 1240 1245
 Leu Lys Asp Glu Ile Val Arg Leu Asn Asp Ser Ile Leu Gln Ala
 1250 1255 1260

Thr Glu Gln Arg Arg Arg Ala Glu Glu Asn Ala Leu Gln Gln Lys
 1265 1270 1275
 Ala Cys Gly Ser Glu Ile Met Gln Lys Lys Gln His Leu Glu Ile
 1280 1285 1290
 Glu Leu Lys Gln Val Met Gln Gln Arg Ser Glu Asp Asn Ala Arg
 1295 1300 1305
 His Lys Gln Ser Leu Glu Glu Ala Ala Lys Thr Ile Gln Asp Lys
 1310 1315 1320
 Asn Lys Glu Ile Glu Arg Leu Lys Ala Glu Phe Gln Glu Glu Ala
 1325 1330 1335
 Lys Arg Arg Trp Glu Tyr Glu Asn Glu Leu Ser Lys Val Arg Asn
 1340 1345 1350
 Asn Tyr Asp Glu Glu Ile Ile Ser Leu Lys Asn Gln Phe Glu Thr
 1355 1360 1365
 Glu Ile Asn Ile Thr Lys Thr Thr Ile His Gln Leu Thr Met Gln
 1370 1375 1380
 Lys Glu Glu Asp Thr Ser Gly Tyr Arg Ala Gln Ile Asp Asn Leu
 1385 1390 1395
 Thr Arg Glu Asn Arg Ser Leu Ser Glu Glu Ile Lys Arg Leu Lys
 1400 1405 1410
 Asn Thr Leu Thr Gln Thr Thr Glu Asn Leu Arg Arg Val Glu Glu
 1415 1420 1425
 Asp Ile Gln Gln Gln Lys Ala Thr Gly Ser Glu Val Ser Gln Arg
 1430 1435 1440
 Lys Gln Gln Leu Glu Val Glu Leu Arg Gln Val Thr Gln Met Arg
 1445 1450 1455
 Thr Glu Glu Ser Val Arg Tyr Lys Gln Ser Leu Asp Asp Ala Ala
 1460 1465 1470
 Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile Glu Arg Leu Lys Gln
 1475 1480 1485
 Leu Ile Asp Lys Glu Thr Asn Asp Arg Lys Cys Leu Glu Asp Glu
 1490 1495 1500
 Asn Ala Arg Leu Gln Arg Val Gln Tyr Asp Leu Gln Lys Ala Asn
 1505 1510 1515
 Ser Ser Ala Thr Glu Thr Ile Asn Lys Leu Lys Val Gln Glu Gln
 1520 1525 1530
 Glu Leu Thr Arg Leu Arg Ile Asp Tyr Glu Arg Val Ser Gln Glu
 1535 1540 1545
 Arg Thr Val Lys Asp Gln Asp Ile Thr Arg Phe Gln Asn Ser Leu
 1550 1555 1560

Lys Glu Leu Gln Leu Gln Lys Gln Lys Val Glu Glu Glu Leu Asn
 1565 1570 1575
 Arg Leu Lys Arg Thr Ala Ser Glu Asp Ser Cys Lys Arg Lys Lys
 1580 1585 1590
 Leu Glu Glu Glu Leu Glu Gly Met Arg Arg Ser Leu Lys Glu Gln
 1595 1600 1605
 Ala Ile Lys Ile Thr Asn Leu Thr Gln Gln Leu Glu Gln Ala Ser
 1610 1615 1620
 Ile Val Lys Lys Arg Ser Glu Asp Asp Leu Arg Gln Gln Arg Asp
 1625 1630 1635
 Val Leu Asp Gly His Leu Arg Glu Lys Gln Arg Thr Gln Glu Glu
 1640 1645 1650
 Leu Arg Arg Leu Ser Ser Glu Val Glu Ala Leu Arg Arg Gln Leu
 1655 1660 1665
 Leu Gln Glu Gln Glu Ser Val Lys Gln Ala His Leu Arg Asn Glu
 1670 1675 1680
 His Phe Gln Lys Ala Ile Glu Asp Lys Ser Arg Ser Leu Asn Glu
 1685 1690 1695
 Ser Lys Ile Glu Ile Glu Arg Leu Gln Ser Leu Thr Glu Asn Leu
 1700 1705 1710
 Thr Lys Glu His Leu Met Leu Glu Glu Glu Leu Arg Asn Leu Arg
 1715 1720 1725
 Leu Glu Tyr Asp Asp Leu Arg Arg Gly Arg Ser Glu Ala Asp Ser
 1730 1735 1740
 Asp Lys Asn Ala Thr Ile Leu Glu Leu Arg Ser Gln Leu Gln Ile
 1745 1750 1755
 Ser Asn Asn Arg Thr Leu Glu Leu Gln Gly Leu Ile Asn Asp Leu
 1760 1765 1770
 Gln Arg Glu Arg Glu Asn Leu Arg Gln Glu Ile Glu Lys Phe Gln
 1775 1780 1785
 Lys Gln Ala Leu Glu Ala Ser Asn Arg Ile Gln Glu Ser Lys Asn
 1790 1795 1800
 Gln Cys Thr Gln Val Val Gln Glu Arg Glu Ser Leu Leu Val Lys
 1805 1810 1815
 Ile Lys Val Leu Glu Gln Asp Lys Ala Arg Leu Gln Arg Leu Glu
 1820 1825 1830
 Asp Glu Leu Asn Arg Ala Lys Ser Thr Leu Glu Ala Glu Thr Arg
 1835 1840 1845
 Val Lys Gln Arg Leu Glu Cys Glu Lys Gln Gln Ile Gln Asn Asp

1850	1855	1860
Leu Asn Gln Trp Lys Thr Gln 1865	Tyr Ser Arg Lys Glu 1870	Glu Ala Ile 1875
Arg Lys Ile Glu Ser Glu Arg 1880	Glu Lys Ser Glu Arg 1885	Glu Lys Asn 1890
Ser Leu Arg Ser Glu Ile Glu 1895	Arg Leu Gln Ala Glu 1900	Ile Lys Arg 1905
Ile Glu Glu Arg Cys Arg Arg 1910	Lys Leu Glu Asp Ser 1915	Thr Arg Glu 1920
Thr Gln Ser Gln Leu Glu Thr 1925	Glu Arg Ser Arg Tyr 1930	Gln Arg Glu 1935
Ile Asp Lys Leu Arg Gln Arg 1940	Pro Tyr Gly Ser His 1945	Arg Glu Thr 1950
Gln Thr Glu Cys Glu Trp Thr 1955	Val Asp Thr Ser Lys 1960	Leu Val Phe 1965
Asp Gly Leu Arg Lys Lys Val 1970	Thr Ala Met Gln Leu 1975	Tyr Glu Cys 1980
Gln Leu Ile Asp Lys Thr Thr 1985	Leu Asp Lys Leu Leu 1990	Lys Gly Lys 1995
Lys Ser Val Glu Glu Val Ala 2000	Ser Glu Ile Gln Pro 2005	Phe Leu Arg 2010
Gly Ala Gly Ser Ile Ala Gly 2015	Ala Ser Ala Ser Pro 2020	Lys Glu Lys 2025
Tyr Ser Leu Val Glu Ala Lys 2030	Arg Lys Lys Leu Ile 2035	Ser Pro Glu 2040
Ser Thr Val Met Leu Leu Glu 2045	Ala Gln Ala Ala Thr 2050	Gly Gly Ile 2055
Ile Asp Pro His Arg Asn Glu 2060	Lys Leu Thr Val Asp 2065	Ser Ala Ile 2070
Ala Arg Asp Leu Ile Asp Phe 2075	Asp Asp Arg Gln Gln 2080	Ile Tyr Ala 2085
Ala Glu Lys Ala Ile Thr Gly 2090	Phe Asp Asp Pro Phe 2095	Ser Gly Lys 2100
Thr Val Ser Val Ser Glu Ala 2105	Ile Lys Lys Asn Leu 2110	Ile Asp Arg 2115
Glu Thr Gly Met Arg Leu Leu 2120	Glu Ala Gln Ile Ala 2125	Ser Gly Gly 2130
Val Val Asp Pro Val Asn Ser 2135	Val Phe Leu Pro Lys 2140	Asp Val Ala 2145

Leu Ala Arg Gly Leu Ile Asp Arg Asp Leu Tyr Arg Ser Leu Asn
 2150 2155 2160
 Asp Pro Arg Asp Ser Gln Lys Asn Phe Val Asp Pro Val Thr Lys
 2165 2170 2175
 Lys Lys Val Ser Tyr Val Gln Leu Lys Glu Arg Cys Arg Ile Glu
 2180 2185 2190
 Pro His Thr Gly Leu Leu Leu Leu Ser Val Gln Lys Arg Ser Met
 2195 2200 2205
 Ser Phe Gln Gly Ile Arg Gln Pro Val Thr Val Thr Glu Leu Val
 2210 2215 2220
 Asp Ser Gly Ile Leu Arg Pro Ser Thr Val Asn Glu Leu Glu Ser
 2225 2230 2235
 Gly Gln Ile Ser Tyr Asp Glu Val Gly Glu Arg Ile Lys Asp Phe
 2240 2245 2250
 Leu Gln Gly Ser Ser Cys Ile Ala Gly Ile Tyr Asn Glu Thr Thr
 2255 2260 2265
 Lys Gln Lys Leu Gly Ile Tyr Glu Ala Met Lys Ile Gly Leu Val
 2270 2275 2280
 Arg Pro Gly Thr Ala Leu Glu Leu Leu Glu Ala Gln Ala Ala Thr
 2285 2290 2295
 Gly Phe Ile Val Asp Pro Val Ser Asn Leu Arg Leu Pro Val Glu
 2300 2305 2310
 Glu Ala Tyr Lys Arg Gly Leu Val Gly Ile Glu Phe Lys Glu Lys
 2315 2320 2325
 Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Asn Asp Pro Glu
 2330 2335 2340
 Thr Gly Asn Ile Ile Ser Leu Phe Gln Ala Met Asn Lys Glu Leu
 2345 2350 2355
 Ile Glu Lys Gly His Gly Ile Arg Leu Leu Glu Ala Gln Ile Ala
 2360 2365 2370
 Thr Gly Gly Ile Ile Asp Pro Lys Glu Ser His Arg Leu Pro Val
 2375 2380 2385
 Asp Ile Ala Tyr Lys Arg Gly Tyr Phe Asn Glu Glu Leu Ser Glu
 2390 2395 2400
 Ile Leu Ser Asp Pro Ser Asp Asp Thr Lys Gly Phe Phe Asp Pro
 2405 2410 2415
 Asn Thr Glu Glu Asn Leu Thr Tyr Leu Gln Leu Lys Glu Arg Cys
 2420 2425 2430
 Ile Lys Asp Glu Glu Thr Gly Leu Cys Leu Leu Pro Leu Lys Glu
 2435 2440 2445

Lys Lys Lys Gln Val Gln Thr Ser Gln Lys Asn Thr Leu Arg Lys
 2450 2455 2460
 Arg Arg Val Val Ile Val Asp Pro Glu Thr Asn Lys Glu Met Ser
 2465 2470 2475
 Val Gln Glu Ala Tyr Lys Lys Gly Leu Ile Asp Tyr Glu Thr Phe
 2480 2485 2490
 Lys Glu Leu Cys Glu Gln Glu Cys Glu Trp Glu Glu Ile Thr Ile
 2495 2500 2505
 Thr Gly Ser Asp Gly Ser Thr Arg Val Val Leu Val Asp Arg Lys
 2510 2515 2520
 Thr Gly Ser Gln Tyr Asp Ile Gln Asp Ala Ile Asp Lys Gly Leu
 2525 2530 2535
 Val Asp Arg Lys Phe Phe Asp Gln Tyr Arg Ser Gly Ser Leu Ser
 2540 2545 2550
 Leu Thr Gln Phe Ala Asp Met Ile Ser Leu Lys Asn Gly Val Gly
 2555 2560 2565
 Thr Ser Ser Ser Met Gly Ser Gly Val Ser Asp Asp Val Phe Ser
 2570 2575 2580
 Ser Ser Arg His Glu Ser Val Ser Lys Ile Ser Thr Ile Ser Ser
 2585 2590 2595
 Val Arg Asn Leu Thr Ile Arg Ser Ser Ser Phe Ser Asp Thr Leu
 2600 2605 2610
 Glu Glu Ser Ser Pro Ile Ala Ala Ile Phe Asp Thr Glu Asn Leu
 2615 2620 2625
 Glu Lys Ile Ser Ile Thr Glu Gly Ile Glu Arg Gly Ile Val Asp
 2630 2635 2640
 Ser Ile Thr Gly Gln Arg Leu Leu Glu Ala Gln Ala Cys Thr Gly
 2645 2650 2655
 Gly Ile Ile His Pro Thr Thr Gly Gln Lys Leu Ser Leu Gln Asp
 2660 2665 2670
 Ala Val Ser Gln Gly Val Ile Asp Gln Asp Met Ala Thr Ser Val
 2675 2680 2685
 Lys Pro Ala Gln Lys Ala Phe Ile Gly Phe Glu Gly Val Lys Gly
 2690 2695 2700
 Lys Lys Lys Met Ser Ala Ala Glu Ala Val Lys Glu Lys Trp Leu
 2705 2710 2715
 Pro Tyr Glu Ala Gly Gln Arg Phe Leu Glu Phe Gln Tyr Leu Thr
 2720 2725 2730
 Gly Gly Leu Val Asp Pro Glu Val His Gly Arg Ile Ser Thr Glu
 2735 2740 2745

Glu Ala Ile Arg Lys Gly Phe Ile Asp Gly Arg Ala Ala Gln Arg
2750 2755 2760

Leu Gln Asp Thr Ser Ser Tyr Ala Lys Ile Leu Thr Cys Pro Lys
2765 2770 2775

Thr Lys Leu Lys Ile Ser Tyr Lys Asp Ala Ile Asn Arg Ser Met
2780 2785 2790

Val Glu Asp Ile Thr Gly Leu Arg Leu Leu Glu Ala Ala Ser Val
2795 2800 2805

Ser Ser Lys Gly Leu Pro Ser Pro Tyr Asn Met Ser Ser Ala Pro
2810 2815 2820

Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg
2825 2830 2835

Ser Gly Ser Arg Ser Gly Ser Arg Arg Gly Ser Phe Asp Ala Thr
2840 2845 2850

Gly Asn Ser Ser Tyr Ser Tyr Ser Tyr Ser Phe Ser Ser Ser Ser
2855 2860 2865

Ile Gly His
2870

<210> 113
<211> 381
<212> PRT
<213> Homo sapiens

<400> 113

Met Trp Arg Leu Met Ser Arg Phe Asn Ala Phe Lys Arg Thr Asn Thr
1 5 10 15

Ile Leu His His Leu Arg Met Ser Lys His Thr Asp Ala Ala Glu Glu
20 25 30

Val Leu Leu Glu Lys Lys Gly Cys Ala Gly Val Ile Thr Leu Asn Arg
35 40 45

Pro Lys Phe Leu Asn Ala Leu Thr Leu Asn Met Ile Arg Gln Ile Tyr
50 55 60

Pro Gln Leu Lys Lys Trp Glu Gln Asp Pro Glu Thr Phe Val Ile Ile
65 70 75 80

Ile Lys Gly Ala Gly Gly Lys Ala Phe Cys Ala Gly Gly Asp Ile Arg
85 90 95

Val Ile Ser Glu Ala Glu Lys Ala Lys Gln Lys Ile Ala Pro Val Phe
100 105 110

Phe Arg Glu Glu Tyr Met Leu Asn Asn Ala Val Gly Ser Cys Gln Lys
115 120 125

Pro Tyr Val Ala Leu Ile His Gly Ile Thr Met Gly Gly Gly Val Gly
130 135 140

Leu Ser Val His Gly Gln Phe Arg Val Ala Thr Glu Lys Cys Leu Phe
145 150 155 160

Ala Met Pro Glu Thr Ala Ile Gly Leu Phe Pro Asp Val Gly Gly Gly
165 170 175

Tyr Phe Phe Ala Thr Thr Pro Arg Lys Thr Trp Leu Leu Pro Cys Ile
180 185 190

Asn Gly Phe Arg Leu Lys Gly Arg Asp Val Tyr Arg Ala Gly Ile Ala
195 200 205

Thr His Phe Val Asp Ser Glu Lys Leu Ala Met Leu Glu Glu Asp Leu
210 215 220

Leu Ala Leu Lys Ser Pro Ser Lys Glu Asn Ile Ala Ser Val Leu Glu
225 230 235 240

Asn Tyr His Thr Glu Ser Lys Ile Asp Arg Asp Lys Ser Phe Ile Leu
245 250 255

Glu Glu His Met Asp Lys Ile Asn Ser Cys Phe Ser Ala Asn Thr Val
260 265 270

Glu Glu Ile Ile Glu Asn Leu Gln Gln Asp Gly Ser Ser Phe Ala Leu
275 280 285

Glu Gln Leu Lys Val Ile Asn Lys Met Ser Pro Thr Ser Leu Lys Ile
290 295 300

Thr Leu Arg Gln Leu Met Glu Gly Ser Ser Lys Thr Leu Gln Glu Val
305 310 315 320

Leu Thr Met Glu Tyr Arg Leu Ser Gln Ala Cys Met Arg Gly His Asp
325 330 335

Phe His Glu Gly Val Arg Ala Val Leu Ile Asp Lys Asp Gln Ser Pro
340 345 350

Lys Trp Lys Pro Ala Asp Leu Lys Glu Val Thr Glu Glu Asp Leu Asn
355 360 365

Asn His Phe Lys Ser Leu Gly Ser Ser Asp Leu Lys Phe
370 375 380

<210> 114
<211> 1139
<212> PRT
<213> Homo sapiens

<400> 114

Met Gln Thr Pro Glu Val Pro Ala Glu Arg Ser Pro Arg Arg Arg Ser
1 5 10 15

Ile Ser Gly Thr Ser Thr Ser Glu Lys Pro Asn Ser Met Asp Thr Ala
20 25 30

Asn Thr Ser Pro Phe Lys Val Pro Gly Phe Phe Ser Lys Arg Leu Lys
35 40 45

Gly Ser Ile Lys Arg Thr Lys Ser Gln Ser Lys Leu Asp Arg Asn Thr
 50 55 60
 Ser Phe Arg Leu Pro Ser Leu Arg Ser Thr Asp Asp Arg Ser Arg Gly
 65 70 75 80
 Leu Pro Lys Leu Lys Glu Ser Arg Ser His Glu Ser Leu Leu Ser Pro
 85 90 95
 Cys Ser Thr Val Glu Cys Leu Asp Leu Gly Arg Gly Glu Pro Val Ser
 100 105 110
 Val Lys Pro Leu His Ser Ser Ile Leu Gly Gln Asp Phe Cys Phe Glu
 115 120 125
 Val Thr Tyr Leu Ser Gly Ser Lys Cys Phe Ser Cys Asn Ser Ala Ser
 130 135 140
 Glu Arg Asp Lys Trp Met Glu Asn Leu Arg Arg Thr Val Gln Pro Asn
 145 150 155 160
 Lys Asp Asn Cys Arg Arg Ala Glu Asn Val Leu Arg Leu Trp Ile Ile
 165 170 175
 Glu Ala Lys Asp Leu Ala Pro Lys Lys Lys Tyr Phe Cys Glu Leu Cys
 180 185 190
 Leu Asp Asp Thr Leu Phe Ala Arg Thr Thr Ser Lys Thr Lys Ala Asp
 195 200 205
 Asn Ile Phe Trp Gly Glu His Phe Glu Phe Phe Ser Leu Pro Pro Leu
 210 215 220
 His Ser Ile Thr Val His Ile Tyr Lys Asp Val Glu Lys Lys Lys Lys
 225 230 235 240
 Lys Asp Lys Asn Asn Tyr Val Gly Leu Val Asn Ile Pro Thr Ala Ser
 245 250 255
 Val Thr Gly Arg Gln Phe Val Glu Lys Trp Tyr Pro Val Ser Thr Pro
 260 265 270
 Thr Pro Asn Lys Gly Lys Thr Gly Gly Pro Ser Ile Arg Ile Lys Ser
 275 280 285
 Arg Phe Gln Thr Ile Thr Ile Leu Pro Met Glu Gln Tyr Lys Glu Phe
 290 295 300
 Ala Glu Phe Val Thr Ser Asn Tyr Thr Met Leu Cys Ser Val Leu Glu
 305 310 315 320
 Pro Val Ile Ser Val Arg Asn Lys Glu Glu Leu Ala Cys Ala Leu Val
 325 330 335
 His Ile Leu Gln Ser Thr Gly Arg Ala Lys Asp Phe Leu Thr Asp Leu
 340 345 350
 Val Met Ser Glu Val Asp Arg Cys Gly Glu His Asp Val Leu Ile Phe

355	360	365
Arg Glu Asn Thr Ile Ala Thr Lys Ser Ile Glu Glu Tyr Leu Lys Leu 370 375 380		
Val Gly Gln Gln Tyr Leu His Asp Ala Leu Gly Glu Phe Ile Lys Ala 385 390 395 400		
Leu Tyr Glu Ser Asp Glu Asn Cys Glu Val Asp Pro Ser Lys Cys Ser 405 410 415		
Ser Ser Glu Leu Ile Asp His Gln Ser Asn Leu Lys Met Cys Cys Glu 420 425 430		
Leu Ala Phe Cys Lys Ile Ile Asn Ser Tyr Cys Val Phe Pro Arg Glu 435 440 445		
Leu Lys Glu Val Phe Ala Ser Trp Lys Gln Gln Cys Leu Asn Arg Gly 450 455 460		
Lys Gln Asp Ile Ser Glu Arg Leu Ile Ser Ala Ser Leu Phe Leu Arg 465 470 475 480		
Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu Phe Asn Leu Met Gln 485 490 495		
Glu Tyr Pro Asp Asp Arg Thr Ser Arg Thr Leu Thr Leu Ile Ala Lys 500 505 510		
Val Ile Gln Asn Leu Ala Asn Phe Ala Lys Phe Gly Asn Lys Glu Glu 515 520 525		
Tyr Met Ala Phe Met Asn Asp Phe Leu Glu His Glu Trp Gly Gly Met 530 535 540		
Lys Arg Phe Leu Leu Glu Ile Ser Asn Pro Asp Thr Ile Ser Asn Thr 545 550 555 560		
Pro Gly Phe Asp Gly Tyr Ile Asp Leu Gly Arg Glu Leu Ser Val Leu 565 570 575		
His Ser Leu Leu Trp Glu Val Val Ser Gln Leu Asp Lys Gly Glu Asn 580 585 590		
Ser Phe Leu Gln Ala Thr Val Ala Lys Leu Gly Pro Leu Pro Arg Val 595 600 605		
Leu Ala Asp Ile Thr Lys Ser Leu Thr Asn Pro Thr Pro Ile Gln Gln 610 615 620		
Gln Leu Arg Arg Phe Thr Glu His Asn Ser Ser Pro Asn Val Ser Gly 625 630 635 640		
Ser Leu Ser Ser Gly Leu Gln Lys Ile Phe Glu Asp Pro Thr Asp Ser 645 650 655		
Asp Leu His Lys Leu Lys Ser Pro Ser Gln Asp Asn Thr Asp Ser Tyr 660 665 670		

Phe Arg Gly Lys Thr Leu Leu Leu Val Gln Gln Ala Ser Ser Gln Ser
 675 680 685
 Met Thr Tyr Ser Glu Lys Asp Glu Arg Glu Ser Ser Leu Pro Asn Gly
 690 695 700
 Arg Ser Val Ser Leu Met Asp Leu Gln Asp Thr His Ala Ala Gln Val
 705 710 715 720
 Glu His Ala Ser Val Met Leu Asp Val Pro Ile Arg Leu Thr Gly Ser
 725 730 735
 Gln Leu Ser Ile Thr Gln Val Ala Ser Ile Lys Gln Leu Arg Glu Thr
 740 745 750
 Gln Ser Thr Pro Gln Ser Ala Pro Gln Val Arg Arg Pro Leu His Pro
 755 760 765
 Ala Leu Asn Gln Pro Gly Gly Leu Gln Pro Leu Ser Phe Gln Asn Pro
 770 775 780
 Val Tyr His Leu Asn Asn Pro Ile Pro Ala Met Pro Lys Ala Ser Ile
 785 790 795 800
 Asp Ser Ser Leu Glu Asn Leu Ser Thr Ala Ser Ser Arg Ser Gln Ser
 805 810 815
 Asn Ser Glu Asp Phe Lys Leu Ser Gly Pro Ser Asn Ser Ser Met Glu
 820 825 830
 Asp Phe Thr Lys Arg Ser Thr Gln Ser Glu Asp Phe Ser Arg Arg His
 835 840 845
 Thr Val Pro Asp Arg His Ile Pro Leu Ala Leu Pro Arg Gln Asn Ser
 850 855 860
 Thr Gly Gln Ala Gln Ile Arg Lys Val Asp Gln Gly Gly Leu Gly Ala
 865 870 875 880
 Arg Ala Lys Ala Pro Pro Ser Leu Pro His Ser Ala Ser Leu Arg Ser
 885 890 895
 Thr Gly Ser Met Ser Val Val Ser Ala Ala Leu Val Ala Glu Pro Val
 900 905 910
 Gln Asn Gly Ser Arg Ser Arg Gln Gln Ser Ser Ser Ser Arg Glu Ser
 915 920 925
 Pro Val Pro Lys Val Arg Ala Ile Gln Arg Gln Gln Thr Gln Gln Val
 930 935 940
 Gln Ser Pro Val Asp Ser Ala Thr Met Ser Pro Val Glu Arg Thr Ala
 945 950 955 960
 Ala Trp Val Leu Asn Asn Gly Gln Tyr Glu Glu Asp Val Glu Glu Thr
 965 970 975
 Glu Gln Asn Leu Asp Glu Ala Lys His Ala Glu Lys Tyr Glu Gln Glu
 980 985 990

Ile Thr Lys Leu Lys Glu Arg Leu Arg Val Ser Ser Arg Arg Leu Glu
995 1000 1005

Glu Tyr Glu Arg Arg Leu Leu Val Gln Glu Gln Gln Met Gln Lys
1010 1015 1020

Leu Leu Leu Glu Tyr Lys Ala Arg Leu Glu Asp Ser Glu Glu Arg
1025 1030 1035

Leu Arg Arg Gln Gln Glu Glu Lys Asp Ser Gln Met Lys Ser Ile
1040 1045 1050

Ile Ser Arg Leu Met Ala Val Glu Glu Glu Leu Lys Lys Asp His
1055 1060 1065

Ala Glu Met Gln Ala Val Ile Asp Ala Lys Gln Lys Ile Ile Asp
1070 1075 1080

Ala Gln Glu Lys Arg Ile Val Ser Leu Asp Ser Ala Asn Thr Arg
1085 1090 1095

Leu Met Ser Ala Leu Thr Gln Val Lys Glu Arg Tyr Ser Met Gln
1100 1105 1110

Val Arg Asn Gly Ile Ser Pro Thr Asn Pro Thr Lys Leu Ser Ile
1115 1120 1125

Thr Glu Asn Gly Glu Phe Lys Asn Ser Ser Cys
1130 1135

<210> 115
<211> 165
<212> PRT
<213> Homo sapiens

<400> 115

Met Thr Leu Glu Glu Phe Ser Ala Gly Glu Gln Lys Thr Glu Arg Met
1 5 10 15

Asp Lys Val Gly Asp Ala Leu Glu Glu Val Leu Ser Lys Ala Leu Ser
20 25 30

Gln Arg Thr Ile Thr Val Gly Val Tyr Glu Ala Ala Lys Leu Leu Asn
35 40 45

Val Asp Pro Asp Asn Val Val Leu Cys Leu Leu Ala Ala Asp Glu Asp
50 55 60

Asp Asp Arg Asp Val Ala Leu Gln Ile His Phe Thr Leu Ile Gln Ala
65 70 75 80

Phe Cys Cys Glu Asn Asp Ile Asn Ile Leu Arg Val Ser Asn Pro Gly
85 90 95

Arg Leu Ala Glu Leu Leu Leu Leu Glu Thr Asp Ala Gly Pro Ala Ala
100 105 110

Ser Glu Gly Ala Glu Gln Pro Pro Asp Leu His Cys Val Leu Val Thr
115 120 125

```

Asn Pro His Ser Ser Gln Trp Lys Asp Pro Ala Leu Ser Gln Leu Ile
130          135          140

Cys Phe Cys Arg Glu Ser Arg Tyr Met Asp Gln Trp Val Pro Val Ile
145          150          155          160

Asn Leu Pro Glu Arg
165

<210> 116
<211> 1163
<212> PRT
<213> Homo sapiens

<400> 116

Met Thr Arg Thr Arg Ala Ala Leu Leu Leu Phe Thr Ala Leu Ala Thr
1      5      10      15

Ser Leu Gly Phe Asn Leu Asp Thr Glu Glu Leu Thr Ala Phe Arg Val
20      25      30

Asp Ser Ala Gly Phe Gly Asp Ser Val Val Gln Tyr Ala Asn Ser Trp
35      40      45

Val Val Val Gly Ala Pro Gln Lys Ile Thr Ala Ala Asn Gln Thr Gly
50      55      60

Gly Leu Tyr Gln Cys Gly Tyr Ser Thr Gly Ala Cys Glu Pro Ile Gly
65      70      75      80

Leu Gln Val Pro Pro Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
85      90      95

Ala Ser Thr Thr Ser Pro Ser Gln Leu Leu Ala Cys Gly Pro Thr Val
100     105     110

His His Glu Cys Gly Arg Asn Met Tyr Leu Thr Gly Leu Cys Phe Leu
115     120     125

Leu Gly Pro Thr Gln Leu Thr Gln Arg Leu Pro Val Ser Arg Gln Glu
130     135     140

Cys Pro Arg Gln Glu Gln Asp Ile Val Phe Leu Ile Asp Gly Ser Gly
145     150     155     160

Ser Ile Ser Ser Arg Asn Phe Ala Thr Met Met Asn Phe Val Arg Ala
165     170     175

Val Ile Ser Gln Phe Gln Arg Pro Ser Thr Gln Phe Ser Leu Met Gln
180     185     190

Phe Ser Asn Lys Phe Gln Thr His Leu Thr Phe Glu Glu Phe Arg Arg
195     200     205

Thr Ser Asn Pro Leu Ser Leu Leu Ala Ser Val His Gln Leu Gln Gly
210     215     220

Phe Thr Tyr Thr Ala Thr Ala Ile Gln Asn Val Val His Arg Leu Phe
225     230     235     240

```

His Ala Ser Tyr Gly Ala Arg Arg Asp Ala Thr Lys Ile Leu Ile Val
 245 250 255
 Ile Thr Asp Gly Lys Lys Glu Gly Asp Thr Leu Asp Tyr Lys Asp Val
 260 265 270
 Ile Pro Met Ala Asp Ala Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val
 275 280 285
 Gly Leu Ala Phe Gln Asn Arg Asn Ser Trp Lys Glu Leu Asn Asp Ile
 290 295 300
 Ala Ser Lys Pro Ser Gln Glu His Ile Phe Lys Val Glu Asp Phe Asp
 305 310 315 320
 Ala Leu Lys Asp Ile Gln Thr Gln Leu Arg Glu Lys Ile Phe Pro Ile
 325 330 335
 Glu Gly Thr Glu Thr Thr Ser Ser Ser Phe Glu Leu Glu Met Ala
 340 345 350
 Gln Glu Gly Phe Ser Ala Val Phe Thr Pro Asp Gly Pro Val Leu Gly
 355 360 365
 Ala Val Gly Ser Phe Thr Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro
 370 375 380
 Asn Met Ser Pro Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp Met
 385 390 395 400
 Arg Asp Ser Tyr Leu Gly Tyr Ser Thr Glu Leu Ala Leu Trp Lys Gly
 405 410 415
 Val Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Thr Gly Lys
 420 425 430
 Ala Val Ile Phe Thr Gln Val Ser Arg Gln Trp Arg Met Lys Ala Glu
 435 440 445
 Val Thr Gly Thr Gln Ile Gly Ser Tyr Phe Gly Pro Ser Leu Cys Ser
 450 455 460
 Val Asp Val Asp Ser Asp Gly Ser Thr Asp Leu Val Leu Ile Gly Pro
 465 470 475 480
 Pro His Tyr Tyr Glu Gln Thr Arg Gly Ala Gln Val Ser Val Cys Pro
 485 490 495
 Leu Pro Arg Gly Trp Arg Arg Trp Trp Cys Asp Ala Val Leu Tyr Gly
 500 505 510
 Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
 515 520 525
 Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Val Ile Gly Ala Pro
 530 535 540
 Gly Glu Glu Glu Asn Arg Gly Ala Val Tyr Leu Phe His Gly Val Leu
 545 550 555 560

Gly Pro Ser Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Gln
 565 570 575
 Leu Ser Ser Arg Leu Gln Tyr Phe Gly Gln Ala Leu Ser Gly Gly Gln
 580 585 590
 Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Arg Gly
 595 600 605
 Gln Val Leu Leu Leu Arg Thr Arg Pro Val Leu Trp Val Gly Val Ser
 610 615 620
 Met Gln Phe Ile Pro Ala Glu Ile Pro Arg Ser Ala Phe Glu Cys Arg
 625 630 635 640
 Glu Gln Val Val Ser Glu Gln Thr Leu Val Gln Ser Asn Ile Cys Leu
 645 650 655
 Tyr Ile Asp Lys Arg Ser Lys Asn Leu Leu Gly Ser Arg Asp Leu Gln
 660 665 670
 Ser Ser Val Thr Leu Asp Leu Ala Leu Asp Pro Gly Arg Leu Ser Pro
 675 680 685
 Arg Ala Thr Phe Gln Glu Thr Lys Asn Arg Ser Leu Ser Arg Val Arg
 690 695 700
 Val Leu Gly Leu Lys Ala His Cys Glu Asn Phe Asn Leu Leu Leu Pro
 705 710 715 720
 Ser Cys Val Glu Asp Ser Val Thr Pro Ile Thr Leu Arg Leu Asn Phe
 725 730 735
 Thr Leu Val Gly Lys Pro Leu Leu Ala Phe Arg Asn Leu Arg Pro Met
 740 745 750
 Leu Ala Ala Asp Ala Gln Arg Tyr Phe Thr Ala Ser Leu Pro Phe Glu
 755 760 765
 Lys Asn Cys Gly Ala Asp His Ile Cys Gln Asp Asn Leu Gly Ile Ser
 770 775 780
 Phe Ser Phe Pro Gly Leu Lys Ser Leu Leu Val Gly Ser Asn Leu Glu
 785 790 795 800
 Leu Asn Ala Glu Val Met Val Trp Asn Asp Gly Glu Asp Ser Tyr Gly
 805 810 815
 Thr Thr Ile Thr Phe Ser His Pro Ala Gly Leu Ser Tyr Arg Tyr Val
 820 825 830
 Ala Glu Gly Gln Lys Gln Gly Gln Leu Arg Ser Leu His Leu Thr Cys
 835 840 845
 Asp Ser Ala Pro Val Gly Ser Gln Gly Thr Trp Ser Thr Ser Cys Arg
 850 855 860
 Ile Asn His Leu Ile Phe Arg Gly Gly Ala Gln Ile Thr Phe Leu Ala

865	870	875	880
Thr Phe Asp Val Ser Pro Lys Ala Val Leu Gly Asp Arg Leu Leu Leu	885	890	895
Thr Ala Asn Val Ser Ser Glu Asn Asn Thr Pro Arg Thr Ser Lys Thr	900	905	910
Thr Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Thr Val Val	915	920	925
Ser Ser His Glu Gln Phe Thr Lys Tyr Leu Asn Phe Ser Glu Ser Glu	930	935	940
Glu Lys Glu Ser His Val Ala Met His Arg Tyr Gln Val Asn Asn Leu	945	950	955
Gly Gln Arg Asp Leu Pro Val Ser Ile Asn Phe Trp Val Pro Val Glu	965	970	975
Leu Asn Gln Glu Ala Val Trp Met Asp Val Glu Val Ser Leu Pro Gln	980	985	990
Asn Pro Ser Leu Arg Cys Ser Ser Glu Lys Ile Ala Gly Pro Ala Ser	995	1000	1005
Asp Phe Leu Ala His Ile Gln Lys Asn Pro Val Leu Asp Cys Ser	1010	1015	1020
Ile Ala Gly Cys Leu Arg Phe Arg Cys Asp Val Pro Ser Phe Ser	1025	1030	1035
Val Gln Glu Glu Leu Asp Phe Thr Leu Lys Gly Asn Leu Ser Phe	1040	1045	1050
Gly Trp Val Arg Gln Ile Leu Gln Lys Lys Val Ser Val Val Ser	1055	1060	1065
Val Ala Glu Ile Thr Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro	1070	1075	1080
Gly Gln Glu Ala Phe Met Arg Ala Gln Thr Thr Thr Val Leu Glu	1085	1090	1095
Lys Tyr Lys Val His Asn Pro Thr Pro Leu Ile Val Gly Ser Ser	1100	1105	1110
Ile Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Val Leu Tyr	1115	1120	1125
Lys Val Gly Phe Phe Lys Arg Gln Tyr Lys Glu Met Met Glu Glu	1130	1135	1140
Ala Asn Gly Gln Ile Ala Pro Glu Asn Gly Thr Gln Thr Pro Ser	1145	1150	1155
Pro Pro Ser Glu Lys	1160		

<210> 117
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 117

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1 5 10 15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
 20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
 35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
 50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
 65 70 75 80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
 85 90 95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
 100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
 115 120 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
 130 135 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
 145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
 165 170 175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
 180 185 190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
 195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
 210 215 220

Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
 225 230 235 240

Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
 245 250 255

Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
 260 265 270

Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
 275 280 285

Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys
 290 295 300
 Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser
 305 310 315 320
 Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
 325 330 335
 <210> 118
 <211> 1251
 <212> PRT
 <213> Homo sapiens
 <400> 118
 Met Glu Leu Ser Asp Val Arg Cys Leu Thr Gly Ser Glu Glu Leu Tyr
 1 5 10 15
 Thr Ile His Pro Thr Pro Pro Ala Gly Asp Gly Arg Ser Ala Ser Arg
 20 25 30
 Pro Gln Arg Leu Leu Trp Gln Thr Ala Val Arg His Ile Thr Glu Gln
 35 40 45
 Arg Phe Ile His Gly His Arg Gly Gly Ser Gly Ser Gly Ser Gly Gly
 50 55 60
 Ser Gly Lys Ala Ser Asp Pro Ala Gly Gly Gly Pro Asn His His Ala
 65 70 75 80
 Pro Gln Leu Ser Gly Asp Ser Ala Leu Pro Leu Tyr Ser Leu Gly Pro
 85 90 95
 Gly Glu Arg Ala His Ser Thr Cys Gly Thr Lys Val Phe Pro Glu Arg
 100 105 110
 Ser Gly Ser Gly Ser Ala Ser Gly Ser Gly Gly Gly Gly Asp Leu Gly
 115 120 125
 Phe Leu His Leu Asp Cys Ala Pro Ser Asn Ser Asp Phe Phe Leu Asn
 130 135 140
 Gly Gly Tyr Ser Tyr Arg Gly Val Ile Phe Pro Thr Leu Arg Asn Ser
 145 150 155 160
 Phe Lys Ser Arg Asp Leu Glu Arg Leu Tyr Gln Arg Tyr Phe Leu Gly
 165 170 175
 Gln Arg Arg Lys Ser Glu Val Val Met Asn Val Leu Asp Val Leu Thr
 180 185 190
 Lys Leu Thr Leu Leu Val Leu His Leu Ser Leu Ala Ser Ala Pro Met
 195 200 205
 Asp Pro Leu Lys Gly Ile Leu Leu Gly Phe Phe Thr Gly Ile Glu Val
 210 215 220
 Val Ile Cys Ala Leu Val Val Val Arg Lys Asp Thr Thr Ser His Thr
 225 230 235 240

Tyr Leu Gln Tyr Ser Gly Val Val Thr Trp Val Ala Met Thr Thr Gln
 245 250 255
 Ile Leu Ala Ala Gly Leu Gly Tyr Gly Leu Leu Gly Asp Gly Ile Gly
 260 265 270
 Tyr Val Leu Phe Thr Leu Phe Ala Thr Tyr Ser Met Leu Pro Leu Pro
 275 280 285
 Leu Thr Trp Ala Ile Leu Ala Gly Leu Gly Thr Ser Leu Leu Gln Val
 290 295 300
 Ile Leu Gln Val Val Ile Pro Arg Leu Ala Val Ile Ser Ile Asn Gln
 305 310 315 320
 Val Val Ala Gln Ala Val Leu Phe Met Cys Met Asn Thr Ala Gly Ile
 325 330 335
 Phe Ile Ser Tyr Leu Ser Asp Arg Ala Gln Arg Gln Ala Phe Leu Glu
 340 345 350
 Thr Arg Arg Cys Val Glu Ala Arg Leu Arg Leu Glu Thr Glu Asn Gln
 355 360 365
 Arg Gln Glu Arg Leu Val Leu Ser Val Leu Pro Arg Phe Val Val Leu
 370 375 380
 Glu Met Ile Asn Asp Met Thr Asn Val Glu Asp Glu His Leu Gln His
 385 390 395 400
 Gln Phe His Arg Ile Tyr Ile His Arg Tyr Glu Asn Val Ser Ile Leu
 405 410 415
 Phe Ala Asp Val Lys Gly Phe Thr Asn Leu Ser Thr Thr Leu Ser Ala
 420 425 430
 Gln Glu Leu Val Arg Met Leu Asn Glu Leu Phe Ala Arg Phe Asp Arg
 435 440 445
 Leu Ala His Glu His His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys
 450 455 460
 Tyr Tyr Cys Val Ser Gly Leu Pro Glu Pro Arg Gln Asp His Ala His
 465 470 475 480
 Cys Cys Val Glu Met Gly Leu Ser Met Ile Lys Thr Ile Arg Tyr Val
 485 490 495
 Arg Ser Arg Thr Lys His Asp Val Asp Met Arg Ile Gly Ile His Ser
 500 505 510
 Gly Ser Val Leu Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp
 515 520 525
 Val Trp Ser Trp Asp Val Asp Ile Ala Asn Lys Leu Glu Ser Gly Gly
 530 535 540
 Ile Pro Gly Arg Ile His Ile Ser Lys Ala Thr Leu Asp Cys Leu Asn
 545 550 555 560

Gly Asp Tyr Asn Val Glu Glu Gly His Gly Lys Glu Arg Asn Glu Phe
 565 570 575
 Leu Arg Lys His Asn Ile Glu Thr Tyr Leu Ile Lys Gln Pro Glu Asp
 580 585 590
 Ser Leu Leu Ser Leu Pro Glu Asp Ile Val Lys Glu Ser Val Ser Ser
 595 600 605
 Ser Asp Arg Arg Asn Ser Gly Ala Thr Phe Thr Glu Gly Ser Trp Ser
 610 615 620
 Pro Glu Leu Pro Phe Asp Asn Ile Val Gly Lys Gln Asn Thr Leu Ala
 625 630 635 640
 Ala Leu Thr Arg Asn Ser Ile Asn Leu Leu Pro Asn His Leu Ala Gln
 645 650 655
 Ala Leu His Val Gln Ser Gly Pro Glu Glu Ile Asn Lys Arg Ile Glu
 660 665 670
 His Thr Ile Asp Leu Arg Ser Gly Asp Lys Leu Arg Arg Glu His Ile
 675 680 685
 Lys Pro Phe Ser Leu Met Phe Lys Asp Ser Ser Leu Glu His Lys Tyr
 690 695 700
 Ser Gln Met Arg Asp Glu Val Phe Lys Ser Asn Leu Val Cys Ala Phe
 705 710 715 720
 Ile Val Leu Leu Phe Ile Thr Ala Ile Gln Ser Leu Leu Pro Ser Ser
 725 730 735
 Arg Val Met Pro Met Thr Ile Gln Phe Ser Ile Leu Ile Met Leu His
 740 745 750
 Ser Ala Leu Val Leu Ile Thr Thr Ala Glu Asp Tyr Lys Cys Leu Pro
 755 760 765
 Leu Ile Leu Arg Lys Thr Cys Cys Trp Ile Asn Glu Thr Tyr Leu Ala
 770 775 780
 Arg Asn Val Ile Ile Phe Ala Ser Ile Leu Ile Asn Phe Leu Gly Ala
 785 790 795 800
 Ile Leu Asn Ile Leu Trp Cys Asp Phe Asp Lys Ser Ile Pro Leu Lys
 805 810 815
 Asn Leu Thr Phe Asn Ser Ser Ala Val Phe Thr Asp Ile Cys Ser Tyr
 820 825 830
 Pro Glu Tyr Phe Val Phe Thr Gly Val Leu Ala Met Val Thr Cys Ala
 835 840 845
 Val Phe Leu Arg Leu Asn Ser Val Leu Lys Leu Ala Val Leu Leu Ile
 850 855 860
 Met Ile Ala Ile Tyr Ala Leu Leu Thr Glu Thr Val Tyr Ala Gly Leu
 865 870 875 880

Phe Leu Arg Tyr Asp Asn Leu Asn His Ser Gly Glu Asp Phe Leu Gly
 885 890 895
 Thr Lys Glu Val Ser Leu Leu Leu Met Ala Met Phe Leu Leu Ala Val
 900 905 910
 Phe Tyr His Gly Gln Gln Leu Glu Tyr Thr Ala Arg Leu Asp Phe Leu
 915 920 925
 Trp Arg Val Gln Ala Lys Glu Glu Ile Asn Glu Met Lys Glu Leu Arg
 930 935 940
 Glu His Asn Glu Asn Met Leu Arg Asn Ile Leu Pro Ser His Val Ala
 945 950 955 960
 Arg His Phe Leu Glu Lys Asp Arg Asp Asn Glu Glu Leu Tyr Ser Gln
 965 970 975
 Ser Tyr Asp Ala Val Gly Val Met Phe Ala Ser Ile Pro Gly Phe Ala
 980 985 990
 Asp Phe Tyr Ser Gln Thr Glu Met Asn Asn Gln Gly Val Glu Cys Leu
 995 1000 1005
 Arg Leu Leu Asn Glu Ile Ile Ala Asp Phe Asp Glu Leu Leu Gly
 1010 1015 1020
 Glu Asp Arg Phe Gln Asp Ile Glu Lys Ile Lys Thr Ile Gly Ser
 1025 1030 1035
 Thr Tyr Met Ala Val Ser Gly Leu Ser Pro Glu Lys Gln Gln Cys
 1040 1045 1050
 Glu Asp Lys Trp Gly His Leu Cys Ala Leu Ala Asp Phe Ser Leu
 1055 1060 1065
 Ala Leu Thr Glu Ser Ile Gln Glu Ile Asn Lys His Ser Phe Asn
 1070 1075 1080
 Asn Phe Glu Leu Arg Ile Gly Ile Ser His Gly Ser Val Val Ala
 1085 1090 1095
 Gly Val Ile Gly Ala Lys Lys Pro Gln Tyr Asp Ile Trp Gly Lys
 1100 1105 1110
 Thr Val Asn Leu Ala Ser Arg Met Asp Ser Thr Gly Val Ser Gly
 1115 1120 1125
 Arg Ile Gln Val Pro Glu Glu Thr Tyr Leu Ile Leu Lys Asp Gln
 1130 1135 1140
 Gly Phe Ala Phe Asp Tyr Arg Gly Glu Ile Tyr Val Lys Gly Ile
 1145 1150 1155
 Ser Glu Gln Glu Gly Lys Ile Lys Thr Tyr Phe Leu Leu Gly Arg
 1160 1165 1170
 Val Gln Pro Asn Pro Phe Ile Leu Pro Pro Arg Arg Leu Pro Gly

1175 1180 1185
 Gln Tyr Ser Leu Ala Ala Val Val Leu Gly Leu Val Gln Ser Leu
 1190 1195 1200
 Asn Arg Gln Arg Gln Lys Gln Leu Leu Asn Glu Asn Asn Asn Thr
 1205 1210 1215
 Gly Ile Ile Lys Gly His Tyr Asn Arg Arg Thr Leu Leu Ser Pro
 1220 1225 1230
 Ser Gly Thr Glu Pro Gly Ala Gln Ala Glu Gly Thr Asp Lys Ser
 1235 1240 1245
 Asp Leu Pro
 1250
 <210> 119
 <211> 143
 <212> PRT
 <213> Homo sapiens
 <400> 119
 Met Gly Lys Cys Arg Gly Leu Arg Thr Ala Arg Lys Leu Arg Ser His
 1 5 10 15
 Arg Arg Asp Gln Lys Trp His Asp Lys Gln Tyr Lys Lys Ala His Leu
 20 25 30
 Gly Thr Ala Leu Lys Ala Asn Pro Phe Gly Gly Ala Ser His Ala Lys
 35 40 45
 Gly Ile Val Leu Glu Lys Val Gly Val Glu Ala Lys Gln Pro Asn Ser
 50 55 60
 Ala Ile Arg Lys Cys Val Arg Val Gln Leu Ile Lys Asn Gly Lys Lys
 65 70 75 80
 Ile Thr Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Ile Glu Glu
 85 90 95
 Asn Asp Glu Val Leu Val Ala Gly Phe Gly Arg Lys Gly His Ala Val
 100 105 110
 Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ala Asn Val
 115 120 125
 Ser Leu Leu Ala Leu Tyr Lys Gly Lys Lys Glu Arg Pro Arg Ser
 130 135 140
 <210> 120
 <211> 144
 <212> PRT
 <213> Homo sapiens
 <400> 120
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu Leu
 1 5 10 15
 Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
 20 25 30

Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys Asn Thr Leu
35 40 45

Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala Phe Phe Cys Val
50 55 60

Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu Gly Leu Asn Met Pro
65 70 75 80

Leu Leu Ala Tyr His Ile Trp Arg Tyr Met Ser Arg Pro Val Met Ser
85 90 95

Gly Pro Gly Leu Tyr Asp Pro Thr Thr Ile Met Asn Ala Asp Ile Leu
100 105 110

Ala Tyr Cys Gln Lys Glu Gly Trp Cys Lys Leu Ala Phe Tyr Leu Leu
115 120 125

Ala Phe Phe Tyr Tyr Leu Tyr Gly Met Ile Tyr Val Leu Val Ser Ser
130 135 140

<210> 121

<211> 1516

<212> PRT

<213> Homo sapiens

<400> 121

Met Ala Pro Ala Lys Ala Thr Asn Val Val Arg Leu Leu Leu Gly Ser
1 5 10 15

Thr Ala Leu Trp Leu Ser Gln Leu Gly Ser Gly Thr Val Ala Ala Ser
20 25 30

Lys Ser Val Thr Ala His Leu Ala Ala Lys Trp Pro Glu Thr Pro Leu
35 40 45

Leu Leu Glu Ala Ser Glu Phe Met Ala Glu Glu Ser Asn Glu Lys Phe
50 55 60

Trp Gln Phe Leu Glu Thr Val Gln Glu Leu Ala Ile Tyr Lys Gln Thr
65 70 75 80

Glu Ser Asp Tyr Ser Tyr Tyr Asn Leu Ile Leu Lys Lys Ala Gly Gln
85 90 95

Phe Leu Asp Asn Leu His Ile Asn Leu Leu Lys Phe Ala Phe Ser Ile
100 105 110

Arg Ala Tyr Ser Pro Ala Ile Gln Met Phe Gln Gln Ile Ala Ala Asp
115 120 125

Glu Pro Pro Pro Asp Gly Cys Asn Ala Phe Val Val Ile His Lys Lys
130 135 140

His Thr Cys Lys Ile Asn Glu Ile Lys Lys Leu Leu Lys Lys Ala Ala
145 150 155 160

Ser Arg Thr Arg Pro Tyr Leu Phe Lys Gly Asp His Lys Phe Pro Thr
165 170 175

Asn Lys Glu Asn Leu Pro Val Val Ile Leu Tyr Ala Glu Met Gly Thr
 180 185 190
 Arg Thr Phe Ser Ala Phe His Lys Val Leu Ser Glu Lys Ala Gln Asn
 195 200 205
 Glu Glu Ile Leu Tyr Val Leu Arg His Tyr Ile Gln Lys Pro Ser Ser
 210 215 220
 Arg Lys Met Tyr Leu Ser Gly Tyr Gly Val Glu Leu Ala Ile Lys Ser
 225 230 235 240
 Thr Glu Tyr Lys Ala Leu Asp Asp Thr Gln Val Lys Thr Val Thr Asn
 245 250 255
 Thr Thr Val Glu Asp Glu Thr Glu Thr Asn Glu Val Gln Gly Phe Leu
 260 265 270
 Phe Gly Lys Leu Lys Glu Ile Tyr Ser Asp Leu Arg Asp Asn Leu Thr
 275 280 285
 Ala Phe His Lys Tyr Leu Ile Glu Ser Asn Lys Gln Met Met Pro Leu
 290 295 300
 Lys Val Trp Glu Leu Gln Asp Leu Ser Phe Gln Ala Ala Ser Gln Ile
 305 310 315 320
 Met Ser Thr Pro Val Tyr Asp Ala Ile Lys Leu Met Lys Asp Ile Ser
 325 330 335
 Gln Asn Phe Pro Ile Lys Ala Arg Ser Leu Thr Arg Ile Ala Val Asn
 340 345 350
 Gln His Met Arg Glu Glu Ile Lys Glu Asn Gln Lys Asp Leu Gln Val
 355 360 365
 Arg Phe Lys Ile Gln Pro Gly Asp Ala Arg Leu Phe Ile Asn Gly Leu
 370 375 380
 Arg Val Asp Met Asp Val Tyr Asp Ala Phe Ser Ile Leu Asp Met Leu
 385 390 395 400
 Lys Leu Glu Gly Lys Met Met Asn Gly Leu Arg Asn Leu Gly Ile Asn
 405 410 415
 Gly Glu Asp Met Ser Lys Phe Leu Lys Leu Asn Ser His Ile Trp Glu
 420 425 430
 Tyr Thr Tyr Val Leu Asp Ile Arg His Ser Ser Ile Met Trp Ile Asn
 435 440 445
 Asp Leu Glu Asn Asp Asp Leu Tyr Ile Thr Trp Pro Thr Ser Cys Gln
 450 455 460
 Lys Leu Leu Lys Pro Val Phe Pro Gly Ser Val Pro Ser Ile Arg Arg
 465 470 475 480
 Asn Phe His Asn Leu Val Leu Phe Ile Asp Pro Ala Gln Glu Tyr Thr

485										490					495				
Leu	Asp	Phe	Ile	Lys	Leu	Ala	Asp	Val	Phe	Tyr	Ser	His	Glu	Val	Pro				
			500					505					510						
Leu	Arg	Ile	Gly	Phe	Val	Phe	Ile	Leu	Asn	Thr	Asp	Asp	Glu	Val	Asp				
		515					520					525							
Gly	Ala	Asn	Asp	Ala	Gly	Val	Ala	Leu	Trp	Arg	Ala	Phe	Asn	Tyr	Ile				
	530					535					540								
Ala	Glu	Glu	Phe	Asp	Ile	Ser	Glu	Ala	Phe	Ile	Ser	Ile	Val	His	Met				
545					550					555					560				
Tyr	Gln	Lys	Val	Lys	Lys	Asp	Gln	Asn	Ile	Leu	Thr	Val	Asp	Asn	Val				
				565					570					575					
Lys	Ser	Val	Leu	Gln	Asn	Thr	Phe	Pro	His	Ala	Asn	Ile	Trp	Asp	Ile				
			580					585					590						
Leu	Gly	Ile	His	Ser	Lys	Tyr	Asp	Glu	Glu	Arg	Lys	Ala	Gly	Ala	Ser				
		595					600					605							
Phe	Tyr	Lys	Met	Thr	Gly	Leu	Gly	Pro	Leu	Pro	Gln	Ala	Leu	Tyr	Asn				
	610					615					620								
Gly	Glu	Pro	Phe	Lys	His	Glu	Glu	Met	Asn	Ile	Lys	Glu	Leu	Lys	Met				
625					630					635					640				
Ala	Val	Leu	Gln	Arg	Met	Met	Asp	Ala	Ser	Val	Tyr	Leu	Gln	Arg	Glu				
				645					650					655					
Val	Phe	Leu	Gly	Thr	Leu	Asn	Asp	Arg	Thr	Asn	Ala	Ile	Asp	Phe	Leu				
			660					665					670						
Met	Asp	Arg	Asn	Asn	Val	Val	Pro	Arg	Ile	Asn	Thr	Leu	Ile	Leu	Arg				
		675					680					685							
Thr	Asn	Gln	Gln	Tyr	Leu	Asn	Leu	Ile	Ser	Thr	Ser	Val	Thr	Ala	Asp				
	690					695					700								
Val	Glu	Asp	Phe	Ser	Thr	Phe	Phe	Phe	Leu	Asp	Ser	Gln	Asp	Lys	Ser				
705					710					715					720				
Ala	Val	Ile	Ala	Lys	Asn	Met	Tyr	Tyr	Leu	Thr	Gln	Asp	Asp	Glu	Ser				
				725					730					735					
Ile	Ile	Ser	Ala	Val	Thr	Leu	Trp	Ile	Ile	Ala	Asp	Phe	Asp	Lys	Pro				
			740					745					750						
Ser	Gly	Arg	Lys	Leu	Leu	Phe	Asn	Ala	Leu	Lys	His	Met	Lys	Thr	Ser				
		755					760					765							
Val	His	Ser	Arg	Leu	Gly	Ile	Ile	Tyr	Asn	Pro	Thr	Ser	Lys	Ile	Asn				
	770					775					780								
Glu	Glu	Asn	Thr	Ala	Ile	Ser	Arg	Gly	Ile	Leu	Ala	Ala	Phe	Leu	Thr				
785					790					795					800				

Gln Lys Asn Met Phe Leu Arg Ser Phe Leu Gly Gln Leu Ala Lys Glu
 805 810 815
 Glu Ile Ala Thr Thr Ile Tyr Ser Gly Asp Lys Ile Lys Thr Phe Leu
 820 825 830
 Ile Glu Gly Met Asp Lys Asn Ala Phe Glu Lys Lys Tyr Asn Thr Val
 835 840 845
 Gly Val Asn Ile Phe Arg Thr His Gln Leu Phe Cys Gln Asp Val Leu
 850 855 860
 Lys Leu Arg Pro Gly Glu Met Gly Ile Val Ser Asn Gly Arg Phe Leu
 865 870 875 880
 Gly Pro Leu Asp Glu Asp Phe Tyr Ala Glu Asp Phe Tyr Leu Leu Glu
 885 890 895
 Lys Ile Thr Phe Ser Asn Leu Gly Glu Lys Ile Lys Gly Ile Val Glu
 900 905 910
 Asn Met Gly Ile Asn Ala Asn Asn Met Ser Asp Phe Ile Met Lys Val
 915 920 925
 Asp Ala Leu Met Ser Ser Val Pro Lys Arg Ala Ser Arg Tyr Asp Val
 930 935 940
 Thr Phe Leu Arg Glu Asn His Ser Val Ile Lys Thr Asn Pro Gln Glu
 945 950 955 960
 Asn Asp Met Phe Phe Asn Val Ile Ala Ile Val Asp Leu Leu Ala Arg
 965 970 975
 Glu Ala Gln Lys Met Ala Gln Leu Leu Val Val Leu Gly Lys Ile Ile
 980 985 990
 Asn Leu Lys Ile Lys Leu Phe Met Asn Cys Arg Gly Arg Leu Ser Glu
 995 1000 1005
 Ala Pro Leu Glu Ser Phe Tyr Arg Phe Val Leu Glu Pro Glu Leu
 1010 1015 1020
 Met Ser Gly Ala Asn Asp Val Ser Ser Leu Gly Pro Val Ala Lys
 1025 1030 1035
 Phe Leu Asp Ile Pro Glu Ser Pro Leu Leu Ile Leu Asn Met Ile
 1040 1045 1050
 Thr Pro Glu Gly Trp Leu Val Glu Thr Val His Ser Asn Cys Asp
 1055 1060 1065
 Leu Asp Asn Ile His Leu Lys Asp Thr Glu Lys Thr Ala Thr Ala
 1070 1075 1080
 Gly Tyr Glu Leu Glu Tyr Leu Leu Leu Glu Gly Gln Cys Phe Asp
 1085 1090 1095
 Lys Val Thr Glu Gln Pro Pro Arg Gly Leu Gln Phe Thr Leu Gly
 1100 1105 1110

Thr Lys Asn Lys Pro Ala Val Val Asp Thr Ile Val Met Ala His
 1115 1120 1125
 His Gly Tyr Phe Gln Leu Lys Ala Asn Pro Gly Ala Trp Ile Leu
 1130 1135 1140
 Arg Leu His Gln Gly Lys Ser Glu Asp Ile Tyr Gln Ile Val Gly
 1145 1150 1155
 His Glu Gly Thr Asp Ser Gln Ala Asp Leu Glu Asp Ile Ile Val
 1160 1165 1170
 Val Leu Asn Ser Phe Lys Ser Lys Ile Leu Lys Val Lys Val Lys
 1175 1180 1185
 Lys Glu Thr Asp Lys Ile Lys Glu Asp Ile Leu Thr Asp Glu Asp
 1190 1195 1200
 Glu Lys Thr Lys Gly Leu Trp Asp Ser Ile Lys Ser Phe Thr Val
 1205 1210 1215
 Ser Leu His Lys Glu Asn Lys Lys Glu Lys Asp Val Leu Asn Ile
 1220 1225 1230
 Phe Ser Val Ala Ser Gly His Leu Tyr Glu Arg Phe Leu Arg Ile
 1235 1240 1245
 Met Met Leu Ser Val Leu Arg Asn Thr Lys Thr Pro Val Lys Phe
 1250 1255 1260
 Trp Leu Leu Lys Asn Tyr Leu Ser Pro Thr Phe Lys Glu Val Ile
 1265 1270 1275
 Pro His Met Ala Lys Glu Tyr Gly Phe Arg Tyr Glu Leu Val Gln
 1280 1285 1290
 Tyr Arg Trp Pro Arg Trp Leu Arg Gln Gln Thr Glu Arg Gln Arg
 1295 1300 1305
 Ile Ile Trp Gly Tyr Lys Ile Leu Phe Leu Asp Val Leu Phe Pro
 1310 1315 1320
 Leu Ala Val Asp Lys Ile Ile Phe Val Asp Ala Asp Gln Ile Val
 1325 1330 1335
 Arg His Asp Leu Lys Glu Leu Arg Asp Phe Asp Leu Asp Gly Ala
 1340 1345 1350
 Pro Tyr Gly Tyr Thr Pro Phe Cys Asp Ser Arg Arg Glu Met Asp
 1355 1360 1365
 Gly Tyr Arg Phe Trp Lys Thr Gly Tyr Trp Ala Ser His Leu Leu
 1370 1375 1380
 Arg Arg Lys Tyr His Ile Ser Ala Leu Tyr Val Val Asp Leu Lys
 1385 1390 1395
 Lys Phe Arg Arg Ile Gly Ala Gly Asp Arg Leu Arg Ser Gln Tyr
 1400 1405 1410

Gln Ala Leu Ser Gln Asp Pro Asn Ser Leu Ser Asn Leu Asp Gln
 1415 1420 1425
 Asp Leu Pro Asn Asn Met Ile Tyr Gln Val Ala Ile Lys Ser Leu
 1430 1435 1440
 Pro Gln Asp Trp Leu Trp Cys Glu Thr Trp Cys Asp Asp Glu Ser
 1445 1450 1455
 Lys Gln Arg Ala Lys Thr Ile Asp Leu Cys Asn Asn Pro Lys Thr
 1460 1465 1470
 Lys Glu Ser Lys Leu Lys Ala Ala Ala Arg Ile Val Pro Glu Trp
 1475 1480 1485
 Val Glu Tyr Asp Ala Glu Ile Arg Gln Leu Leu Asp His Leu Glu
 1490 1495 1500
 Asn Lys Lys Gln Asp Thr Ile Leu Thr His Asp Glu Leu
 1505 1510 1515
 <210> 122
 <211> 798
 <212> PRT
 <213> Homo sapiens
 <400> 122
 Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys
 1 5 10 15
 Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala
 20 25 30
 Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys
 35 40 45
 Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys
 50 55 60
 Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro Pro Asp Asp Ile
 65 70 75 80
 Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr
 85 90 95
 Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His
 100 105 110
 Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro
 115 120 125
 Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp
 130 135 140
 Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu
 145 150 155 160
 Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile
 165 170 175

Thr Ser Asp Phe Arg Ile Gly Phe Gly Ser Phe Val Glu Lys Thr Val
 180 185 190
 Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr
 195 200 205
 Ser Glu Gln Asn Cys Thr Thr Pro Phe Ser Tyr Lys Asn Val Leu Ser
 210 215 220
 Leu Thr Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys Gln Arg
 225 230 235 240
 Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met
 245 250 255
 Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg
 260 265 270
 Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly
 275 280 285
 Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu
 290 295 300
 Asn Asn Met Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala
 305 310 315 320
 His Leu Val Gln Lys Leu Ser Glu Asn Asn Ile Gln Thr Ile Phe Ala
 325 330 335
 Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile
 340 345 350
 Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile
 355 360 365
 Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu
 370 375 380
 Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser Tyr
 385 390 395 400
 Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser
 405 410 415
 Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ser
 420 425 430
 Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu
 435 440 445
 Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys
 450 455 460
 Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly
 465 470 475 480
 Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val

Page 176

<210> 123
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 123

```

Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly
1          5          10          15

Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu
20          25          30

Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp
35          40          45

Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His
50          55          60

Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser
65          70          75          80

Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr
85          90          95

Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala
100         105         110

Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr
115         120         125

Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp
130         135         140

Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser
145         150         155         160

Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val
165         170         175

Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr
180         185         190

Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala
195         200         205

Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly
210         215         220

Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys
225         230         235         240

Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile
245         250         255

Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln
260         265         270

Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser
275         280         285

```

Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp
 290 295 300

Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg
 305 310 315

<210> 124
 <211> 351
 <212> PRT
 <213> Homo sapiens

<400> 124

Met Gln Arg Ala Leu Pro Gly Ala Arg Gln His Leu Gly Ala Ile Leu
 1 5 10 15

Ala Ser Ala Ser Val Val Val Lys Ala Leu Cys Ala Ala Val Leu Phe
 20 25 30

Leu Tyr Leu Leu Ser Phe Ala Val Asp Thr Gly Cys Leu Ala Val Thr
 35 40 45

Pro Gly Tyr Leu Phe Pro Pro Asn Phe Trp Ile Trp Thr Leu Ala Thr
 50 55 60

His Gly Leu Met Glu Gln His Val Trp Asp Val Ala Ile Ser Leu Thr
 65 70 75 80

Thr Val Val Val Ala Gly Arg Leu Leu Glu Pro Leu Trp Gly Ala Leu
 85 90 95

Glu Leu Leu Ile Phe Phe Ser Val Val Asn Val Ser Val Gly Leu Leu
 100 105 110

Gly Ala Phe Ala Tyr Leu Leu Thr Tyr Met Ala Ser Phe Asn Leu Val
 115 120 125

Tyr Leu Phe Thr Val Arg Ile His Gly Ala Leu Gly Phe Leu Gly Gly
 130 135 140

Val Leu Val Ala Leu Lys Gln Thr Met Gly Asp Cys Val Val Leu Arg
 145 150 155 160

Val Pro Gln Val Arg Val Ser Val Met Pro Met Leu Leu Leu Ala Leu
 165 170 175

Leu Leu Leu Leu Arg Leu Ala Thr Leu Leu Gln Ser Pro Ala Leu Ala
 180 185 190

Ser Tyr Gly Phe Gly Leu Leu Ser Ser Trp Val Tyr Leu Arg Phe Tyr
 195 200 205

Gln Arg His Ser Arg Gly Arg Gly Asp Met Ala Asp His Phe Ala Phe
 210 215 220

Ala Thr Phe Phe Pro Glu Ile Leu Gln Pro Val Val Gly Leu Leu Ala
 225 230 235 240

Asn Leu Val His Ser Leu Leu Val Lys Val Lys Ile Cys Gln Lys Thr
 245 250 255

Val Lys Arg Tyr Asp Val Gly Ala Pro Ser Ser Ile Thr Ile Ser Leu
260 265 270

Pro Gly Thr Asp Pro Gln Asp Ala Glu Arg Arg Arg Gln Leu Ala Leu
275 280 285

Lys Ala Leu Asn Glu Arg Leu Lys Arg Val Glu Asp Gln Ser Ile Trp
290 295 300

Pro Ser Met Asp Asp Asp Glu Glu Glu Ser Gly Ala Lys Val Asp Ser
305 310 315 320

Pro Leu Pro Ser Asp Lys Ala Pro Thr Pro Pro Gly Lys Gly Ala Ala
325 330 335

Pro Glu Ser Ser Leu Ile Thr Phe Glu Ala Ala Pro Pro Thr Leu
340 345 350

<210> 125
<211> 310
<212> PRT
<213> Homo sapiens

<400> 125

Met Arg Arg Ala Ala Leu Trp Leu Trp Leu Cys Ala Leu Ala Leu Ser
1 5 10 15

Leu Gln Leu Ala Leu Pro Gln Ile Val Ala Thr Asn Leu Pro Pro Glu
20 25 30

Asp Gln Asp Gly Ser Gly Asp Asp Ser Asp Asn Phe Ser Gly Ser Gly
35 40 45

Ala Gly Ala Leu Gln Asp Ile Thr Leu Ser Gln Gln Thr Pro Ser Thr
50 55 60

Trp Lys Asp Thr Gln Leu Leu Thr Ala Ile Pro Thr Ser Pro Glu Pro
65 70 75 80

Thr Gly Leu Glu Ala Thr Ala Ala Ser Thr Ser Thr Leu Pro Ala Gly
85 90 95

Glu Gly Pro Lys Glu Gly Glu Ala Val Val Leu Pro Glu Val Glu Pro
100 105 110

Gly Leu Thr Ala Arg Glu Gln Glu Ala Thr Pro Arg Pro Arg Glu Thr
115 120 125

Thr Gln Leu Pro Thr Thr His Gln Ala Ser Thr Thr Thr Ala Thr Thr
130 135 140

Ala Gln Glu Pro Ala Thr Ser His Pro His Arg Asp Met Gln Pro Gly
145 150 155 160

His His Glu Thr Ser Thr Pro Ala Gly Pro Ser Gln Ala Asp Leu His
165 170 175

Thr Pro His Thr Glu Asp Gly Gly Pro Ser Ala Thr Glu Arg Ala Ala
180 185 190

Glu Asp Gly Ala Ser Ser Gln Leu Pro Ala Ala Glu Gly Ser Gly Glu
195 200 205

Gln Asp Phe Thr Phe Glu Thr Ser Gly Glu Asn Thr Ala Val Val Ala
210 215 220

Val Glu Pro Asp Arg Arg Asn Gln Ser Pro Val Asp Gln Gly Ala Thr
225 230 235 240

Gly Ala Ser Gln Gly Leu Leu Asp Arg Lys Glu Val Leu Gly Gly Val
245 250 255

Ile Ala Gly Gly Leu Val Gly Leu Ile Phe Ala Val Cys Leu Val Gly
260 265 270

Phe Met Leu Tyr Arg Met Lys Lys Lys Asp Glu Gly Ser Tyr Ser Leu
275 280 285

Glu Glu Pro Lys Gln Ala Asn Gly Gly Ala Tyr Gln Lys Pro Thr Lys
290 295 300

Gln Glu Glu Phe Tyr Ala
305 310

<210> 126
<211> 2174
<212> PRT
<213> Homo sapiens

<400> 126

Met Ser Ala Ser Phe Val Pro Asn Gly Ala Ser Leu Glu Asp Cys His
1 5 10 15

Cys Asn Leu Phe Cys Leu Ala Asp Leu Thr Gly Ile Lys Trp Lys Lys
20 25 30

Tyr Val Trp Gln Gly Pro Thr Ser Ala Pro Ile Leu Phe Pro Val Thr
35 40 45

Glu Glu Asp Pro Ile Leu Ser Ser Phe Ser Arg Cys Leu Lys Ala Asp
50 55 60

Val Leu Gly Val Trp Arg Arg Asp Gln Arg Pro Gly Arg Arg Glu Leu
65 70 75 80

Trp Ile Phe Trp Trp Gly Glu Asp Pro Val Leu Leu Thr Leu Phe Thr
85 90 95

Met Thr Tyr Gln Lys Lys Lys Met Glu Cys Gly Arg Met Asp Phe Pro
100 105 110

Met Asn Ala Val Leu Cys Phe Ser Lys Ala Val His Asn Leu Leu Glu
115 120 125

Arg Cys Leu Met Asn Arg Asn Phe Val Arg Ile Gly Lys Trp Phe Val
130 135 140

Lys Pro Tyr Glu Lys Asp Glu Lys Pro Ile Asn Lys Ser Glu His Leu
145 150 155 160

Ser Cys Ser Phe Thr Phe Phe Leu His Gly Asp Ser Asn Val Cys Thr
 165 170 175
 Ser Val Glu Ile Asn Gln His Gln Pro Val Tyr Leu Leu Ser Glu Glu
 180 185 190
 His Ile Thr Leu Ala Gln Gln Ser Asn Ser Pro Phe Gln Val Ile Leu
 195 200 205
 Cys Pro Phe Gly Leu Asn Gly Thr Leu Thr Gly Gln Ala Phe Lys Met
 210 215 220
 Ser Asp Ser Ala Thr Lys Lys Leu Ile Gly Glu Trp Lys Gln Phe Tyr
 225 230 235 240
 Pro Ile Ser Cys Cys Leu Lys Glu Met Ser Glu Glu Lys Gln Glu Asp
 245 250 255
 Met Asp Trp Glu Asp Asp Ser Leu Ala Ala Val Glu Val Leu Val Ala
 260 265 270
 Gly Val Arg Met Ile Tyr Pro Ala Cys Phe Val Leu Val Pro Gln Ser
 275 280 285
 Asp Ile Pro Thr Pro Ser Pro Val Gly Ser Thr His Cys Ser Ser Ser
 290 295 300
 Cys Leu Gly Val His Gln Val Pro Ala Ser Thr Arg Asp Pro Ala Met
 305 310 315 320
 Ser Ser Val Thr Leu Thr Pro Pro Thr Ser Pro Glu Glu Val Gln Thr
 325 330 335
 Val Asp Pro Gln Ser Val Gln Lys Trp Val Lys Phe Ser Ser Val Ser
 340 345 350
 Asp Gly Phe Asn Ser Asp Ser Thr Ser His His Gly Gly Lys Ile Pro
 355 360 365
 Arg Lys Leu Ala Asn His Val Val Asp Arg Val Trp Gln Glu Cys Asn
 370 375 380
 Met Asn Arg Ala Gln Asn Lys Lys Lys Tyr Ser Ala Ser Ser Gly Gly
 385 390 395 400
 Leu Cys Glu Glu Ala Thr Ala Ala Lys Val Ala Ser Trp Asp Phe Val
 405 410 415
 Glu Ala Thr Gln Arg Thr Asn Cys Ser Cys Leu Arg His Lys Asn Leu
 420 425 430
 Lys Ser Arg Asn Ala Gly Gln Gln Gly Gln Ala Pro Ser Leu Gly Gln
 435 440 445
 Gln Gln Gln Ile Leu Pro Lys His Lys Thr Asn Glu Lys Gln Glu Lys
 450 455 460
 Ser Glu Glu Pro Gln Lys Arg Pro Leu Thr Pro Phe His His Arg Val
 465 470 475 480

Ser Val Ser Asp Asp Val Gly Met Asp Ala Asp Ser Ala Ser Gln Arg
 485 490 495
 Leu Val Ile Ser Ala Pro Asp Ser Gln Val Arg Phe Ser Asn Ile Arg
 500 505 510
 Thr Asn Asp Val Ala Lys Thr Pro Gln Met His Gly Thr Glu Met Ala
 515 520 525
 Asn Ser Pro Gln Pro Pro Pro Leu Ser Pro His Pro Cys Asp Val Val
 530 535 540
 Asp Glu Gly Val Thr Lys Thr Pro Ser Thr Pro Gln Ser Gln His Phe
 545 550 555 560
 Tyr Gln Met Pro Thr Pro Asp Pro Leu Val Pro Ser Lys Pro Met Glu
 565 570 575
 Asp Arg Ile Asp Ser Leu Ser Gln Ser Phe Pro Pro Gln Tyr Gln Glu
 580 585 590
 Ala Val Glu Pro Thr Val Tyr Val Gly Thr Ala Val Asn Leu Glu Glu
 595 600 605
 Asp Glu Ala Asn Ile Ala Trp Lys Tyr Tyr Lys Phe Pro Lys Lys Lys
 610 615 620
 Asp Val Glu Phe Leu Pro Pro Gln Leu Pro Ser Asp Lys Phe Lys Asp
 625 630 635 640
 Asp Pro Val Gly Pro Phe Gly Gln Glu Ser Val Thr Ser Val Thr Glu
 645 650 655
 Leu Met Val Gln Cys Lys Lys Pro Leu Lys Val Ser Asp Glu Leu Val
 660 665 670
 Gln Gln Tyr Gln Ile Lys Asn Gln Cys Leu Ser Ala Ile Ala Ser Asp
 675 680 685
 Ala Glu Gln Glu Pro Lys Ile Asp Pro Tyr Ala Phe Val Glu Gly Asp
 690 695 700
 Glu Glu Phe Leu Phe Pro Asp Lys Lys Asp Arg Gln Asn Ser Glu Arg
 705 710 715 720
 Glu Ala Gly Lys Lys His Lys Val Glu Asp Gly Thr Ser Ser Val Thr
 725 730 735
 Val Leu Ser His Glu Glu Asp Ala Met Ser Leu Phe Ser Pro Ser Ile
 740 745 750
 Lys Gln Asp Ala Pro Arg Pro Thr Ser His Ala Arg Pro Pro Ser Thr
 755 760 765
 Ser Leu Ile Tyr Asp Ser Asp Leu Ala Val Ser Tyr Thr Asp Leu Asp
 770 775 780
 Asn Leu Phe Asn Ser Asp Glu Asp Glu Leu Thr Pro Gly Ser Lys Arg
 785 790 795 800

Ser Ala Asn Gly Ser Asp Asp Lys Ala Ser Cys Lys Glu Ser Lys Thr
 805 810 815
 Gly Asn Leu Asp Pro Leu Ser Cys Ile Ser Thr Ala Asp Leu His Lys
 820 825 830
 Met Tyr Pro Thr Pro Pro Ser Leu Glu Gln His Ile Met Gly Phe Ser
 835 840 845
 Pro Met Asn Met Asn Asn Lys Glu Tyr Gly Ser Met Asp Thr Thr Pro
 850 855 860
 Gly Gly Thr Val Leu Glu Gly Asn Ser Ser Ser Ile Gly Ala Gln Phe
 865 870 875 880
 Lys Ile Glu Val Asp Glu Gly Phe Cys Ser Pro Lys Pro Ser Glu Ile
 885 890 895
 Lys Asp Phe Ser Tyr Val Tyr Lys Pro Glu Asn Cys Gln Ile Leu Val
 900 905 910
 Gly Cys Ser Met Phe Ala Pro Leu Lys Thr Leu Pro Ser Gln Tyr Leu
 915 920 925
 Pro Leu Ile Lys Leu Pro Glu Glu Cys Ile Tyr Arg Gln Ser Trp Thr
 930 935 940
 Val Gly Lys Leu Glu Leu Leu Ser Ser Gly Pro Ser Met Pro Phe Ile
 945 950 955 960
 Lys Glu Gly Asp Gly Ser Asn Met Asp Gln Glu Tyr Gly Thr Ala Tyr
 965 970 975
 Thr Pro Gln Thr His Thr Ser Cys Gly Met Pro Pro Ser Ser Ala Pro
 980 985 990
 Pro Ser Asn Ser Gly Ala Gly Ile Leu Pro Ser Pro Ser Thr Pro Arg
 995 1000 1005
 Phe Pro Thr Pro Arg Thr Pro Arg Thr Pro Arg Thr Pro Arg Gly
 1010 1015 1020
 Ala Gly Gly Pro Ala Ser Ala Gln Gly Ser Val Lys Tyr Glu Asn
 1025 1030 1035
 Ser Asp Leu Tyr Ser Pro Ala Ser Thr Pro Ser Thr Cys Arg Pro
 1040 1045 1050
 Leu Asn Ser Val Glu Pro Ala Thr Val Pro Ser Ile Pro Glu Ala
 1055 1060 1065
 His Ser Leu Tyr Val Asn Leu Ile Leu Ser Glu Ser Val Met Asn
 1070 1075 1080
 Leu Phe Lys Asp Cys Asn Ser Asp Ser Cys Cys Ile Cys Val Cys
 1085 1090 1095
 Asn Met Asn Ile Lys Gly Ala Asp Val Gly Val Tyr Ile Pro Asp

1100	1105	1110
Pro Thr Gln Glu Ala Gln Tyr 1115	Arg Cys Thr Cys Gly 1120	Phe Ser Ala 1125
Val Met Asn Arg Lys Phe Gly 1130	Asn Asn Ser Gly 1135	Leu Phe Leu Glu 1140
Asp Glu Leu Asp Ile Ile Gly 1145	Arg Asn Thr Asp Cys 1150	Gly Lys Glu 1155
Ala Glu Lys Arg Phe Glu Ala 1160	Leu Arg Ala Thr Ser 1165	Ala Glu His 1170
Val Asn Gly Gly Leu Lys Glu 1175	Ser Glu Lys Leu Ser 1180	Asp Asp Leu 1185
Ile Leu Leu Leu Gln Asp Gln 1190	Cys Thr Asn Leu Phe 1195	Ser Pro Phe 1200
Gly Ala Ala Asp Gln Asp Pro 1205	Phe Pro Lys Ser Gly 1210	Val Ile Ser 1215
Asn Trp Val Arg Val Glu Glu 1220	Arg Asp Cys Cys Asn 1225	Asp Cys Tyr 1230
Leu Ala Leu Glu His Gly Arg 1235	Gln Phe Met Asp Asn 1240	Met Ser Gly 1245
Gly Lys Val Asp Glu Ala Leu 1250	Val Lys Ser Ser Cys 1255	Leu His Pro 1260
Trp Ser Lys Arg Asn Asp Val 1265	Ser Met Gln Cys Ser 1270	Gln Asp Ile 1275
Leu Arg Met Leu Leu Ser Leu 1280	Gln Pro Val Leu Gln 1285	Asp Ala Ile 1290
Gln Lys Lys Arg Thr Val Arg 1295	Pro Trp Gly Val Gln 1300	Gly Pro Leu 1305
Thr Trp Gln Gln Phe His Lys 1310	Met Ala Gly Arg Gly 1315	Ser Tyr Gly 1320
Thr Asp Glu Ser Pro Glu Pro 1325	Leu Pro Ile Pro Thr 1330	Phe Leu Leu 1335
Gly Tyr Asp Tyr Asp Tyr Leu 1340	Val Leu Ser Pro Phe 1345	Ala Leu Pro 1350
Tyr Trp Glu Arg Leu Met Leu 1355	Glu Pro Tyr Gly Ser 1360	Gln Arg Asp 1365
Ile Ala Tyr Val Val Leu Cys 1370	Pro Glu Asn Glu Ala 1375	Leu Leu Asn 1380
Gly Ala Lys Ser Phe Phe Arg 1385	Asp Leu Thr Ala Ile 1390	Tyr Glu Ser 1395

Cys Arg Leu Gly Gln His Arg Pro Val Ser Arg Leu Leu Thr Asp
 1400 1405 1410
 Gly Ile Met Arg Val Gly Ser Thr Ala Ser Lys Lys Leu Ser Glu
 1415 1420 1425
 Lys Leu Val Ala Glu Trp Phe Ser Gln Ala Ala Asp Gly Asn Asn
 1430 1435 1440
 Glu Ala Phe Ser Lys Leu Lys Leu Tyr Ala Gln Val Cys Arg Tyr
 1445 1450 1455
 Asp Leu Gly Pro Tyr Leu Ala Ser Leu Pro Leu Asp Ser Ser Leu
 1460 1465 1470
 Leu Ser Gln Pro Asn Leu Val Ala Pro Thr Ser Gln Ser Leu Ile
 1475 1480 1485
 Thr Pro Pro Gln Met Thr Asn Thr Gly Asn Ala Asn Thr Pro Ser
 1490 1495 1500
 Ala Thr Leu Ala Ser Ala Ala Ser Ser Thr Met Thr Val Thr Ser
 1505 1510 1515
 Gly Val Ala Ile Ser Thr Ser Val Ala Thr Ala Asn Ser Thr Leu
 1520 1525 1530
 Thr Thr Ala Ser Thr Ser Ser Ser Ser Ser Ser Asn Leu Asn Ser
 1535 1540 1545
 Gly Val Ser Ser Asn Lys Leu Pro Ser Phe Pro Pro Phe Gly Ser
 1550 1555 1560
 Met Asn Ser Asn Ala Ala Gly Ser Met Ser Thr Gln Ala Asn Thr
 1565 1570 1575
 Val Gln Ser Gly Gln Leu Gly Gly Gln Gln Thr Ser Ala Leu Gln
 1580 1585 1590
 Thr Ala Gly Ile Ser Gly Glu Ser Ser Ser Leu Pro Thr Gln Pro
 1595 1600 1605
 His Pro Asp Val Ser Glu Ser Thr Met Asp Arg Asp Lys Val Gly
 1610 1615 1620
 Ile Pro Thr Asp Gly Asp Ser His Ala Val Thr Tyr Pro Pro Ala
 1625 1630 1635
 Ile Val Val Tyr Ile Ile Asp Pro Phe Thr Tyr Glu Asn Thr Asp
 1640 1645 1650
 Glu Ser Thr Asn Ser Ser Ser Val Trp Thr Leu Gly Leu Leu Arg
 1655 1660 1665
 Cys Phe Leu Glu Met Val Gln Thr Leu Pro Pro His Ile Lys Ser
 1670 1675 1680
 Thr Val Ser Val Gln Ile Ile Pro Cys Gln Tyr Leu Leu Gln Pro
 1685 1690 1695

Val Lys His Glu Asp Arg Glu Ile Tyr Pro Gln His Leu Lys Ser
 1700 1705 1710
 Leu Ala Phe Ser Ala Phe Thr Gln Cys Arg Arg Pro Leu Pro Thr
 1715 1720 1725
 Ser Thr Asn Val Lys Thr Leu Thr Gly Phe Gly Pro Gly Leu Ala
 1730 1735 1740
 Met Glu Thr Ala Leu Arg Ser Pro Asp Arg Pro Glu Cys Ile Arg
 1745 1750 1755
 Leu Tyr Ala Pro Pro Phe Ile Leu Ala Pro Val Lys Asp Lys Gln
 1760 1765 1770
 Thr Glu Leu Gly Glu Thr Phe Gly Glu Ala Gly Gln Lys Tyr Asn
 1775 1780 1785
 Val Leu Phe Val Gly Tyr Cys Leu Ser His Asp Gln Arg Trp Ile
 1790 1795 1800
 Leu Ala Ser Cys Thr Asp Leu Tyr Gly Glu Leu Leu Glu Thr Cys
 1805 1810 1815
 Ile Ile Asn Ile Asp Val Pro Asn Arg Ala Arg Arg Lys Lys Ser
 1820 1825 1830
 Ser Ala Arg Lys Phe Gly Leu Gln Lys Leu Trp Glu Trp Cys Leu
 1835 1840 1845
 Gly Leu Val Gln Met Ser Ser Leu Pro Trp Arg Val Val Ile Gly
 1850 1855 1860
 Arg Leu Gly Arg Ile Gly His Gly Glu Leu Lys Asp Trp Ser Cys
 1865 1870 1875
 Leu Leu Ser Arg Arg Asn Leu Gln Ser Leu Ser Lys Arg Leu Lys
 1880 1885 1890
 Asp Met Cys Arg Met Cys Gly Ile Ser Ala Ala Asp Ser Pro Ser
 1895 1900 1905
 Ile Leu Ser Ala Cys Leu Val Ala Met Glu Pro Gln Gly Ser Phe
 1910 1915 1920
 Val Ile Met Pro Asp Ser Val Ser Thr Gly Ser Val Phe Gly Arg
 1925 1930 1935
 Ser Thr Thr Leu Asn Met Gln Thr Ser Gln Leu Asn Thr Pro Gln
 1940 1945 1950
 Asp Thr Ser Cys Thr His Ile Leu Val Phe Pro Thr Ser Ala Ser
 1955 1960 1965
 Val Gln Val Ala Ser Ala Thr Tyr Thr Thr Glu Asn Leu Asp Leu
 1970 1975 1980
 Ala Phe Asn Pro Asn Asn Asp Gly Ala Asp Gly Met Gly Ile Phe
 1985 1990 1995

Asp Leu Leu Asp Thr Gly Asp Asp Leu Asp Pro Asp Ile Ile Asn
 2000 2005 2010
 Ile Leu Pro Ala Ser Pro Thr Gly Ser Pro Val His Ser Pro Gly
 2015 2020 2025
 Ser His Tyr Pro His Gly Gly Asp Ala Gly Lys Gly Gln Ser Thr
 2030 2035 2040
 Asp Arg Leu Leu Ser Thr Glu Pro His Glu Glu Val Pro Asn Ile
 2045 2050 2055
 Leu Gln Gln Pro Leu Ala Leu Gly Tyr Phe Val Ser Thr Ala Lys
 2060 2065 2070
 Ala Gly Pro Leu Pro Asp Trp Phe Trp Ser Ala Cys Pro Gln Ala
 2075 2080 2085
 Gln Tyr Gln Cys Pro Leu Phe Leu Lys Ala Ser Leu His Leu His
 2090 2095 2100
 Val Pro Ser Val Gln Ser Asp Glu Leu Leu His Ser Lys His Ser
 2105 2110 2115
 His Pro Leu Asp Ser Asn Gln Thr Ser Asp Val Leu Arg Phe Val
 2120 2125 2130
 Leu Glu Gln Tyr Asn Ala Leu Ser Trp Leu Thr Cys Asp Pro Ala
 2135 2140 2145
 Thr Gln Asp Arg Arg Ser Cys Leu Pro Ile His Phe Val Val Leu
 2150 2155 2160
 Asn Gln Leu Tyr Asn Phe Ile Met Asn Met Leu
 2165 2170
 <210> 127
 <211> 415
 <212> PRT
 <213> Homo sapiens
 <400> 127
 Met Glu Leu Arg Val Gly Asn Arg Tyr Arg Leu Gly Arg Lys Ile Gly
 1 5 10 15
 Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly Thr Asp Ile Ala Ala Gly
 20 25 30
 Glu Glu Val Ala Ile Lys Leu Glu Cys Val Lys Thr Lys His Pro Gln
 35 40 45
 Leu His Ile Glu Ser Lys Ile Tyr Lys Met Met Gln Gly Gly Val Gly
 50 55 60
 Ile Pro Thr Ile Arg Trp Cys Gly Ala Glu Gly Asp Tyr Asn Val Met
 65 70 75 80
 Val Met Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys
 85 90 95

Ser Arg Lys Phe Ser Leu Lys Thr Val Leu Leu Leu Ala Asp Gln Met
 100 105 110
 Ile Ser Arg Ile Glu Tyr Ile His Ser Lys Asn Phe Ile His Arg Asp
 115 120 125
 Val Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Lys Lys Gly Asn Leu
 130 135 140
 Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ala Arg
 145 150 155 160
 Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
 165 170 175
 Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
 180 185 190
 Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Asn Leu
 195 200 205
 Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Ala Thr Lys Arg Gln Lys
 210 215 220
 Tyr Glu Arg Ile Ser Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu
 225 230 235 240
 Cys Lys Gly Tyr Pro Ser Glu Phe Ala Thr Tyr Leu Asn Phe Cys Arg
 245 250 255
 Ser Leu Arg Phe Asp Asp Lys Pro Asp Tyr Ser Tyr Leu Arg Gln Leu
 260 265 270
 Phe Arg Asn Leu Phe His Arg Gln Gly Phe Ser Tyr Asp Tyr Val Phe
 275 280 285
 Asp Trp Asn Met Leu Lys Phe Gly Ala Ser Arg Ala Ala Asp Asp Ala
 290 295 300
 Glu Arg Glu Arg Arg Asp Arg Glu Glu Arg Leu Arg His Ser Arg Asn
 305 310 315 320
 Pro Ala Thr Arg Gly Leu Pro Ser Thr Asp Ser Gly Arg Leu Arg Gly
 325 330 335
 Thr Gln Glu Val Ala Pro Pro Thr Pro Leu Thr Pro Thr Ser His Thr
 340 345 350
 Ala Asn Thr Ser Pro Arg Pro Val Ser Gly Met Glu Arg Glu Arg Lys
 355 360 365
 Val Ser Met Arg Leu His Arg Gly Ala Pro Val Asn Ile Ser Ser Ser
 370 375 380
 Asp Leu Thr Gly Arg Gln Asp Thr Ser Arg Met Ser Thr Ser Gln Ile
 385 390 395 400
 Pro Gly Arg Val Ala Ser Ser Gly Leu Gln Ser Val Val His Arg

405 410 415

<210> 128
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 128

Met Thr Glu Trp Glu Thr Ala Ala Pro Ala Val Ala Glu Thr Pro Asp
 1 5 10 15

Ile Lys Leu Phe Gly Lys Trp Ser Thr Asp Asp Val Gln Ile Asn Asp
 20 25 30

Ile Ser Leu Gln Asp Tyr Ile Ala Val Lys Glu Lys Tyr Ala Lys Tyr
 35 40 45

Leu Pro His Ser Ala Gly Arg Tyr Ala Ala Asn Ala Phe Arg Lys Ala
 50 55 60

Gln Cys Pro Ile Val Glu Arg Leu Thr Asn Ser Met Met Met His Gly
 65 70 75 80

Arg Asn Asn Gly Lys Lys Leu Met Thr Val Arg Ile Val Lys His Ala
 85 90 95

Phe Glu Ile Ile His Leu Leu Thr Gly Glu Asn Pro Leu Gln Val Leu
 100 105 110

Val Asn Ala Ile Ile Asn Ser Gly Pro Arg Glu Asp Ser Thr Arg Ile
 115 120 125

Gly Arg Ala Gly Thr Val Arg Arg Gln Ala Val Asp Val Ser Pro Leu
 130 135 140

Arg Arg Val Asn Gln Ala Ile Trp Leu Leu Cys Thr Gly Ala Arg Glu
 145 150 155 160

Ala Ala Phe Arg Asn Ile Lys Thr Ile Ala Glu Cys Leu Ala Asp Glu
 165 170 175

Leu Ile Asn Ala Ala Lys Gly Ser Ser Asn Ser Tyr Ala Ile Lys Lys
 180 185 190

Lys Asp Glu Leu Glu Arg Val Ala Lys Ser Asn Arg
 195 200

<210> 129
 <211> 694
 <212> PRT
 <213> Homo sapiens

<400> 129

Met Glu Asn Lys Ser Leu Glu Ser Ser Gln Thr Asp Leu Lys Leu Val
 1 5 10 15

Ala His Pro Arg Ala Lys Ser Lys Val Trp Lys Tyr Phe Gly Phe Asp
 20 25 30

Thr Asn Ala Glu Gly Cys Ile Leu Gln Trp Lys Lys Ile Tyr Cys Arg
 35 40 45

Ile Cys Met Ala Gln Ile Ala Tyr Ser Gly Asn Thr Ser Asn Leu Ser
 50 55 60
 Tyr His Leu Glu Lys Asn His Pro Glu Glu Phe Cys Glu Phe Val Lys
 65 70 75 80
 Ser Asn Thr Glu Gln Met Arg Glu Ala Phe Ala Thr Ala Phe Ser Lys
 85 90 95
 Leu Lys Pro Glu Ser Ser Gln Gln Pro Gly Gln Asp Ala Leu Ala Val
 100 105 110
 Lys Ala Gly His Gly Tyr Asp Ser Lys Lys Gln Gln Glu Leu Thr Ala
 115 120 125
 Ala Val Leu Gly Leu Ile Cys Glu Gly Leu Tyr Pro Ala Ser Ile Val
 130 135 140
 Asp Glu Pro Thr Phe Lys Val Leu Leu Lys Thr Ala Asp Pro Arg Tyr
 145 150 155 160
 Glu Leu Pro Ser Arg Lys Tyr Ile Ser Thr Lys Ala Ile Pro Glu Lys
 165 170 175
 Tyr Gly Ala Val Arg Glu Val Ile Leu Lys Glu Leu Ala Glu Ala Thr
 180 185 190
 Trp Cys Gly Ile Ser Thr Asp Met Trp Arg Ser Glu Asn Gln Asn Arg
 195 200 205
 Ala Tyr Val Thr Leu Ala Ala His Phe Leu Gly Leu Gly Ala Pro Asn
 210 215 220
 Cys Leu Ser Met Gly Ser Arg Cys Leu Lys Thr Phe Glu Val Pro Glu
 225 230 235 240
 Glu Asn Thr Ala Glu Thr Ile Thr Arg Val Leu Tyr Glu Val Phe Ile
 245 250 255
 Glu Trp Gly Ile Ser Ala Lys Val Phe Gly Ala Thr Thr Asn Tyr Gly
 260 265 270
 Lys Asp Ile Val Lys Ala Cys Ser Leu Leu Asp Val Ala Val His Met
 275 280 285
 Pro Cys Leu Gly His Thr Phe Asn Ala Gly Ile Gln Gln Ala Phe Gln
 290 295 300
 Leu Pro Lys Leu Gly Ala Leu Leu Ser Arg Cys Arg Lys Leu Val Glu
 305 310 315 320
 Tyr Phe Gln Gln Ser Ala Val Ala Met Tyr Met Leu Tyr Glu Lys Gln
 325 330 335
 Lys Gln Gln Asn Val Ala His Cys Met Leu Val Ser Asn Arg Val Ser
 340 345 350
 Trp Trp Gly Ser Thr Leu Ala Met Leu Gln Arg Leu Lys Glu Gln Gln

```

355          360          365
Phe Val Ile Ala Gly Val Leu Val Glu Asp Ser Asn Asn His His Leu
370          375          380
Met Leu Glu Ala Ser Glu Trp Ala Thr Ile Glu Gly Leu Val Glu Leu
385          390          395          400
Leu Gln Pro Phe Lys Gln Val Ala Glu Met Leu Ser Ala Ser Arg Tyr
405          410          415
Pro Thr Ile Ser Met Val Lys Pro Leu Leu His Met Leu Leu Asn Thr
420          425          430
Thr Leu Asn Ile Lys Glu Thr Asp Ser Lys Glu Leu Ser Met Ala Lys
435          440          445
Glu Val Ile Ala Lys Glu Leu Ser Lys Thr Tyr Gln Glu Thr Pro Glu
450          455          460
Ile Asp Met Phe Leu Asn Val Ala Thr Phe Leu Asp Pro Arg Tyr Lys
465          470          475          480
Arg Leu Pro Phe Leu Ser Ala Phe Glu Arg Gln Gln Val Glu Asn Arg
485          490          495
Val Val Glu Glu Ala Lys Gly Leu Leu Asp Lys Val Lys Asp Gly Gly
500          505          510
Tyr Arg Pro Ala Glu Asp Lys Ile Phe Pro Val Pro Glu Glu Pro Pro
515          520          525
Val Lys Lys Leu Met Arg Thr Ser Thr Pro Pro Pro Ala Ser Val Ile
530          535          540
Asn Asn Met Leu Ala Glu Ile Phe Cys Gln Thr Gly Gly Val Glu Asp
545          550          555          560
Gln Glu Glu Trp His Ala Gln Val Val Glu Glu Leu Ser Asn Phe Lys
565          570          575
Ser Gln Lys Val Leu Gly Leu Asn Glu Asp Pro Leu Lys Trp Trp Ser
580          585          590
Asp Arg Leu Ala Leu Phe Pro Leu Leu Pro Lys Val Leu Gln Lys Tyr
595          600          605
Trp Cys Val Thr Ala Thr Arg Val Ala Pro Glu Arg Leu Phe Gly Ser
610          615          620
Ala Ala Asn Val Val Ser Ala Lys Arg Asn Arg Leu Ala Pro Ala His
625          630          635          640
Val Asp Glu Gln Val Phe Leu Tyr Glu Asn Ala Arg Ser Gly Ala Glu
645          650          655
Ala Glu Pro Glu Asp Gln Asp Glu Gly Glu Trp Gly Leu Asp Gln Glu
660          665          670

```

Gln Val Phe Ser Leu Gly Asp Gly Val Ser Gly Gly Phe Phe Gly Ile
675 680 685

Arg Asp Ser Ser Phe Leu
690

<210> 130
<211> 729
<212> PRT
<213> Homo sapiens

<400> 130

Met Gly Lys Lys Tyr Lys Asn Ile Val Leu Leu Lys Gly Leu Glu Val
1 5 10 15

Ile Asn Asp Tyr His Phe Arg Met Val Lys Ser Leu Leu Ser Asn Asp
20 25 30

Leu Lys Leu Asn Leu Lys Met Arg Glu Glu Tyr Asp Lys Ile Gln Ile
35 40 45

Ala Asp Leu Met Glu Glu Lys Phe Arg Gly Asp Ala Gly Leu Gly Lys
50 55 60

Leu Ile Lys Ile Phe Glu Asp Ile Pro Thr Leu Glu Asp Leu Ala Glu
65 70 75 80

Thr Leu Lys Lys Glu Lys Leu Lys Val Lys Gly Pro Ala Leu Ser Arg
85 90 95

Lys Arg Lys Lys Glu Val His Ala Thr Ser Pro Ala Pro Ser Thr Ser
100 105 110

Ser Thr Val Lys Thr Glu Gly Ala Glu Ala Thr Pro Gly Ala Gln Lys
115 120 125

Arg Lys Lys Ser Thr Lys Glu Lys Ala Gly Pro Lys Gly Ser Lys Val
130 135 140

Ser Glu Glu Gln Thr Gln Pro Pro Ser Pro Ala Gly Ala Gly Met Ser
145 150 155 160

Thr Ala Met Gly Arg Ser Pro Ser Pro Lys Thr Ser Leu Ser Ala Pro
165 170 175

Pro Asn Ser Ser Ser Thr Glu Asn Pro Lys Thr Val Ala Lys Cys Gln
180 185 190

Val Thr Pro Arg Arg Asn Val Leu Gln Lys Arg Pro Val Ile Val Lys
195 200 205

Val Leu Ser Thr Thr Lys Pro Phe Glu Tyr Glu Thr Pro Glu Met Glu
210 215 220

Lys Lys Ile Met Phe His Ala Thr Val Ala Thr Gln Thr Gln Phe Phe
225 230 235 240

His Val Lys Val Leu Asn Thr Ser Leu Lys Glu Lys Phe Asn Gly Lys
245 250 255

Lys Ile Ile Ile Ile Ser Asp Tyr Leu Glu Tyr Asp Ser Leu Leu Glu
 260 265 270
 Val Asn Glu Glu Ser Thr Val Ser Glu Ala Gly Pro Asn Gln Thr Phe
 275 280 285
 Glu Val Pro Asn Lys Ile Ile Asn Arg Ala Lys Glu Thr Leu Lys Ile
 290 295 300
 Asp Ile Leu His Lys Lys Gln Ala Ser Gly Asn Ile Val Tyr Gly Val Phe
 305 310 315 320
 Met Leu His Lys Lys Thr Val Asn Gln Lys Thr Thr Ile Tyr Glu Ile
 325 330 335
 Gln Asp Asp Arg Gly Lys Met Asp Val Val Gly Thr Gly Gln Cys His
 340 345 350
 Asn Ile Pro Cys Glu Glu Gly Asp Lys Leu Gln Leu Phe Cys Phe Arg
 355 360 365
 Leu Arg Lys Lys Asn Gln Met Ser Lys Leu Ile Ser Glu Met His Ser
 370 375 380
 Phe Ile Gln Ile Lys Lys Lys Thr Asn Pro Arg Asn Asn Asp Pro Lys
 385 390 395 400
 Ser Met Lys Leu Pro Gln Glu Gln Arg Gln Leu Pro Tyr Pro Ser Glu
 405 410 415
 Ala Ser Thr Thr Phe Pro Glu Ser His Leu Arg Thr Pro Gln Met Pro
 420 425 430
 Pro Thr Thr Pro Ser Ser Ser Phe Phe Thr Lys Lys Ser Glu Asp Thr
 435 440 445
 Ile Ser Lys Met Asn Asp Phe Met Arg Met Gln Ile Leu Lys Glu Gly
 450 455 460
 Ser His Phe Pro Gly Pro Phe Met Thr Ser Ile Gly Pro Ala Glu Ser
 465 470 475 480
 His Pro His Thr Pro Gln Met Pro Pro Ser Thr Pro Ser Ser Ser Phe
 485 490 495
 Leu Thr Thr Leu Lys Pro Arg Leu Lys Thr Glu Pro Glu Glu Val Ser
 500 505 510
 Ile Glu Asp Ser Ala Gln Ser Asp Leu Lys Glu Val Met Val Leu Asn
 515 520 525
 Ala Thr Glu Ser Phe Val Tyr Glu Pro Lys Glu Gln Lys Lys Met Phe
 530 535 540
 His Ala Thr Val Ala Thr Glu Asn Glu Val Phe Arg Val Lys Val Phe
 545 550 555 560
 Asn Ile Asp Leu Lys Glu Lys Phe Thr Pro Lys Lys Ile Ile Ala Ile
 565 570 575

Ala Asn Tyr Val Cys Arg Asn Gly Phe Leu Glu Val Tyr Pro Phe Thr
580 585 590

Leu Val Ala Asp Val Asn Ala Asp Arg Asn Met Glu Ile Pro Lys Gly
595 600 605

Leu Ile Arg Ser Ala Ser Val Thr Pro Lys Ile Asn Gln Leu Cys Ser
610 615 620

Gln Thr Lys Gly Ser Phe Val Asn Gly Val Phe Glu Val His Lys Lys
625 630 635 640

Asn Val Arg Gly Glu Phe Thr Tyr Tyr Glu Ile Gln Asp Asn Thr Gly
645 650 655

Lys Met Glu Val Val Val His Gly Arg Leu Asn Thr Ile Asn Cys Glu
660 665 670

Glu Gly Asp Lys Leu Lys Leu Thr Ser Phe Glu Leu Ala Pro Lys Ser
675 680 685

Gly Asn Thr Gly Glu Leu Arg Ser Val Ile His Ser His Ile Lys Val
690 695 700

Ile Lys Thr Arg Lys Asn Lys Lys Asp Ile Leu Asn Pro Asp Ser Ser
705 710 715 720

Met Glu Thr Ser Pro Asp Phe Phe Phe
725

<210> 131
<211> 216
<212> PRT
<213> Homo sapiens

<400> 131

Met Leu Arg Leu Ser Glu Arg Asn Met Lys Val Leu Leu Ala Ala Ala
1 5 10 15

Leu Ile Ala Gly Ser Val Phe Phe Leu Leu Leu Pro Gly Pro Ser Ala
20 25 30

Ala Asp Glu Lys Lys Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe
35 40 45

Asp Leu Arg Ile Gly Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu
50 55 60

Phe Gly Lys Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala
65 70 75 80

Thr Gly Glu Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val
85 90 95

Ile Lys Asp Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly
100 105 110

Thr Gly Gly Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe
115 120 125

Lys Leu Lys His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly
130 135 140

Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala
145 150 155 160

Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met
165 170 175

Glu Val Val Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys
180 185 190

Pro Leu Lys Asp Val Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu
195 200 205

Lys Pro Phe Ala Ile Ala Lys Glu
210 215

<210> 132
<211> 208
<212> PRT
<213> Homo sapiens

<400> 132

Met Lys Leu Leu Pro Ser Val Val Leu Lys Leu Phe Leu Ala Ala Val
1 5 10 15

Leu Ser Ala Leu Val Thr Gly Glu Ser Leu Glu Arg Leu Arg Arg Gly
20 25 30

Leu Ala Ala Gly Thr Ser Asn Pro Asp Pro Pro Thr Val Ser Thr Asp
35 40 45

Gln Leu Leu Pro Leu Gly Gly Gly Arg Asp Arg Lys Val Arg Asp Leu
50 55 60

Gln Glu Ala Asp Leu Asp Leu Leu Arg Val Thr Leu Ser Ser Lys Pro
65 70 75 80

Gln Ala Leu Ala Thr Pro Asn Lys Glu Glu His Gly Lys Arg Lys Lys
85 90 95

Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr
100 105 110

Lys Asp Phe Cys Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg
115 120 125

Ala Pro Ser Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His
130 135 140

Gly Leu Ser Leu Pro Val Glu Asn Arg Leu Tyr Thr Tyr Asp His Thr
145 150 155 160

Thr Ile Leu Ala Val Val Ala Val Val Leu Ser Ser Val Cys Leu Leu
165 170 175

Val Ile Val Gly Leu Leu Met Phe Arg Tyr His Arg Arg Gly Gly Tyr
180 185 190

Asp Val Glu Asn Glu Glu Lys Val Lys Leu Gly Met Thr Asn Ser His
195 200 205

<210> 133
<211> 178
<212> PRT
<213> Homo sapiens

<400> 133

Met Thr Thr Leu Arg Ala Phe Thr Cys Asp Asp Leu Phe Arg Phe Asn
1 5 10 15

Asn Ile Asn Leu Asp Pro Leu Thr Glu Thr Tyr Gly Ile Pro Phe Tyr
20 25 30

Leu Gln Tyr Leu Ala His Trp Pro Glu Tyr Phe Ile Val Ala Glu Ala
35 40 45

Pro Gly Gly Glu Leu Met Gly Tyr Ile Met Gly Lys Ala Glu Gly Ser
50 55 60

Val Ala Arg Glu Glu Trp His Gly His Val Thr Ala Leu Ser Val Ala
65 70 75 80

Pro Glu Phe Arg Arg Leu Gly Leu Ala Ala Lys Leu Met Glu Leu Leu
85 90 95

Glu Glu Ile Ser Glu Arg Lys Gly Gly Phe Phe Val Asp Leu Phe Val
100 105 110

Arg Val Ser Asn Gln Val Ala Val Asn Met Tyr Lys Gln Leu Gly Tyr
115 120 125

Ser Val Tyr Arg Thr Val Ile Glu Tyr Tyr Ser Ala Ser Asn Gly Glu
130 135 140

Pro Asp Glu Asp Ala Tyr Asp Met Arg Lys Ala Leu Ser Arg Asp Thr
145 150 155 160

Glu Lys Lys Ser Ile Ile Pro Leu Pro His Pro Val Arg Pro Glu Asp
165 170 175

Ile Glu

<210> 134
<211> 185
<212> PRT
<213> Homo sapiens

<400> 134

Met Gly Pro Glu Arg His Leu Ser Gly Ala Pro Ala Arg Met Ala Thr
1 5 10 15

Val Val Leu Gly Gly Asp Thr Met Gly Pro Glu Arg Ile Phe Pro Asn
20 25 30

Gln Thr Glu Glu Leu Gly His Gln Gly Pro Ser Glu Gly Thr Gly Asp
35 40 45

Trp Ser Ser Glu Glu Pro Glu Glu Glu Gln Glu Glu Thr Gly Ser Gly
50 55 60

Pro Ala Gly Tyr Ser Tyr Gln Pro Leu Asn Gln Asp Pro Glu Gln Glu
65 70 75 80

Glu Val Glu Leu Ala Pro Val Gly Asp Gly Asp Val Val Ala Asp Ile
85 90 95

Gln Asp Arg Ile Gln Ala Leu Gly Leu His Leu Pro Asp Pro Pro Leu
100 105 110

Glu Ser Glu Asp Glu Asp Glu Glu Gly Ala Thr Ala Leu Asn Asn His
115 120 125

Ser Ser Ile Pro Met Asp Pro Glu His Val Glu Leu Val Lys Arg Thr
130 135 140

Met Ala Gly Val Ser Leu Pro Ala Pro Gly Val Pro Ala Trp Ala Arg
145 150 155 160

Glu Ile Ser Asp Ala Gln Trp Glu Asp Val Val Gln Lys Ala Leu Gln
165 170 175

Ala Arg Gln Ala Ser Pro Ala Trp Lys
180 185

<210> 135
<211> 397
<212> PRT
<213> Homo sapiens

<400> 135

Met Asn Ala Gly Ser Asp Pro Val Val Ile Val Ser Ala Ala Arg Thr
1 5 10 15

Ile Ile Gly Ser Phe Asn Gly Ala Leu Ala Ala Val Pro Val Gln Asp
20 25 30

Leu Gly Ser Thr Val Ile Lys Glu Val Leu Lys Arg Ala Thr Val Ala
35 40 45

Pro Glu Asp Val Ser Glu Val Ile Phe Gly His Val Leu Ala Ala Gly
50 55 60

Cys Gly Gln Asn Pro Val Arg Gln Ala Ser Val Gly Ala Gly Ile Pro
65 70 75 80

Tyr Ser Val Pro Ala Trp Ser Cys Gln Met Ile Cys Gly Ser Gly Leu
85 90 95

Lys Ala Val Cys Leu Ala Val Gln Ser Ile Gly Ile Gly Asp Ser Ser
100 105 110

Ile Val Val Ala Gly Gly Met Glu Asn Met Ser Lys Ala Pro His Leu
115 120 125

Ala Tyr Leu Arg Thr Gly Val Lys Ile Gly Glu Met Pro Leu Thr Asp
130 135 140

Ser Ile Leu Cys Asp Gly Leu Thr Asp Ala Phe His Asn Cys His Met
145 150 155 160

Gly Ile Thr Ala Glu Asn Val Ala Thr Lys Trp Gln Val Ser Arg Glu
165 170 175

Asp Gln Asp Lys Val Ala Val Leu Ser Gln Asn Arg Thr Glu Asn Ala
180 185 190

Gln Lys Ala Gly His Phe Asp Lys Glu Ile Val Pro Val Leu Val Ser
195 200 205

Thr Arg Lys Gly Leu Ile Glu Val Lys Thr Asp Glu Phe Pro Arg His
210 215 220

Gly Ser Asn Ile Glu Ala Met Ser Lys Leu Lys Pro Tyr Phe Leu Thr
225 230 235 240

Asp Gly Thr Gly Thr Val Thr Pro Ala Asn Ala Ser Gly Ile Asn Asp
245 250 255

Gly Ala Ala Ala Val Ala Leu Met Lys Lys Ser Glu Ala Asp Lys Arg
260 265 270

Gly Leu Thr Pro Leu Ala Arg Ile Val Ser Trp Ser Gln Val Gly Val
275 280 285

Glu Pro Ser Ile Met Gly Ile Gly Pro Ile Pro Ala Ile Lys Gln Ala
290 295 300

Val Thr Lys Ala Gly Trp Ser Leu Glu Asp Val Asp Ile Phe Glu Ile
305 310 315 320

Asn Glu Ala Phe Ala Ala Val Ser Ala Ala Ile Val Lys Glu Leu Gly
325 330 335

Leu Asn Pro Glu Lys Val Asn Ile Glu Gly Gly Ala Ile Ala Leu Gly
340 345 350

His Pro Leu Gly Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His
355 360 365

Thr Leu Glu Arg Met Gly Arg Ser Arg Gly Val Ala Ala Leu Cys Ile
370 375 380

Gly Gly Gly Met Gly Ile Ala Met Cys Val Gln Arg Glu
385 390 395

<210> 136

<211> 556

<212> PRT

<213> Homo sapiens

<400> 136

Met Glu Gly Pro Leu Ser Val Phe Gly Asp Arg Ser Thr Gly Glu Thr
1 5 10 15

Ile Arg Ser Gln Asn Val Met Ala Ala Ala Ser Ile Ala Asn Ile Val
20 25 30

Lys Ser Ser Leu Gly Pro Val Gly Leu Asp Lys Met Leu Val Asp Asp
 35 40 45
 Ile Gly Asp Val Thr Ile Thr Asn Asp Gly Ala Thr Ile Leu Lys Leu
 50 55 60
 Leu Glu Val Glu His Pro Ala Ala Lys Val Leu Cys Glu Leu Ala Asp
 65 70 75 80
 Leu Gln Asp Lys Glu Val Gly Asp Gly Thr Thr Ser Val Val Ile Ile
 85 90 95
 Ala Ala Glu Leu Leu Lys Asn Ala Asp Glu Leu Val Lys Gln Lys Ile
 100 105 110
 His Pro Thr Ser Val Ile Ser Gly Tyr Arg Leu Ala Cys Lys Glu Ala
 115 120 125
 Val Arg Tyr Ile Asn Glu Asn Leu Ile Val Asn Thr Asp Glu Leu Gly
 130 135 140
 Arg Asp Cys Leu Ile Asn Ala Ala Lys Thr Ser Met Ser Ser Lys Ile
 145 150 155 160
 Ile Gly Ile Asn Gly Asp Phe Phe Ala Asn Met Val Val Asp Ala Val
 165 170 175
 Leu Ala Ile Lys Tyr Thr Asp Ile Arg Gly Gln Pro Arg Tyr Pro Val
 180 185 190
 Asn Ser Val Asn Ile Leu Lys Ala His Gly Arg Ser Gln Met Glu Ser
 195 200 205
 Met Leu Ile Ser Gly Tyr Ala Leu Asn Cys Val Val Gly Ser Gln Gly
 210 215 220
 Met Pro Lys Arg Ile Val Asn Ala Lys Ile Ala Cys Leu Asp Phe Ser
 225 230 235 240
 Leu Gln Lys Thr Lys Met Lys Leu Gly Val Gln Val Val Ile Thr Asp
 245 250 255
 Pro Glu Lys Leu Asp Gln Ile Arg Gln Arg Glu Ser Asp Ile Thr Lys
 260 265 270
 Glu Arg Ile Gln Lys Ile Leu Ala Thr Gly Ala Asn Val Ile Leu Thr
 275 280 285
 Thr Gly Gly Ile Asp Asp Met Cys Leu Lys Tyr Phe Val Glu Ala Gly
 290 295 300
 Ala Met Ala Val Arg Arg Val Leu Lys Arg Asp Leu Lys Arg Ile Ala
 305 310 315 320
 Lys Ala Ser Gly Ala Thr Ile Leu Ser Thr Leu Ala Asn Leu Glu Gly
 325 330 335
 Glu Glu Thr Phe Glu Ala Ala Met Leu Gly Gln Ala Glu Glu Val Val
 340 345 350

Gln Glu Arg Ile Cys Asp Asp Glu Leu Ile Leu Ile Lys Asn Thr Lys
355 360 365

Ala Arg Thr Ser Ala Ser Ile Ile Leu Arg Gly Ala Asn Asp Phe Met
370 375 380

Cys Asp Glu Met Glu Arg Ser Leu His Asp Ala Leu Cys Val Val Lys
385 390 395 400

Arg Val Leu Glu Ser Lys Ser Val Val Pro Gly Gly Gly Ala Val Glu
405 410 415

Ala Ala Leu Ser Ile Tyr Leu Glu Asn Tyr Ala Thr Ser Met Gly Ser
420 425 430

Arg Glu Gln Leu Ala Ile Ala Glu Phe Ala Arg Ser Leu Leu Val Ile
435 440 445

Pro Asn Thr Leu Ala Val Asn Ala Ala Gln Asp Ser Thr Asp Leu Val
450 455 460

Ala Lys Leu Arg Ala Phe His Asn Glu Ala Gln Val Asn Pro Glu Arg
465 470 475 480

Lys Asn Leu Lys Trp Ile Gly Leu Asp Leu Ser Asn Gly Lys Pro Arg
485 490 495

Asp Asn Lys Gln Ala Gly Val Phe Glu Pro Thr Ile Val Lys Val Lys
500 505 510

Ser Leu Lys Phe Ala Thr Glu Ala Ala Ile Thr Ile Leu Arg Ile Asp
515 520 525

Asp Leu Ile Lys Leu His Pro Glu Ile Leu Arg Ile Lys His Gly Ser
530 535 540

Tyr Glu Asp Ala Val His Ser Gly Ala Leu Asn Asp
545 550 555

<210> 137
<211> 266
<212> PRT
<213> Homo sapiens

<400> 137

Met Pro Lys Gly Lys Lys Ala Lys Gly Lys Lys Val Ala Pro Ala Pro
1 5 10 15

Ala Val Val Lys Lys Gln Glu Ala Lys Lys Val Val Asn Pro Leu Phe
20 25 30

Glu Lys Arg Pro Lys Asn Phe Gly Ile Gly Gln Asp Ile Gln Pro Lys
35 40 45

Arg Asp Leu Thr Arg Phe Val Lys Trp Pro Arg Tyr Ile Arg Leu Gln
50 55 60

Arg Gln Arg Ala Ile Leu Tyr Lys Arg Leu Lys Val Pro Pro Ala Ile
65 70 75 80

Asn Gln Phe Thr Gln Ala Leu Asp Arg Gln Thr Ala Thr Gln Leu Leu
85 90 95

Lys Leu Ala His Lys Tyr Arg Pro Glu Thr Lys Gln Glu Lys Lys Gln
100 105 110

Arg Leu Leu Ala Arg Ala Glu Lys Lys Ala Ala Gly Lys Gly Asp Val
115 120 125

Pro Thr Lys Arg Pro Pro Val Leu Arg Ala Gly Val Asn Thr Val Thr
130 135 140

Thr Leu Val Glu Asn Lys Lys Ala Gln Leu Val Val Ile Ala His Asp
145 150 155 160

Val Asp Pro Ile Glu Leu Val Val Phe Leu Pro Ala Leu Cys Arg Lys
165 170 175

Met Gly Val Pro Tyr Cys Ile Ile Lys Gly Lys Ala Arg Leu Gly Arg
180 185 190

Leu Val His Arg Lys Thr Cys Thr Thr Val Ala Phe Thr Gln Val Asn
195 200 205

Ser Glu Asp Lys Gly Ala Leu Ala Lys Leu Val Glu Ala Ile Arg Thr
210 215 220

Asn Tyr Asn Asp Arg Tyr Asp Glu Ile Arg Arg His Trp Gly Gly Asn
225 230 235 240

Val Leu Gly Pro Lys Ser Val Ala Arg Ile Ala Lys Leu Glu Lys Ala
245 250 255

Lys Ala Lys Glu Leu Ala Thr Lys Leu Gly
260 265

<210> 138
<211> 160
<212> PRT
<213> Homo sapiens

<400> 138

Met Asp Cys Gln Asn Gly His Gln His Ile Ser Gln Glu Leu Glu Val
1 5 10 15

Leu Arg Ile His Met Gln Leu Val Thr Val Gln Phe Thr Gln Leu Gly
20 25 30

Lys Gly Ala Leu Glu Ile Ile Gln Val Leu Cys Gly Ile Ser Gln Gly
35 40 45

Ser Gln His Leu Leu Ala Met Cys Leu Asp Phe Gly Val Ala His Asp
50 55 60

Gly Arg Gly Arg Gly Gln Val Ala Lys Ala Val Lys Glu Pro Leu Gly
65 70 75 80

Pro Trp Val Asp Asn Gln Glu Pro Ser Gln Gly Phe Ser Ser Ser Ile
85 90 95

Phe His Ile His Leu Ala Pro Gln Ala Cys Asp Ser Ser Leu Val Leu
100 105 110

Leu Cys Glu Met Thr His Gly Val Trp Thr Arg Ser Leu Leu Ile Thr
115 120 125

Ser Asp Val Pro Glu Ala Ser Val Thr Gln Ile Leu Leu Cys Ala Met
130 135 140

Trp Thr Leu Pro Ser His Ala Thr Thr Arg Glu Leu Thr Gln Trp Val
145 150 155 160

<210> 139
<211> 172
<212> PRT
<213> Homo sapiens

<400> 139

Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp
1 5 10 15

Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu
20 25 30

Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile
35 40 45

Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
50 55 60

Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
65 70 75 80

Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
85 90 95

Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
100 105 110

Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
115 120 125

Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
130 135 140

Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Tyr Met
145 150 155 160

Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
165 170

<210> 140
<211> 133
<212> PRT
<213> Homo sapiens

<400> 140

Met Asn Asp Thr Val Thr Ile Arg Thr Arg Lys Phe Met Thr Asn Arg
1 5 10 15

Leu Leu Gln Arg Lys Gln Met Val Ile Asp Val Leu His Pro Gly Lys
20 25 30

Ala Thr Val Pro Lys Thr Glu Ile Arg Glu Lys Leu Ala Lys Met Tyr
35 40 45

Lys Thr Thr Pro Asp Val Ile Phe Val Phe Gly Phe Arg Thr His Phe
50 55 60

Gly Gly Gly Lys Thr Thr Gly Phe Gly Met Ile Tyr Asp Ser Leu Asp
65 70 75 80

Tyr Ala Lys Lys Asn Glu Pro Lys His Arg Leu Ala Arg His Gly Leu
85 90 95

Tyr Glu Lys Lys Lys Thr Ser Arg Lys Gln Arg Lys Glu Arg Lys Asn
100 105 110

Arg Met Lys Lys Val Arg Gly Thr Ala Lys Ala Asn Val Gly Ala Gly
115 120 125

Lys Lys Pro Lys Glu
130

<210> 141
<211> 604
<212> PRT
<213> Homo sapiens

<400> 141

Met Asn Ile Val Glu Asn Ser Ile Phe Leu Ser Asn Leu Met Lys Ser
1 5 10 15

Ala Tyr Thr Phe Glu Leu Lys Tyr Asp Leu Ser Cys Glu Leu Tyr Arg
20 25 30

Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu Arg
35 40 45

Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys Val
50 55 60

Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Arg Gly Asp
65 70 75 80

Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser Cys Arg Phe Val
85 90 95

Gln Ser Leu Asn Ser Val Asn Asn Leu Glu Ala Thr Ser Gln Pro Thr
100 105 110

Phe Pro Ser Ser Val Thr Asn Ser Thr His Ser Leu Leu Pro Gly Thr
115 120 125

Glu Asn Ser Gly Tyr Phe Arg Gly Ser Tyr Ser Asn Ser Pro Ser Asn
130 135 140

Pro Val Asn Ser Arg Ala Asn Gln Asp Phe Ser Ala Leu Met Arg Ser
145 150 155 160

Ser Tyr His Cys Ala Met Asn Asn Glu Asn Ala Arg Leu Leu Thr Phe
 165 170 175
 Gln Thr Trp Pro Leu Thr Phe Leu Ser Pro Thr Asp Leu Ala Lys Ala
 180 185 190
 Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys
 195 200 205
 Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn Ala Met Ser Glu
 210 215 220
 His Leu Arg His Phe Pro Lys Cys Pro Phe Ile Glu Asn Gln Leu Gln
 225 230 235 240
 Asp Thr Ser Arg Tyr Thr Val Ser Asn Leu Ser Met Gln Thr His Ala
 245 250 255
 Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu Val Asn
 260 265 270
 Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp
 275 280 285
 Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
 290 295 300
 Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu
 305 310 315 320
 Tyr Leu Ile Arg Ile Lys Gly Gln Glu Phe Ile Arg Gln Val Gln Ala
 325 330 335
 Ser Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Ser Pro
 340 345 350
 Gly Asp Glu Asn Ala Glu Ser Ser Ile Ile His Phe Glu Pro Gly Glu
 355 360 365
 Asp His Ser Glu Asp Ala Ile Met Met Asn Thr Pro Val Ile Asn Ala
 370 375 380
 Ala Val Glu Met Gly Phe Ser Arg Ser Leu Val Lys Gln Thr Val Gln
 385 390 395 400
 Arg Lys Ile Leu Ala Thr Gly Glu Asn Tyr Arg Leu Val Asn Asp Leu
 405 410 415
 Val Leu Asp Leu Leu Asn Ala Glu Asp Glu Ile Arg Glu Glu Glu Arg
 420 425 430
 Glu Arg Ala Thr Glu Glu Lys Glu Ser Asn Asp Leu Leu Leu Ile Arg
 435 440 445
 Lys Asn Arg Met Ala Leu Phe Gln His Leu Thr Cys Val Ile Pro Ile
 450 455 460
 Leu Asp Ser Leu Leu Thr Ala Gly Ile Ile Asn Glu Gln Glu His Asp
 465 470 475 480

Val Ile Lys Gln Lys Thr Gln Thr Ser Leu Gln Ala Arg Glu Leu Ile
 485 490 495
 Asp Thr Ile Leu Val Lys Gly Asn Ile Ala Ala Thr Val Phe Arg Asn
 500 505 510
 Ser Leu Gln Glu Ala Glu Ala Val Leu Tyr Glu His Leu Phe Val Gln
 515 520 525
 Gln Asp Ile Lys Tyr Ile Pro Thr Glu Asp Val Ser Asp Leu Pro Val
 530 535 540
 Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys
 545 550 555 560
 Met Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val
 565 570 575
 Val Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg
 580 585 590
 Ser Thr Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
 595 600
 <210> 142
 <211> 624
 <212> PRT
 <213> Homo sapiens
 <400> 142
 Met Gln Pro Asp Pro Arg Pro Ser Gly Ala Gly Ala Cys Cys Arg Phe
 1 5 10 15
 Leu Pro Leu Gln Ser Gln Cys Pro Glu Gly Ala Gly Asp Ala Val Met
 20 25 30
 Tyr Ala Ser Thr Glu Cys Lys Ala Glu Val Thr Pro Ser Gln His Gly
 35 40 45
 Asn Arg Thr Phe Ser Tyr Thr Leu Glu Asp His Thr Lys Gln Ala Phe
 50 55 60
 Gly Ile Met Asn Glu Leu Arg Leu Ser Gln Gln Leu Cys Asp Val Thr
 65 70 75 80
 Leu Gln Val Lys Tyr Gln Asp Ala Pro Ala Ala Gln Phe Met Ala His
 85 90 95
 Lys Val Val Leu Ala Ser Ser Ser Pro Val Phe Lys Ala Met Phe Thr
 100 105 110
 Asn Gly Leu Arg Glu Gln Gly Met Glu Val Val Ser Ile Glu Gly Ile
 115 120 125
 His Pro Lys Val Met Glu Arg Leu Ile Glu Phe Ala Tyr Thr Ala Ser
 130 135 140
 Ile Ser Met Gly Glu Lys Cys Val Leu His Val Met Asn Gly Ala Val
 145 150 155 160

Met Tyr Gln Ile Asp Ser Val Val Arg Ala Cys Ser Asp Phe Leu Val
 165 170 175
 Gln Gln Leu Asp Pro Ser Asn Ala Ile Gly Ile Ala Asn Phe Ala Glu
 180 185 190
 Gln Ile Gly Cys Val Glu Leu His Gln Arg Ala Arg Glu Tyr Ile Tyr
 195 200 205
 Met His Phe Gly Glu Val Ala Lys Gln Glu Glu Phe Phe Asn Leu Ser
 210 215 220
 His Cys Gln Leu Val Thr Leu Ile Ser Arg Asp Asp Leu Asn Val Arg
 225 230 235 240
 Cys Glu Ser Glu Val Phe His Ala Cys Ile Asn Trp Val Lys Tyr Asp
 245 250 255
 Cys Glu Gln Arg Arg Phe Tyr Val Gln Ala Leu Leu Arg Ala Val Arg
 260 265 270
 Cys His Ser Leu Thr Pro Asn Phe Leu Gln Met Gln Leu Gln Lys Cys
 275 280 285
 Glu Ile Leu Gln Ser Asp Ser Arg Cys Lys Asp Tyr Leu Val Lys Ile
 290 295 300
 Phe Glu Glu Leu Thr Leu His Lys Pro Thr Gln Val Met Pro Cys Arg
 305 310 315 320
 Ala Pro Lys Val Gly Arg Leu Ile Tyr Thr Ala Gly Gly Tyr Phe Arg
 325 330 335
 Gln Ser Leu Ser Tyr Leu Glu Ala Tyr Asn Pro Ser Asn Gly Thr Trp
 340 345 350
 Leu Arg Leu Ala Asp Leu Gln Val Pro Arg Ser Gly Leu Ala Gly Cys
 355 360 365
 Val Val Gly Gly Leu Leu Tyr Ala Val Gly Gly Arg Asn Asn Ser Pro
 370 375 380
 Asp Gly Asn Thr Asp Ser Ser Ala Leu Asp Cys Tyr Asn Pro Met Thr
 385 390 395 400
 Asn Gln Trp Ser Pro Cys Ala Pro Met Ser Val Pro Arg Asn Arg Ile
 405 410 415
 Gly Val Gly Val Ile Asp Gly His Ile Tyr Ala Val Gly Gly Ser His
 420 425 430
 Gly Cys Ile His His Asn Ser Val Glu Arg Tyr Glu Pro Glu Arg Asp
 435 440 445
 Glu Trp His Leu Val Ala Pro Met Leu Thr Arg Arg Ile Gly Val Gly
 450 455 460
 Val Ala Val Leu Asn Arg Leu Leu Tyr Ala Val Gly Gly Phe Asp Gly
 465 470 475 480

Thr Asn Arg Leu Asn Ser Ala Glu Cys Tyr Tyr Pro Glu Arg Asn Glu
485 490 495

Trp Arg Met Ile Thr Ala Met Asn Thr Ile Arg Ser Gly Ala Gly Val
500 505 510

Cys Val Leu His Asn Cys Ile Tyr Ala Ala Gly Gly Tyr Asp Gly Gln
515 520 525

Asp Gln Leu Asn Ser Val Glu Arg Tyr Asp Val Glu Thr Glu Thr Trp
530 535 540

Thr Phe Val Ala Pro Met Lys His Arg Arg Ser Ala Leu Gly Ile Thr
545 550 555 560

Val His Gln Gly Arg Ile Tyr Val Leu Gly Gly Tyr Asp Gly His Thr
565 570 575

Phe Leu Asp Ser Val Glu Cys Tyr Asp Pro Asp Thr Asp Thr Trp Ser
580 585 590

Glu Val Thr Arg Met Thr Ser Gly Arg Ser Gly Val Gly Val Ala Val
595 600 605

Thr Met Glu Pro Cys Arg Lys Gln Ile Asp Gln Gln Asn Cys Thr Cys
610 615 620

<210> 143

<211> 389

<212> PRT

<213> Homo sapiens

<400> 143

Met Leu Ser Leu Arg Val Pro Leu Ala Pro Ile Thr Asp Pro Gln Gln
1 5 10 15

Leu Gln Leu Ser Pro Leu Lys Gly Leu Ser Leu Val Asp Lys Glu Asn
20 25 30

Thr Pro Pro Ala Leu Ser Gly Thr Arg Val Leu Ala Ser Lys Thr Ala
35 40 45

Arg Arg Ile Phe Gln Glu Pro Thr Glu Pro Lys Thr Lys Ala Ala Ala
50 55 60

Pro Gly Val Glu Asp Glu Pro Leu Leu Arg Glu Asn Pro Arg Arg Phe
65 70 75 80

Val Ile Phe Pro Ile Glu Tyr His Asp Ile Trp Gln Met Tyr Lys Lys
85 90 95

Ala Glu Ala Ser Phe Trp Thr Ala Glu Glu Val Asp Leu Ser Lys Asp
100 105 110

Ile Gln His Trp Glu Ser Leu Lys Pro Glu Glu Arg Tyr Phe Ile Ser
115 120 125

His Val Leu Ala Phe Phe Ala Ala Ser Asp Gly Ile Val Asn Glu Asn
130 135 140

Leu Val Glu Arg Phe Ser Gln Glu Val Gln Ile Thr Glu Ala Arg Cys
 145 150 155 160
 Phe Tyr Gly Phe Gln Ile Ala Met Glu Asn Ile His Ser Glu Met Tyr
 165 170 175
 Ser Leu Leu Ile Asp Thr Tyr Ile Lys Asp Pro Lys Glu Arg Glu Phe
 180 185 190
 Leu Phe Asn Ala Ile Glu Thr Met Pro Cys Val Lys Lys Lys Ala Asp
 195 200 205
 Trp Ala Leu Arg Trp Ile Gly Asp Lys Glu Ala Thr Tyr Gly Glu Arg
 210 215 220
 Val Val Ala Phe Ala Ala Val Glu Gly Ile Phe Phe Ser Gly Ser Phe
 225 230 235 240
 Ala Ser Ile Phe Trp Leu Lys Lys Arg Gly Leu Met Pro Gly Leu Thr
 245 250 255
 Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu His Cys Asp Phe
 260 265 270
 Ala Cys Leu Met Phe Lys His Leu Val His Lys Pro Ser Glu Glu Arg
 275 280 285
 Val Arg Glu Ile Ile Ile Asn Ala Val Arg Ile Glu Gln Glu Phe Leu
 290 295 300
 Thr Glu Ala Leu Pro Val Lys Leu Ile Gly Met Asn Cys Thr Leu Met
 305 310 315 320
 Lys Gln Tyr Ile Glu Phe Val Ala Asp Arg Leu Met Leu Glu Leu Gly
 325 330 335
 Phe Ser Lys Val Phe Arg Val Glu Asn Pro Phe Asp Phe Met Glu Asn
 340 345 350
 Ile Ser Leu Glu Gly Lys Thr Asn Phe Phe Glu Lys Arg Val Gly Glu
 355 360 365
 Tyr Gln Arg Met Gly Val Met Ser Ser Pro Thr Glu Asn Ser Phe Thr
 370 375 380
 Leu Asp Ala Asp Phe
 385

<210> 144
 <211> 281
 <212> PRT
 <213> Homo sapiens

<400> 144

Met Ala Thr Asn Phe Leu Ala His Glu Lys Ile Trp Phe Asp Lys Phe
 1 5 10 15

Lys Tyr Asp Asp Ala Glu Arg Arg Phe Tyr Glu Gln Met Asn Gly Pro
 20 25 30

Val Arg Gly Ala Ser Arg Gln Glu Asn Gly Ala Thr Val Ile Leu Arg
35 40 45

Asp Ile Ala Arg Ala Arg Glu Asn Ile Gln Lys Ser Leu Ala Gly Ser
50 55 60

Ser Gly Pro Gly Ala Ser Ser Gly Thr Ser Gly Asp His Gly Glu Leu
65 70 75 80

Val Val Arg Ile Ala Ser Leu Glu Val Glu Asn Gln Ser Leu Arg Gly
85 90 95

Val Val Gln Glu Leu Gln Gln Ala Ile Ser Lys Leu Glu Ala Arg Leu
100 105 110

Asn Val Leu Glu Lys Ser Ser Pro Gly His Arg Ala Thr Ala Pro Gln
115 120 125

Thr Gln His Val Ser Pro Met Arg Gln Val Glu Pro Pro Ala Lys Lys
130 135 140

Pro Ala Thr Pro Ala Glu Asp Asp Glu Asp Asp Asp Ile Asp Leu Phe
145 150 155 160

Gly Ser Asp Asn Glu Glu Glu Asp Lys Glu Ala Ala Gln Leu Arg Glu
165 170 175

Glu Arg Leu Arg Gln Tyr Ala Glu Lys Lys Ala Lys Lys Pro Ala Leu
180 185 190

Val Ala Lys Ser Ser Ile Leu Leu Asp Val Lys Pro Trp Asp Asp Glu
195 200 205

Thr Asp Met Ala Gln Leu Glu Ala Cys Val Arg Ser Ile Gln Leu Asp
210 215 220

Gly Leu Val Trp Gly Ala Ser Lys Leu Val Pro Val Gly Tyr Gly Ile
225 230 235 240

Arg Lys Leu Gln Ile Gln Cys Val Val Glu Asp Asp Lys Val Gly Thr
245 250 255

Asp Leu Leu Glu Glu Glu Ile Thr Lys Phe Glu Glu His Val Gln Ser
260 265 270

Val Asp Ile Ala Ala Phe Asn Lys Ile
275 280

<210> 145
<211> 269
<212> PRT
<213> Homo sapiens

<400> 145

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
1 5 10 15

Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
20 25 30

Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu
 35 40 45
 Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu
 50 55 60
 Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln
 65 70 75 80
 Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu
 85 90 95
 Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg
 100 105 110
 Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr
 115 120 125
 Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala
 130 135 140
 Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile
 145 150 155 160
 Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn
 165 170 175
 Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
 180 185 190
 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
 195 200 205
 Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
 210 215 220
 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
 225 230 235 240
 Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
 245 250 255
 Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Val
 260 265

 <210> 146
 <211> 1231
 <212> PRT
 <213> Homo sapiens

 <400> 146
 Met Arg Leu Leu Ala Lys Ile Ile Cys Leu Met Leu Trp Ala Ile Cys
 1 5 10 15
 Val Ala Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile
 20 25 30
 Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala
 35 40 45

Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met
 50 55 60
 Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys
 65 70 75 80
 Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe
 85 90 95
 Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr
 100 105 110
 Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu
 115 120 125
 Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val
 130 135 140
 Lys Cys Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser
 145 150 155 160
 Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe
 165 170 175
 Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys
 180 185 190
 Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile
 195 200 205
 Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys
 210 215 220
 Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly
 225 230 235 240
 Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp
 245 250 255
 Arg Pro Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile
 260 265 270
 Pro Asn Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp
 275 280 285
 Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly
 290 295 300
 Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys
 305 310 315 320
 Thr Leu Lys Pro Cys Asp Tyr Pro Asp Ile Lys His Gly Gly Leu Tyr
 325 330 335
 His Glu Asn Met Arg Arg Pro Tyr Phe Pro Val Ala Val Gly Lys Tyr
 340 345 350
 Tyr Ser Tyr Tyr Cys Asp Glu His Phe Glu Thr Pro Ser Gly Ser Tyr

355 360 365
 Trp Asp His Ile His Cys Thr Gln Asp Gly Trp Ser Pro Ala Val Pro
 370 375 380
 Cys Leu Arg Lys Cys Tyr Phe Pro Tyr Leu Glu Asn Gly Tyr Asn Gln
 385 390 395 400
 Asn His Gly Arg Lys Phe Val Gln Gly Lys Ser Ile Asp Val Ala Cys
 405 410 415
 His Pro Gly Tyr Ala Leu Pro Lys Ala Gln Thr Thr Val Thr Cys Met
 420 425 430
 Glu Asn Gly Trp Ser Pro Thr Pro Arg Cys Ile Arg Val Lys Thr Cys
 435 440 445
 Ser Lys Ser Ser Ile Asp Ile Glu Asn Gly Phe Ile Ser Glu Ser Gln
 450 455 460
 Tyr Thr Tyr Ala Leu Lys Glu Lys Ala Lys Tyr Gln Cys Lys Leu Gly
 465 470 475 480
 Tyr Val Thr Ala Asp Gly Glu Thr Ser Gly Ser Ile Arg Cys Gly Lys
 485 490 495
 Asp Gly Trp Ser Ala Gln Pro Thr Cys Ile Lys Ser Cys Asp Ile Pro
 500 505 510
 Val Phe Met Asn Ala Arg Thr Lys Asn Asp Phe Thr Trp Phe Lys Leu
 515 520 525
 Asn Asp Thr Leu Asp Tyr Glu Cys His Asp Gly Tyr Glu Ser Asn Thr
 530 535 540
 Gly Ser Thr Thr Gly Ser Ile Val Cys Gly Tyr Asn Gly Trp Ser Asp
 545 550 555 560
 Leu Pro Ile Cys Tyr Glu Arg Glu Cys Glu Leu Pro Lys Ile Asp Val
 565 570 575
 His Leu Val Pro Asp Arg Lys Lys Asp Gln Tyr Lys Val Gly Glu Val
 580 585 590
 Leu Lys Phe Ser Cys Lys Pro Gly Phe Thr Ile Val Gly Pro Asn Ser
 595 600 605
 Val Gln Cys Tyr His Phe Gly Leu Ser Pro Asp Leu Pro Ile Cys Lys
 610 615 620
 Glu Gln Val Gln Ser Cys Gly Pro Pro Pro Glu Leu Leu Asn Gly Asn
 625 630 635 640
 Val Lys Glu Lys Thr Lys Glu Glu Tyr Gly His Ser Glu Val Val Glu
 645 650 655
 Tyr Tyr Cys Asn Pro Arg Phe Leu Met Lys Gly Pro Asn Lys Ile Gln
 660 665 670

Cys Val Asp Gly Glu Trp Thr Thr Leu Pro Val Cys Ile Val Glu Glu
 675 680 685
 Ser Thr Cys Gly Asp Ile Pro Glu Leu Glu His Gly Trp Ala Gln Leu
 690 695 700
 Ser Ser Pro Pro Tyr Tyr Tyr Gly Asp Ser Val Glu Phe Asn Cys Ser
 705 710 715 720
 Glu Ser Phe Thr Met Ile Gly His Arg Ser Ile Thr Cys Ile His Gly
 725 730 735
 Val Trp Thr Gln Leu Pro Gln Cys Val Ala Ile Asp Lys Leu Lys Lys
 740 745 750
 Cys Lys Ser Ser Asn Leu Ile Ile Leu Glu Glu His Leu Lys Asn Lys
 755 760 765
 Lys Glu Phe Asp His Asn Ser Asn Ile Arg Tyr Arg Cys Arg Gly Lys
 770 775 780
 Glu Gly Trp Ile His Thr Val Cys Ile Asn Gly Arg Trp Asp Pro Glu
 785 790 795 800
 Val Asn Cys Ser Met Ala Gln Ile Gln Leu Cys Pro Pro Pro Pro Gln
 805 810 815
 Ile Pro Asn Ser His Asn Met Thr Thr Thr Leu Asn Tyr Arg Asp Gly
 820 825 830
 Glu Lys Val Ser Val Leu Cys Gln Glu Asn Tyr Leu Ile Gln Glu Gly
 835 840 845
 Glu Glu Ile Thr Cys Lys Asp Gly Arg Trp Gln Ser Ile Pro Leu Cys
 850 855 860
 Val Glu Lys Ile Pro Cys Ser Gln Pro Pro Gln Ile Glu His Gly Thr
 865 870 875 880
 Ile Asn Ser Ser Arg Ser Ser Gln Glu Ser Tyr Ala His Gly Thr Lys
 885 890 895
 Leu Ser Tyr Thr Cys Glu Gly Gly Phe Arg Ile Ser Glu Glu Asn Glu
 900 905 910
 Thr Thr Cys Tyr Met Gly Lys Trp Ser Ser Pro Pro Gln Cys Glu Gly
 915 920 925
 Leu Pro Cys Lys Ser Pro Pro Glu Ile Ser His Gly Val Val Ala His
 930 935 940
 Met Ser Asp Ser Tyr Gln Tyr Gly Glu Glu Val Thr Tyr Lys Cys Phe
 945 950 955 960
 Glu Gly Phe Gly Ile Asp Gly Pro Ala Ile Ala Lys Cys Leu Gly Glu
 965 970 975
 Lys Trp Ser His Pro Pro Ser Cys Ile Lys Thr Asp Cys Leu Ser Leu
 980 985 990

Pro Ser Phe Glu Asn Ala Ile Pro Met Gly Glu Lys Lys Asp Val Tyr
995 1000 1005

Lys Ala Gly Glu Gln Val Thr Tyr Thr Cys Ala Thr Tyr Tyr Lys
1010 1015 1020

Met Asp Gly Ala Ser Asn Val Thr Cys Ile Asn Ser Arg Trp Thr
1025 1030 1035

Gly Arg Pro Thr Cys Arg Asp Thr Ser Cys Val Asn Pro Pro Thr
1040 1045 1050

Val Gln Asn Ala Tyr Ile Val Ser Arg Gln Met Ser Lys Tyr Pro
1055 1060 1065

Ser Gly Glu Arg Val Arg Tyr Gln Cys Arg Ser Pro Tyr Glu Met
1070 1075 1080

Phe Gly Asp Glu Glu Val Met Cys Leu Asn Gly Asn Trp Thr Glu
1085 1090 1095

Pro Pro Gln Cys Lys Asp Ser Thr Gly Lys Cys Gly Pro Pro Pro
1100 1105 1110

Pro Ile Asp Asn Gly Asp Ile Thr Ser Phe Pro Leu Ser Val Tyr
1115 1120 1125

Ala Pro Ala Ser Ser Val Glu Tyr Gln Cys Gln Asn Leu Tyr Gln
1130 1135 1140

Leu Glu Gly Asn Lys Arg Ile Thr Cys Arg Asn Gly Gln Trp Ser
1145 1150 1155

Glu Pro Pro Lys Cys Leu His Pro Cys Val Ile Ser Arg Glu Ile
1160 1165 1170

Met Glu Asn Tyr Asn Ile Ala Leu Arg Trp Thr Ala Lys Gln Lys
1175 1180 1185

Leu Tyr Ser Arg Thr Gly Glu Ser Val Glu Phe Val Cys Lys Arg
1190 1195 1200

Gly Tyr Arg Leu Ser Ser Arg Ser His Thr Leu Arg Thr Thr Cys
1205 1210 1215

Trp Asp Gly Lys Leu Glu Tyr Pro Thr Cys Ala Lys Arg
1220 1225 1230

<210> 147
<211> 364
<212> PRT
<213> Homo sapiens

<400> 147

Met Tyr Leu Ser Arg Phe Leu Ser Ile His Ala Leu Trp Val Thr Val
1 5 10 15

Ser Ser Val Met Gln Pro Tyr Pro Leu Val Trp Gly His Tyr Asp Leu
20 25 30

Cys Lys Thr Gln Ile Tyr Thr Glu Glu Gly Lys Val Trp Asp Tyr Met
 35 40 45
 Ala Cys Gln Pro Glu Ser Thr Asp Met Thr Lys Tyr Leu Lys Val Lys
 50 55 60
 Leu Asp Pro Pro Asp Ile Thr Cys Gly Asp Pro Pro Glu Thr Phe Cys
 65 70 75 80
 Ala Met Gly Asn Pro Tyr Met Cys Asn Asn Glu Cys Asp Ala Ser Thr
 85 90 95
 Pro Glu Leu Ala His Pro Pro Glu Leu Met Phe Asp Phe Glu Gly Arg
 100 105 110
 His Pro Ser Thr Phe Trp Gln Ser Ala Thr Trp Lys Glu Tyr Pro Lys
 115 120 125
 Pro Leu Gln Val Asn Ile Thr Leu Ser Trp Ser Lys Thr Ile Glu Leu
 130 135 140
 Thr Asp Asn Ile Val Ile Thr Phe Glu Ser Gly Arg Pro Asp Gln Met
 145 150 155 160
 Ile Leu Glu Lys Ser Leu Asp Tyr Gly Arg Thr Trp Gln Pro Tyr Gln
 165 170 175
 Tyr Tyr Ala Thr Asp Cys Leu Asp Ala Phe His Met Asp Pro Lys Ser
 180 185 190
 Val Lys Asp Leu Ser Gln His Thr Val Leu Glu Ile Ile Cys Thr Glu
 195 200 205
 Glu Tyr Ser Thr Gly Tyr Thr Thr Asn Ser Lys Ile Ile His Phe Glu
 210 215 220
 Ile Lys Asp Arg Phe Ala Phe Phe Ala Gly Pro Arg Leu Arg Asn Met
 225 230 235 240
 Ala Ser Leu Tyr Gly Gln Leu Asp Thr Thr Lys Lys Leu Arg Asp Phe
 245 250 255
 Phe Thr Val Thr Asp Leu Arg Ile Arg Leu Leu Arg Pro Ala Val Gly
 260 265 270
 Glu Ile Phe Val Asp Glu Leu His Leu Ala Arg Tyr Phe Tyr Ala Ile
 275 280 285
 Ser Asp Ile Lys Val Arg Gly Arg Cys Lys Cys Asn Leu His Ala Thr
 290 295 300
 Val Cys Val Tyr Asp Asn Ser Lys Leu Thr Cys Glu Cys Glu His Asn
 305 310 315 320
 Thr Thr Gly Pro Asp Cys Gly Lys Cys Lys Lys Asn Tyr Gln Gly Arg
 325 330 335
 Pro Trp Ser Pro Gly Ser Tyr Leu Pro Ile Pro Lys Gly Thr Ala Asn
 340 345 350

Thr Cys Ile Pro Ser Ile Ser Ser Ile Gly Ser Lys
 355 360

<210> 148
 <211> 3210
 <212> PRT
 <213> Homo sapiens

<400> 148

Met Ser Trp Ala Leu Glu Glu Trp Lys Glu Gly Leu Pro Thr Arg Thr
 1 5 10 15

Leu Gln Lys Ile Gln Glu Leu Glu Gly Gln Leu Asp Lys Leu Lys Lys
 20 25 30

Glu Lys Gln Gln Arg Gln Phe Gln Leu Asp Ser Leu Glu Ala Ala Pro
 35 40 45

Gln Lys Gln Thr Gln Lys Val Glu Asn Glu Lys Thr Glu Gly Thr Asn
 50 55 60

Leu Lys Arg Glu Asn Gln Arg Leu Met Glu Ile Cys Glu Ser Leu Glu
 65 70 75 80

Lys Thr Lys Gln Lys Ile Ser His Glu Leu Gln Val Lys Glu Ser Gln
 85 90 95

Val Asn Phe Gln Glu Gly Gln Leu Asn Ser Gly Lys Lys Gln Ile Glu
 100 105 110

Lys Leu Glu Gln Glu Leu Lys Arg Cys Lys Ser Glu Leu Glu Arg Ser
 115 120 125

Gln Gln Ala Ala Gln Ser Ala Asp Val Ser Leu Asn Pro Cys Asn Thr
 130 135 140

Pro Gln Lys Ile Phe Thr Thr Pro Leu Thr Pro Ser Gln Tyr Tyr Ser
 145 150 155 160

Gly Ser Lys Tyr Glu Asp Leu Lys Glu Lys Tyr Asn Lys Glu Val Glu
 165 170 175

Glu Arg Lys Arg Leu Glu Ala Glu Val Lys Ala Leu Gln Ala Lys Lys
 180 185 190

Ala Ser Gln Thr Leu Pro Gln Ala Thr Met Asn His Arg Asp Ile Ala
 195 200 205

Arg His Gln Ala Ser Ser Ser Val Phe Ser Trp Gln Gln Glu Lys Thr
 210 215 220

Pro Ser His Leu Ser Ser Asn Ser Gln Arg Thr Pro Ile Arg Arg Asp
 225 230 235 240

Phe Ser Ala Ser Tyr Phe Ser Gly Glu Leu Glu Val Thr Pro Ser Arg
 245 250 255

Ser Thr Leu Gln Ile Gly Lys Arg Asp Ala Asn Ser Ser Phe Phe Gly
 260 265 270

Asn Ser Ser Ser Pro His Leu Leu Asp Gln Leu Lys Ala Gln Asn Gln
 275 280 285
 Glu Leu Arg Asn Lys Ile Asn Glu Leu Glu Leu Arg Leu Gln Gly His
 290 295 300
 Glu Lys Glu Met Lys Gly Gln Val Asn Lys Phe Gln Glu Leu Gln Leu
 305 310 315 320
 Gln Leu Glu Lys Ala Lys Val Glu Leu Ile Glu Lys Glu Lys Val Leu
 325 330 335
 Asn Lys Cys Arg Asp Glu Leu Val Arg Thr Thr Ala Gln Tyr Asp Gln
 340 345 350
 Ala Ser Thr Lys Tyr Thr Ala Leu Glu Gln Lys Leu Lys Lys Leu Thr
 355 360 365
 Glu Asp Leu Ser Cys Gln Arg Gln Asn Ala Glu Ser Ala Arg Cys Ser
 370 375 380
 Leu Glu Gln Lys Ile Lys Glu Lys Glu Lys Glu Phe Gln Glu Glu Leu
 385 390 395 400
 Ser Arg Gln Gln Arg Ser Phe Gln Thr Leu Asp Gln Glu Cys Ile Gln
 405 410 415
 Met Lys Ala Arg Leu Thr Gln Glu Leu Gln Gln Ala Lys Asn Met His
 420 425 430
 Asn Val Leu Gln Ala Glu Leu Asp Lys Leu Thr Ser Val Lys Gln Gln
 435 440 445
 Leu Glu Asn Asn Leu Glu Glu Phe Lys Gln Lys Leu Cys Arg Ala Glu
 450 455 460
 Gln Ala Phe Gln Ala Ser Gln Ile Lys Glu Asn Glu Leu Arg Arg Ser
 465 470 475 480
 Met Glu Glu Met Lys Lys Glu Asn Asn Leu Leu Lys Ser His Ser Glu
 485 490 495
 Gln Lys Ala Arg Glu Val Cys His Leu Glu Ala Glu Leu Lys Asn Ile
 500 505 510
 Lys Gln Cys Leu Asn Gln Ser Gln Asn Phe Ala Glu Glu Met Lys Ala
 515 520 525
 Lys Asn Thr Ser Gln Glu Thr Met Leu Arg Asp Leu Gln Glu Lys Ile
 530 535 540
 Asn Gln Gln Glu Asn Ser Leu Thr Leu Glu Lys Leu Lys Leu Ala Val
 545 550 555 560
 Ala Asp Leu Glu Lys Gln Arg Asp Cys Ser Gln Asp Leu Leu Lys Lys
 565 570 575
 Arg Glu His His Ile Glu Gln Leu Asn Asp Lys Leu Ser Lys Thr Glu

580	585	590
Lys Glu Ser Lys Ala Leu Leu Ser	Ala Leu Glu Leu Lys Lys Lys Glu	
595	600	605
Tyr Glu Glu Leu Lys Glu Glu Lys Thr Leu Phe Ser Cys Trp Lys Ser		
610	615	620
Glu Asn Glu Lys Leu Leu Thr Gln Met Glu Ser Glu Lys Glu Asn Leu		
625	630	635
Gln Ser Lys Ile Asn His Leu Glu Thr Cys Leu Lys Thr Gln Gln Ile		
645	650	655
Lys Ser His Glu Tyr Asn Glu Arg Val Arg Thr Leu Glu Met Asp Arg		
660	665	670
Glu Asn Leu Ser Val Glu Ile Arg Asn Leu His Asn Val Leu Asp Ser		
675	680	685
Lys Ser Val Glu Val Glu Thr Gln Lys Leu Ala Tyr Met Glu Leu Gln		
690	695	700
Gln Lys Ala Glu Phe Ser Asp Gln Lys His Gln Lys Glu Ile Glu Asn		
705	710	715
Met Cys Leu Lys Thr Ser Gln Leu Thr Gly Gln Val Glu Asp Leu Glu		
725	730	735
His Lys Leu Gln Leu Leu Ser Asn Glu Ile Met Asp Lys Asp Arg Cys		
740	745	750
Tyr Gln Asp Leu His Ala Glu Tyr Glu Ser Leu Arg Asp Leu Leu Lys		
755	760	765
Ser Lys Asp Ala Ser Leu Val Thr Asn Glu Asp His Gln Arg Ser Leu		
770	775	780
Leu Ala Phe Asp Gln Gln Pro Ala Met His His Ser Phe Ala Asn Ile		
785	790	795
Ile Gly Glu Gln Gly Ser Met Pro Ser Glu Arg Ser Glu Cys Arg Leu		
805	810	815
Glu Ala Asp Gln Ser Pro Lys Asn Ser Ala Ile Leu Gln Asn Arg Val		
820	825	830
Asp Ser Leu Glu Phe Ser Leu Glu Ser Gln Lys Gln Met Asn Ser Asp		
835	840	845
Leu Gln Lys Gln Cys Glu Glu Leu Val Gln Ile Lys Gly Glu Ile Glu		
850	855	860
Glu Asn Leu Met Lys Ala Glu Gln Met His Gln Ser Phe Val Ala Glu		
865	870	875
Thr Ser Gln Arg Ile Ser Lys Leu Gln Glu Asp Thr Ser Ala His Gln		
885	890	895

Asn Val Val Ala Glu Thr Leu Ser Ala Leu Glu Asn Lys Glu Lys Glu
 900 905 910
 Leu Gln Leu Leu Asn Asp Lys Val Glu Thr Glu Gln Ala Glu Ile Gln
 915 920 925
 Glu Leu Lys Lys Ser Asn His Leu Leu Glu Asp Ser Leu Lys Glu Leu
 930 935 940
 Gln Leu Leu Ser Glu Thr Leu Ser Leu Glu Lys Lys Glu Met Ser Ser
 945 950 955 960
 Ile Ile Ser Leu Asn Lys Arg Glu Ile Glu Glu Leu Thr Gln Glu Asn
 965 970 975
 Gly Thr Leu Lys Glu Ile Asn Ala Ser Leu Asn Gln Glu Lys Met Asn
 980 985 990
 Leu Ile Gln Lys Ser Glu Ser Phe Ala Asn Tyr Ile Asp Glu Arg Glu
 995 1000 1005
 Lys Ser Ile Ser Glu Leu Ser Asp Gln Tyr Lys Gln Glu Lys Leu
 1010 1015 1020
 Ile Leu Leu Gln Arg Cys Glu Glu Thr Gly Asn Ala Tyr Glu Asp
 1025 1030 1035
 Leu Ser Gln Lys Tyr Lys Ala Ala Gln Glu Lys Asn Ser Lys Leu
 1040 1045 1050
 Glu Cys Leu Leu Asn Glu Cys Thr Ser Leu Cys Glu Asn Arg Lys
 1055 1060 1065
 Asn Glu Leu Glu Gln Leu Lys Glu Ala Phe Ala Lys Glu His Gln
 1070 1075 1080
 Glu Phe Leu Thr Lys Leu Ala Phe Ala Glu Glu Arg Asn Gln Asn
 1085 1090 1095
 Leu Met Leu Glu Leu Glu Thr Val Gln Gln Ala Leu Arg Ser Glu
 1100 1105 1110
 Met Thr Asp Asn Gln Asn Asn Ser Lys Ser Glu Ala Gly Gly Leu
 1115 1120 1125
 Lys Gln Glu Ile Met Thr Leu Lys Glu Glu Gln Asn Lys Met Gln
 1130 1135 1140
 Lys Glu Val Asn Asp Leu Leu Gln Glu Asn Glu Gln Leu Met Lys
 1145 1150 1155
 Val Met Lys Thr Lys His Glu Cys Gln Asn Leu Glu Ser Glu Pro
 1160 1165 1170
 Ile Arg Asn Ser Val Lys Glu Arg Glu Ser Glu Arg Asn Gln Cys
 1175 1180 1185
 Asn Phe Lys Pro Gln Met Asp Leu Glu Val Lys Glu Ile Ser Leu
 1190 1195 1200

Asp Ser Tyr Asn Ala Gln Leu Val Gln Leu Glu Ala Met Leu Arg
 1205 1210 1215
 Asn Lys Glu Leu Lys Leu Gln Glu Ser Glu Lys Glu Lys Glu Cys
 1220 1225 1230
 Leu Gln His Glu Leu Gln Thr Ile Arg Gly Asp Leu Glu Thr Ser
 1235 1240 1245
 Asn Leu Gln Asp Met Gln Ser Gln Glu Ile Ser Gly Leu Lys Asp
 1250 1255 1260
 Cys Glu Ile Asp Ala Glu Glu Lys Tyr Ile Ser Gly Pro His Glu
 1265 1270 1275
 Leu Ser Thr Ser Gln Asn Asp Asn Ala His Leu Gln Cys Ser Leu
 1280 1285 1290
 Gln Thr Thr Met Asn Lys Leu Asn Glu Leu Glu Lys Ile Cys Glu
 1295 1300 1305
 Ile Leu Gln Ala Glu Lys Tyr Glu Leu Val Thr Glu Leu Asn Asp
 1310 1315 1320
 Ser Arg Ser Glu Cys Ile Thr Ala Thr Arg Lys Met Ala Glu Glu
 1325 1330 1335
 Val Gly Lys Leu Leu Asn Glu Val Lys Ile Leu Asn Asp Asp Ser
 1340 1345 1350
 Gly Leu Leu His Gly Glu Leu Val Glu Asp Ile Pro Gly Gly Glu
 1355 1360 1365
 Phe Gly Glu Gln Pro Asn Glu Gln His Pro Val Ser Leu Ala Pro
 1370 1375 1380
 Leu Asp Glu Ser Asn Ser Tyr Glu His Leu Thr Leu Ser Asp Lys
 1385 1390 1395
 Glu Val Gln Met His Phe Ala Glu Leu Gln Glu Lys Phe Leu Ser
 1400 1405 1410
 Leu Gln Ser Glu His Lys Ile Leu His Asp Gln His Cys Gln Met
 1415 1420 1425
 Ser Ser Lys Met Ser Glu Leu Gln Thr Tyr Val Asp Ser Leu Lys
 1430 1435 1440
 Ala Glu Asn Leu Val Leu Ser Thr Asn Leu Arg Asn Phe Gln Gly
 1445 1450 1455
 Asp Leu Val Lys Glu Met Gln Leu Gly Leu Glu Glu Gly Leu Val
 1460 1465 1470
 Pro Ser Leu Ser Ser Ser Cys Val Pro Asp Ser Ser Ser Leu Ser
 1475 1480 1485
 Ser Leu Gly Asp Ser Ser Phe Tyr Arg Ala Leu Leu Glu Gln Thr
 1490 1495 1500

Gly Asp Met Ser Leu Leu Ser Asn Leu Glu Gly Ala Val Ser Ala
 1505 1510 1515
 Asn Gln Cys Ser Val Asp Glu Val Phe Cys Ser Ser Leu Gln Thr
 1520 1525 1530
 Tyr Val Asp Ser Leu Lys Ala Glu Asn Leu Val Leu Ser Thr Asn
 1535 1540 1545
 Leu Arg Asn Phe Gln Gly Asp Leu Val Lys Glu Met Gln Leu Gly
 1550 1555 1560
 Leu Glu Glu Gly Leu Val Pro Ser Leu Ser Ser Ser Cys Val Pro
 1565 1570 1575
 Asp Ser Ser Ser Leu Ser Ser Leu Gly Asp Ser Ser Phe Tyr Arg
 1580 1585 1590
 Ala Leu Leu Glu Gln Thr Gly Asp Met Ser Leu Leu Ser Asn Leu
 1595 1600 1605
 Glu Gly Val Val Ser Ala Asn Gln Cys Ser Val Asp Glu Val Phe
 1610 1615 1620
 Cys Ser Ser Leu Gln Glu Glu Asn Leu Thr Arg Lys Glu Thr Pro
 1625 1630 1635
 Ser Ala Pro Ala Lys Gly Val Glu Glu Leu Glu Ser Leu Cys Glu
 1640 1645 1650
 Val Tyr Arg Gln Ser Leu Glu Lys Leu Glu Glu Lys Met Glu Ser
 1655 1660 1665
 Gln Gly Ile Met Lys Asn Lys Glu Ile Gln Glu Leu Glu Gln Leu
 1670 1675 1680
 Leu Ser Ser Glu Arg Gln Glu Leu Asp Cys Leu Arg Lys Gln Tyr
 1685 1690 1695
 Leu Ser Glu Asn Glu Gln Trp Gln Gln Lys Leu Thr Ser Val Thr
 1700 1705 1710
 Leu Glu Met Glu Ser Lys Leu Ala Ala Glu Lys Lys Gln Thr Glu
 1715 1720 1725
 Gln Leu Ser Leu Glu Leu Glu Val Ala Arg Leu Gln Leu Gln Gly
 1730 1735 1740
 Leu Asp Leu Ser Ser Arg Ser Leu Leu Gly Ile Asp Thr Glu Asp
 1745 1750 1755
 Ala Ile Gln Gly Arg Asn Glu Ser Cys Asp Ile Ser Lys Glu His
 1760 1765 1770
 Thr Ser Glu Thr Thr Glu Arg Thr Pro Lys His Asp Val His Gln
 1775 1780 1785
 Ile Cys Asp Lys Asp Ala Gln Gln Asp Leu Asn Leu Asp Ile Glu

1790	1795	1800
Lys Ile Thr Glu Thr Gly Ala 1805	Val Lys Pro Thr Gly 1810	Glu Cys Ser 1815
Gly Glu Gln Ser Pro Asp Thr 1820	Asn Tyr Glu Pro 1825	Pro Gly Glu Asp 1830
Lys Thr Gln Gly Ser Ser Glu 1835	Cys Ile Ser Glu 1840	Leu Ser Phe Ser 1845
Gly Pro Asn Ala Leu Val Pro 1850	Met Asp Phe Leu 1855	Gly Asn Gln Glu 1860
Asp Ile His Asn Leu Gln Leu 1865	Arg Val Lys Glu Thr 1870	Ser Asn Glu 1875
Asn Leu Arg Leu Leu His Val 1880	Ile Glu Asp Arg 1885	Asp Arg Lys Val 1890
Glu Ser Leu Leu Asn Glu Met 1895	Lys Glu Leu Asp 1900	Ser Lys Leu His 1905
Leu Gln Glu Val Gln Leu Met 1910	Thr Lys Ile Glu Ala 1915	Cys Ile Glu 1920
Leu Glu Lys Ile Val Gly Glu 1925	Leu Lys Lys Glu Asn 1930	Ser Asp Leu 1935
Ser Glu Lys Leu Glu Tyr Phe 1940	Ser Cys Asp His 1945	Gln Glu Leu Leu 1950
Gln Arg Val Glu Thr Ser Glu 1955	Gly Leu Asn Ser Asp 1960	Leu Glu Met 1965
His Ala Asp Lys Ser Ser Arg 1970	Glu Asp Ile Gly 1975	Asp Asn Val Ala 1980
Lys Val Asn Asp Ser Trp Lys 1985	Glu Arg Phe Leu 1990	Asp Val Glu Asn 1995
Glu Leu Ser Arg Ile Arg Ser 2000	Glu Lys Ala Ser 2005	Ile Glu His Glu 2010
Ala Leu Tyr Leu Glu Ala Asp 2015	Leu Glu Val Val 2020	Gln Thr Glu Lys 2025
Leu Cys Leu Glu Lys Asp Asn 2030	Glu Asn Lys Gln 2035	Lys Val Ile Val 2040
Cys Leu Glu Glu Glu Leu Ser 2045	Val Val Thr Ser 2050	Glu Arg Asn Gln 2055
Leu Arg Gly Glu Leu Asp Thr 2060	Met Ser Lys Lys 2065	Thr Thr Ala Leu 2070
Asp Gln Leu Ser Glu Lys Met 2075	Lys Glu Lys Thr 2080	Gln Glu Leu Glu 2085

Ser His Gln Ser Glu Cys Leu His Cys Ile Gln Val Ala Glu Ala
 2090 2095 2100
 Glu Val Lys Glu Lys Thr Glu Leu Leu Gln Thr Leu Ser Ser Asp
 2105 2110 2115
 Val Ser Glu Leu Leu Lys Asp Lys Thr His Leu Gln Glu Lys Leu
 2120 2125 2130
 Gln Ser Leu Glu Lys Asp Ser Gln Ala Leu Ser Leu Thr Lys Cys
 2135 2140 2145
 Glu Leu Glu Asn Gln Ile Ala Gln Leu Asn Lys Glu Lys Glu Leu
 2150 2155 2160
 Leu Val Lys Glu Ser Glu Ser Leu Gln Ala Arg Leu Ser Glu Ser
 2165 2170 2175
 Asp Tyr Glu Lys Leu Asn Val Ser Lys Ala Leu Glu Ala Ala Leu
 2180 2185 2190
 Val Glu Lys Gly Glu Phe Ala Leu Arg Leu Ser Ser Thr Gln Glu
 2195 2200 2205
 Glu Val His Gln Leu Arg Arg Gly Ile Glu Lys Leu Arg Val Arg
 2210 2215 2220
 Ile Glu Ala Asp Glu Lys Lys Gln Leu His Ile Ala Glu Lys Leu
 2225 2230 2235
 Lys Glu Arg Glu Arg Glu Asn Asp Ser Leu Lys Asp Lys Val Glu
 2240 2245 2250
 Asn Leu Glu Arg Glu Leu Gln Met Ser Glu Glu Asn Gln Glu Leu
 2255 2260 2265
 Val Ile Leu Asp Ala Glu Asn Ser Lys Ala Glu Val Glu Thr Leu
 2270 2275 2280
 Lys Thr Gln Ile Glu Glu Met Ala Arg Ser Leu Lys Val Phe Glu
 2285 2290 2295
 Leu Asp Leu Val Thr Leu Arg Ser Glu Lys Glu Asn Leu Thr Lys
 2300 2305 2310
 Gln Ile Gln Glu Lys Gln Gly Gln Leu Ser Glu Leu Asp Lys Leu
 2315 2320 2325
 Leu Ser Ser Phe Lys Ser Leu Leu Glu Glu Lys Glu Gln Ala Glu
 2330 2335 2340
 Ile Gln Ile Lys Glu Glu Ser Lys Thr Ala Val Glu Met Leu Gln
 2345 2350 2355
 Asn Gln Leu Lys Glu Leu Asn Glu Ala Val Ala Ala Leu Cys Gly
 2360 2365 2370
 Asp Gln Glu Ile Met Lys Ala Thr Glu Gln Ser Leu Asp Pro Pro
 2375 2380 2385

Ile Glu Glu Glu His Gln Leu Arg Asn Ser Ile Glu Lys Leu Arg
 2390 2395 2400
 Ala Arg Leu Glu Ala Asp Glu Lys Lys Gln Leu Cys Val Leu Gln
 2405 2410 2415
 Gln Leu Lys Glu Ser Glu His His Ala Asp Leu Leu Lys Gly Arg
 2420 2425 2430
 Val Glu Asn Leu Glu Arg Glu Leu Glu Ile Ala Arg Thr Asn Gln
 2435 2440 2445
 Glu His Ala Ala Leu Glu Ala Glu Asn Ser Lys Gly Glu Val Glu
 2450 2455 2460
 Thr Leu Lys Ala Lys Ile Glu Gly Met Thr Gln Ser Leu Arg Gly
 2465 2470 2475
 Leu Glu Leu Asp Val Val Thr Ile Arg Ser Glu Lys Glu Asp Leu
 2480 2485 2490
 Thr Asn Glu Leu Gln Lys Glu Gln Glu Arg Ile Ser Glu Leu Glu
 2495 2500 2505
 Ile Ile Asn Ser Ser Phe Glu Asn Ile Leu Gln Glu Lys Glu Gln
 2510 2515 2520
 Glu Lys Val Gln Met Lys Glu Lys Ser Ser Thr Ala Met Glu Met
 2525 2530 2535
 Leu Gln Thr Gln Leu Lys Glu Leu Asn Glu Arg Val Ala Ala Leu
 2540 2545 2550
 His Asn Asp Gln Glu Ala Cys Lys Ala Lys Glu Gln Asn Leu Ser
 2555 2560 2565
 Ser Gln Val Glu Cys Leu Glu Leu Glu Lys Ala Gln Leu Leu Gln
 2570 2575 2580
 Gly Leu Asp Glu Ala Lys Asn Asn Tyr Ile Val Leu Gln Ser Ser
 2585 2590 2595
 Val Asn Gly Leu Ile Gln Glu Val Glu Asp Gly Lys Gln Lys Leu
 2600 2605 2610
 Glu Lys Lys Asp Glu Glu Ile Ser Arg Leu Lys Asn Gln Ile Gln
 2615 2620 2625
 Asp Gln Glu Gln Leu Val Ser Lys Leu Ser Gln Val Glu Gly Glu
 2630 2635 2640
 His Gln Leu Trp Lys Glu Gln Asn Leu Glu Leu Arg Asn Leu Thr
 2645 2650 2655
 Val Glu Leu Glu Gln Lys Ile Gln Val Leu Gln Ser Lys Asn Ala
 2660 2665 2670
 Ser Leu Gln Asp Thr Leu Glu Val Leu Gln Ser Ser Tyr Lys Asn
 2675 2680 2685

Leu Glu Asn Glu Leu Glu Leu Thr Lys Met Asp Lys Met Ser Phe
 2690 2695 2700
 Val Glu Lys Val Asn Lys Met Thr Ala Lys Glu Thr Glu Leu Gln
 2705 2710 2715
 Arg Glu Met His Glu Met Ala Gln Lys Thr Ala Glu Leu Gln Glu
 2720 2725 2730
 Glu Leu Ser Gly Glu Lys Asn Arg Leu Ala Gly Glu Leu Gln Leu
 2735 2740 2745
 Leu Leu Glu Glu Ile Lys Ser Ser Lys Asp Gln Leu Lys Glu Leu
 2750 2755 2760
 Thr Leu Glu Asn Ser Glu Leu Lys Lys Ser Leu Asp Cys Met His
 2765 2770 2775
 Lys Asp Gln Val Glu Lys Glu Gly Lys Val Arg Glu Glu Ile Ala
 2780 2785 2790
 Glu Tyr Gln Leu Arg Leu His Glu Ala Glu Lys Lys His Gln Ala
 2795 2800 2805
 Leu Leu Leu Asp Thr Asn Lys Gln Tyr Glu Val Glu Ile Gln Thr
 2810 2815 2820
 Tyr Arg Glu Lys Leu Thr Ser Lys Glu Glu Cys Leu Ser Ser Gln
 2825 2830 2835
 Lys Leu Glu Ile Asp Leu Leu Lys Ser Ser Lys Glu Glu Leu Asn
 2840 2845 2850
 Asn Ser Leu Lys Ala Thr Thr Gln Ile Leu Glu Glu Leu Lys Lys
 2855 2860 2865
 Thr Lys Met Asp Asn Leu Lys Tyr Val Asn Gln Leu Lys Lys Glu
 2870 2875 2880
 Asn Glu Arg Ala Gln Gly Lys Met Lys Leu Leu Ile Lys Ser Cys
 2885 2890 2895
 Lys Gln Leu Glu Glu Glu Lys Glu Ile Leu Gln Lys Glu Leu Ser
 2900 2905 2910
 Gln Leu Gln Ala Ala Gln Glu Lys Gln Lys Thr Gly Thr Val Met
 2915 2920 2925
 Asp Thr Lys Val Asp Glu Leu Thr Thr Glu Ile Lys Glu Leu Lys
 2930 2935 2940
 Glu Thr Leu Glu Glu Lys Thr Lys Glu Ala Asp Glu Tyr Leu Asp
 2945 2950 2955
 Lys Tyr Cys Ser Leu Leu Ile Ser His Glu Lys Leu Glu Lys Ala
 2960 2965 2970
 Lys Glu Met Leu Glu Thr Gln Val Ala His Leu Cys Ser Gln Gln

2975 2980 2985
 Ser Lys Gln Asp Ser Arg Gly Ser Pro Leu Leu Gly Pro Val Val
 2990 2995 3000
 Pro Gly Pro Ser Pro Ile Pro Ser Val Thr Glu Lys Arg Leu Ser
 3005 3010 3015
 Ser Gly Gln Asn Lys Ala Ser Gly Lys Arg Gln Arg Ser Ser Gly
 3020 3025 3030
 Ile Trp Glu Asn Gly Gly Gly Pro Thr Pro Ala Thr Pro Glu Ser
 3035 3040 3045
 Phe Ser Lys Lys Ser Lys Lys Ala Val Met Ser Gly Ile His Pro
 3050 3055 3060
 Ala Glu Asp Thr Glu Gly Thr Glu Phe Glu Pro Glu Gly Leu Pro
 3065 3070 3075
 Glu Val Val Lys Lys Gly Phe Ala Asp Ile Pro Thr Gly Lys Thr
 3080 3085 3090
 Ser Pro Tyr Ile Leu Arg Arg Thr Thr Met Ala Thr Arg Thr Ser
 3095 3100 3105
 Pro Arg Leu Ala Ala Gln Lys Leu Ala Leu Ser Pro Leu Ser Leu
 3110 3115 3120
 Gly Lys Glu Asn Leu Ala Glu Ser Ser Lys Pro Thr Ala Gly Gly
 3125 3130 3135
 Ser Arg Ser Gln Lys Val Lys Val Ala Gln Arg Ser Pro Val Asp
 3140 3145 3150
 Ser Gly Thr Ile Leu Arg Glu Pro Thr Thr Lys Ser Val Pro Val
 3155 3160 3165
 Asn Asn Leu Pro Glu Arg Ser Pro Thr Asp Ser Pro Arg Glu Gly
 3170 3175 3180
 Leu Arg Val Lys Arg Gly Arg Leu Val Pro Ser Pro Lys Ala Gly
 3185 3190 3195
 Leu Glu Ser Lys Gly Ser Glu Asn Cys Lys Val Gln
 3200 3205 3210

 <210> 149
 <211> 108
 <212> PRT
 <213> Homo sapiens

 <400> 149
 Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
 1 5 10 15
 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
 20 25 30
 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

35 40 45
 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
 50 55 60
 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
 65 70 75 80
 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
 85 90 95
 Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
 100 105
 <210> 150
 <211> 253
 <212> PRT
 <213> Homo sapiens
 <400> 150
 Met Ala Arg Ser Leu Leu Leu Pro Leu Gln Ile Leu Leu Leu Ser Leu
 1 5 10 15
 Ala Leu Glu Thr Ala Gly Glu Glu Ala Gln Gly Asp Lys Ile Ile Asp
 20 25 30
 Gly Ala Pro Cys Ala Arg Gly Ser His Pro Trp Gln Val Ala Leu Leu
 35 40 45
 Ser Gly Asn Gln Leu His Cys Gly Gly Val Leu Val Asn Glu Arg Trp
 50 55 60
 Val Leu Thr Ala Ala His Cys Lys Met Asn Glu Tyr Thr Val His Leu
 65 70 75 80
 Gly Ser Asp Thr Leu Gly Asp Arg Arg Ala Gln Arg Ile Lys Ala Ser
 85 90 95
 Lys Ser Phe Arg His Pro Gly Tyr Ser Thr Gln Thr His Val Asn Asp
 100 105 110
 Leu Met Leu Val Lys Leu Asn Ser Gln Ala Arg Leu Ser Ser Met Val
 115 120 125
 Lys Lys Val Arg Leu Pro Ser Arg Cys Glu Pro Pro Gly Thr Thr Cys
 130 135 140
 Thr Val Ser Gly Trp Gly Thr Thr Thr Ser Pro Asp Val Thr Phe Pro
 145 150 155 160
 Ser Asp Leu Met Cys Val Asp Val Lys Leu Ile Ser Pro Gln Asp Cys
 165 170 175
 Thr Lys Val Tyr Lys Asp Leu Leu Glu Asn Ser Met Leu Cys Ala Gly
 180 185 190
 Ile Pro Asp Ser Lys Lys Asn Ala Cys Asn Gly Asp Ser Gly Gly Pro
 195 200 205
 Leu Val Cys Arg Gly Thr Leu Gln Gly Leu Val Ser Trp Gly Thr Phe

210 215 220
 Pro Cys Gly Gln Pro Asn Asp Pro Gly Val Tyr Thr Gln Val Cys Lys
 225 230 235 240

 Phe Thr Lys Trp Ile Asn Asp Thr Met Lys Lys His Arg
 245 250

 <210> 151
 <211> 495
 <212> PRT
 <213> Homo sapiens

 <400> 151-

 Met Val Thr Trp Leu Tyr Arg Phe Leu Pro Thr Ser Asn Met Ala Ala
 1 5 10 15

 Lys Leu Arg Ser Leu Leu Pro Pro Asp Leu Arg Leu Gln Phe Trp Leu
 20 25 30

 His Ala Arg Leu Gln Lys Cys Phe Leu Ser Arg Gly Cys Gly Ser Tyr
 35 40 45

 Cys Ala Gly Ala Lys Ala Ser Pro Leu Pro Gly Lys Met Ala Met Gly
 50 55 60

 Leu Met Cys Gly Arg Arg Glu Leu Leu Arg Leu Leu Gln Ser Gly Arg
 65 70 75 80

 Arg Val His Ser Val Ala Gly Pro Ser Gln Trp Leu Gly Lys Pro Leu
 85 90 95

 Thr Thr Arg Leu Leu Phe Pro Val Ala Pro Cys Cys Cys Arg Pro His
 100 105 110

 Tyr Leu Phe Leu Ala Ala Ser Gly Pro Arg Ser Leu Ser Thr Ser Ala
 115 120 125

 Ile Ser Phe Ala Glu Val Gln Val Gln Ala Pro Pro Val Val Ala Ala
 130 135 140

 Thr Pro Ser Pro Thr Ala Val Pro Glu Val Ala Ser Gly Glu Thr Ala
 145 150 155 160

 Asp Val Val Gln Thr Ala Ala Glu Gln Ser Phe Ala Glu Leu Gly Leu
 165 170 175

 Gly Ser Tyr Thr Pro Val Gly Leu Ile Gln Asn Leu Leu Glu Phe Met
 180 185 190

 His Val Asp Leu Gly Leu Pro Trp Trp Gly Ala Ile Ala Ala Cys Thr
 195 200 205

 Val Phe Ala Arg Cys Leu Ile Phe Pro Leu Ile Val Thr Gly Gln Arg
 210 215 220

 Glu Ala Ala Arg Ile His Asn His Leu Pro Glu Ile Gln Lys Phe Ser
 225 230 235 240

 Ser Arg Ile Arg Glu Ala Lys Leu Ala Gly Asp His Ile Glu Tyr Tyr

245 250 255
 Lys Ala Ser Ser Glu Met Ala Leu Tyr Gln Lys Lys His Gly Ile Lys
 260 265 270
 Leu Tyr Lys Pro Leu Ile Leu Pro Val Thr Gln Ala Pro Ile Phe Ile
 275 280 285
 Ser Phe Phe Ile Ala Leu Arg Glu Met Ala Asn Leu Pro Val Pro Ser
 290 295 300
 Leu Gln Thr Gly Gly Leu Trp Trp Phe Gln Asp Leu Thr Val Ser Asp
 305 310 315 320
 Pro Ile Tyr Ile Leu Pro Leu Ala Val Thr Ala Thr Met Trp Ala Val
 325 330 335
 Leu Glu Leu Gly Ala Glu Thr Gly Val Gln Ser Ser Asp Leu Gln Trp
 340 345 350
 Met Arg Asn Val Ile Arg Met Met Pro Leu Ile Thr Leu Pro Ile Thr
 355 360 365
 Met His Phe Pro Thr Ala Val Phe Met Tyr Trp Leu Ser Ser Asn Leu
 370 375 380
 Phe Ser Leu Val Gln Val Ser Cys Leu Arg Ile Pro Ala Val Arg Thr
 385 390 395 400
 Val Leu Lys Ile Pro Gln Arg Val Val His Asp Leu Asp Lys Leu Pro
 405 410 415
 Pro Arg Glu Gly Phe Leu Glu Ser Phe Lys Lys Gly Trp Lys Asn Ala
 420 425 430
 Glu Met Thr Arg Gln Leu Arg Glu Arg Glu Gln Arg Met Arg Asn Gln
 435 440 445
 Leu Glu Leu Ala Ala Arg Gly Pro Leu Arg Gln Thr Phe Thr His Asn
 450 455 460
 Pro Leu Leu Gln Pro Gly Lys Asp Asn Pro Pro Asn Ile Pro Ser Ser
 465 470 475 480
 Ser Ser Lys Pro Lys Ser Lys Tyr Pro Trp His Asp Thr Leu Gly
 485 490 495

<210> 152
 <211> 351
 <212> PRT
 <213> Homo sapiens

<400> 152

Met Gly Asn Ala Ala Thr Ala Lys Lys Gly Ser Glu Val Glu Ser Val
 1 5 10 15

Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp Glu
 20 25 30

Asn Pro Thr Gln Asn Asn Ala Gly Leu Glu Asp Phe Glu Arg Lys Lys

35	40	45
Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His Lys 50 55 60		
Ala Thr Glu Gln Tyr Tyr Ala Met Lys Ile Leu Asp Lys Gln Lys Val 65 70 75 80		
Val Lys Leu Lys Gln Ile Glu His Thr Leu Asn Glu Lys Arg Ile Leu 85 90 95		
Gln Ala Val Asn Phe Pro Phe Leu Val Arg Leu Glu Tyr Ala Phe Lys 100 105 110		
Asp Asn Ser Asn Leu Tyr Met Val Met Glu Tyr Val Pro Gly Gly Glu 115 120 125		
Met Phe Ser His Leu Arg Arg Ile Gly Arg Phe Ser Glu Pro His Ala 130 135 140		
Arg Phe Tyr Ala Ala Gln Ile Val Leu Thr Phe Glu Tyr Leu His Ser 145 150 155 160		
Leu Asp Leu Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Ile Asp 165 170 175		
His Gln Gly Tyr Ile Gln Val Thr Asp Phe Gly Phe Ala Lys Arg Val 180 185 190		
Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro 195 200 205		
Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala 210 215 220		
Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe 225 230 235 240		
Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val 245 250 255		
Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn 260 265 270		
Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asn Gly 275 280 285		
Val Ser Asp Ile Lys Thr His Lys Trp Phe Ala Thr Thr Asp Trp Ile 290 295 300		
Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Arg 305 310 315 320		
Gly Ser Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Asp Ile 325 330 335		
Arg Val Ser Ile Thr Glu Lys Cys Ala Lys Glu Phe Gly Glu Phe 340 345 350		

<210> 153
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 153

Met Val Phe Arg Arg Phe Val Glu Val Gly Arg Val Ala Tyr Val Ser
 1 5 10 15

Phe Gly Pro His Ala Gly Lys Leu Val Ala Ile Val Asp Val Ile Asp
 20 25 30

Gln Asn Arg Ala Leu Val Asp Gly Bro Cys Thr Gln Val Arg Arg Gln
 35 40 45

Ala Met Pro Phe Lys Cys Met Gln Leu Thr Asp Phe Ile Leu Lys Phe
 50 55 60

Leu His Ser Ala His Gln Lys Tyr Val Arg Gln Ala Trp Gln Lys Ala
 65 70 75 80

Asp Ile Asn Thr Lys Trp Ala Ala Thr Arg Trp Ala Lys Lys Ile Glu
 85 90 95

Ala Arg Glu Arg Lys Ala Lys Met Thr Asp Phe Asp Arg Phe Lys Val
 100 105 110

Met Lys Ala Lys Lys Met Arg Asn Arg Ile Ile Lys Asn Glu Val Lys
 115 120 125

Lys Leu Gln Lys Ala Ala Leu Leu Lys Ala Ser Pro Lys Lys Ala Pro
 130 135 140

Gly Thr Lys Gly Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
 145 150 155 160

Ala Ala Ala Ala Lys Val Pro Ala Lys Lys Ile Thr Ala Ala Ser Lys
 165 170 175

Lys Ala Pro Ala Gln Lys Val Pro Ala Gln Lys Ala Thr Gly Gln Lys
 180 185 190

Ala Ala Pro Ala Pro Lys Ala Gln Lys Gly Gln Lys Ala Pro Ala Gln
 195 200 205

Lys Ala Pro Ala Pro Lys Ala Ser Gly Lys Lys Ala
 210 215 220

<210> 154
 <211> 492
 <212> PRT
 <213> Homo sapiens

<400> 154

Met Ala Pro Val Gly Val Glu Lys Lys Leu Leu Leu Gly Pro Asn Gly
 1 5 10 15

Pro Ala Val Ala Ala Ala Gly Asp Leu Thr Ser Glu Glu Glu Gly
 20 25 30

Gln Ser Leu Trp Ser Ser Ile Leu Ser Glu Val Ser Thr Arg Ala Arg

35	40	45
Ser Lys Leu Pro Ser Gly Lys Asn Ile Leu Val Phe Gly Glu Asp Gly		
50	55	60
Ser Gly Lys Thr Thr Leu Met Thr Lys Leu Gln Gly Ala Glu His Gly		
65	70	75
Lys Lys Gly Arg Gly Leu Glu Tyr Leu Tyr Leu Ser Val His Asp Glu		
	85	90
Asp Arg Asp Asp His Thr Arg Cys Asn Val Trp Ile Leu Asp Gly Asp		
	100	105
Leu Tyr His Lys Gly Leu Leu Lys Phe Ala Val Ser Ala Glu Ser Leu		
	115	120
Pro Glu Thr Leu Val Ile Phe Val Ala Asp Met Ser Arg Pro Trp Thr		
	130	135
Val Met Glu Ser Leu Gln Lys Trp Ala Ser Val Leu Arg Glu His Ile		
	145	150
Asp Lys Met Lys Ile Pro Pro Glu Lys Met Arg Glu Leu Glu Arg Lys		
	165	170
Phe Val Lys Asp Phe Gln Asp Tyr Met Glu Pro Glu Glu Gly Cys Gln		
	180	185
Gly Ser Pro Gln Arg Arg Gly Pro Leu Thr Ser Gly Ser Asp Glu Glu		
	195	200
Asn Val Ala Leu Pro Leu Gly Asp Asn Val Leu Thr His Asn Leu Gly		
	210	215
Ile Pro Val Leu Val Val Cys Thr Lys Cys Asp Ala Val Ser Val Leu		
	225	230
Glu Lys Glu His Asp Tyr Arg Asp Glu His Leu Asp Phe Ile Gln Ser		
	245	250
His Leu Arg Arg Phe Cys Leu Gln Tyr Gly Ala Ala Leu Ile Tyr Thr		
	260	265
Ser Val Lys Glu Glu Lys Asn Leu Asp Leu Leu Tyr Lys Tyr Ile Val		
	275	280
His Lys Thr Tyr Gly Phe His Phe Thr Thr Pro Ala Leu Val Val Glu		
	290	295
Lys Asp Ala Val Phe Ile Pro Ala Gly Trp Asp Asn Glu Lys Lys Ile		
	305	310
Ala Ile Leu His Glu Asn Phe Thr Thr Val Lys Pro Glu Asp Ala Tyr		
	325	330
Glu Asp Phe Ile Val Lys Pro Pro Val Arg Lys Leu Val His Asp Lys		
	340	345
		350

Glu Leu Ala Ala Glu Asp Glu Gln Val Phe Leu Met Lys Gln Gln Ser
355 360 365

Leu Leu Ala Lys Gln Pro Ala Thr Pro Thr Arg Ala Ser Glu Ser Pro
370 375 380

Ala Arg Gly Pro Ser Gly Ser Pro Arg Thr Gln Gly Arg Gly Gly Pro
385 390 395 400

Ala Ser Val Pro Ser Ser Ser Pro Gly Thr Ser Val Lys Lys Pro Asp
405 410 415

Pro Asn Ile Lys Asn Asn Ala Ala Ser Glu Gly Val Leu Ala Ser Phe
420 425 430

Phe Asn Ser Leu Leu Ser Lys Lys Thr Gly Ser Pro Gly Ser Pro Gly
435 440 445

Ala Gly Gly Val Gln Ser Thr Ala Lys Lys Ser Gly Gln Lys Thr Val
450 455 460

Leu Ser Asn Val Gln Glu Glu Leu Asp Arg Met Thr Arg Lys Pro Asp
465 470 475 480

Ser Met Val Thr Asn Ser Ser Thr Glu Asn Glu Ala
485 490

<210> 155
<211> 2230
<212> PRT
<213> Homo sapiens

<400> 155

Met Phe Lys Lys Leu Lys Gln Lys Ile Ser Glu Glu Gln Gln Gln Leu
1 5 10 15

Gln Gln Ala Leu Ala Pro Ala Gln Ala Ser Ser Asn Ser Ser Thr Pro
20 25 30

Thr Arg Met Arg Ser Arg Thr Ser Ser Phe Thr Glu Gln Leu Asp Glu
35 40 45

Gly Thr Pro Asn Arg Glu Ser Gly Asp Thr Gln Ser Phe Ala Gln Lys
50 55 60

Leu Gln Leu Arg Val Pro Ser Val Glu Ser Leu Phe Arg Ser Pro Ile
65 70 75 80

Lys Glu Ser Leu Phe Arg Ser Ser Ser Lys Glu Ser Leu Val Arg Thr
85 90 95

Ser Ser Arg Glu Ser Leu Asn Arg Leu Asp Leu Asp Ser Ser Thr Ala
100 105 110

Ser Phe Asp Pro Pro Ser Asp Met Asp Ser Glu Ala Glu Asp Leu Val
115 120 125

Gly Asn Ser Asp Ser Leu Asn Lys Glu Gln Leu Ile Gln Arg Leu Arg
130 135 140

Arg Met Glu Arg Ser Leu Ser Ser Tyr Arg Gly Lys Tyr Ser Glu Leu
 145 150 155 160
 Val Thr Ala Tyr Gln Met Leu Gln Arg Glu Lys Lys Lys Leu Gln Gly
 165 170 175
 Ile Leu Ser Gln Ser Gln Asp Lys Ser Leu Arg Arg Ile Ala Glu Leu
 180 185 190
 Arg Glu Glu Leu Gln Met Asp Gln Gln Ala Lys Lys His Leu Gln Glu
 195 200 205
 Glu Phe Asp Ala Ser Leu Glu Glu Lys Asp Gln Tyr Ile Ser Val Leu
 210 215 220
 Gln Thr Gln Val Ser Leu Leu Lys Gln Arg Leu Arg Asn Gly Pro Met
 225 230 235 240
 Asn Val Asp Val Leu Lys Pro Leu Pro Gln Leu Glu Pro Gln Ala Glu
 245 250 255
 Val Phe Thr Lys Glu Glu Asn Pro Glu Ser Asp Gly Glu Pro Val Val
 260 265 270
 Glu Asp Gly Thr Ser Val Lys Thr Leu Glu Thr Leu Gln Gln Arg Val
 275 280 285
 Lys Arg Gln Glu Asn Leu Leu Lys Arg Cys Lys Glu Thr Ile Gln Ser
 290 295 300
 His Lys Glu Gln Cys Thr Leu Leu Thr Ser Glu Lys Glu Ala Leu Gln
 305 310 315 320
 Glu Gln Leu Asp Glu Arg Leu Gln Glu Leu Glu Lys Ile Lys Asp Leu
 325 330 335
 His Met Ala Glu Lys Thr Lys Leu Ile Thr Gln Leu Arg Asp Ala Lys
 340 345 350
 Asn Leu Ile Glu Gln Leu Glu Gln Asp Lys Gly Met Val Ile Ala Glu
 355 360 365
 Thr Lys Arg Gln Met His Glu Thr Leu Glu Met Lys Glu Glu Glu Ile
 370 375 380
 Ala Gln Leu Arg Ser Arg Ile Lys Gln Met Thr Thr Gln Gly Glu Glu
 385 390 395 400
 Leu Arg Glu Gln Lys Glu Lys Ser Glu Arg Ala Ala Phe Glu Glu Leu
 405 410 415
 Glu Lys Ala Leu Ser Thr Ala Gln Lys Thr Glu Glu Ala Arg Arg Lys
 420 425 430
 Leu Lys Ala Glu Met Asp Glu Gln Ile Lys Thr Ile Glu Lys Thr Ser
 435 440 445
 Glu Glu Glu Arg Ile Ser Leu Gln Gln Glu Leu Ser Arg Val Lys Gln
 450 455 460

Glu Val Val Asp Val Met Lys Lys Ser Ser Glu Glu Gln Ile Ala Lys
 465 470 475 480
 Leu Gln Lys Leu His Glu Lys Glu Leu Ala Arg Lys Glu Gln Glu Leu
 485 490 495
 Thr Lys Lys Leu Gln Thr Arg Glu Arg Glu Phe Gln Glu Gln Met Lys
 500 505 510
 Val Ala Leu Glu Lys Ser Gln Ser Glu Tyr Leu Lys Ile Ser Gln Glu
 515 520 525
 Lys Glu Gln Gln Glu Ser Leu Ala Leu Glu Glu Leu Glu Leu Gln Lys
 530 535 540
 Lys Ala Ile Leu Thr Glu Ser Glu Asn Lys Leu Arg Asp Leu Gln Gln
 545 550 555 560
 Glu Ala Glu Thr Tyr Arg Thr Arg Ile Leu Glu Leu Glu Ser Ser Leu
 565 570 575
 Glu Lys Ser Leu Gln Glu Asn Lys Asn Gln Ser Lys Asp Leu Ala Val
 580 585 590
 His Leu Glu Ala Glu Lys Asn Lys His Asn Lys Glu Ile Thr Val Met
 595 600 605
 Val Glu Lys His Lys Thr Glu Leu Glu Ser Leu Lys His Gln Gln Asp
 610 615 620
 Ala Leu Trp Thr Glu Lys Leu Gln Val Leu Lys Gln Gln Tyr Gln Thr
 625 630 635 640
 Glu Met Glu Lys Leu Arg Glu Lys Cys Glu Gln Glu Lys Glu Thr Leu
 645 650 655
 Leu Lys Asp Lys Glu Ile Ile Phe Gln Ala His Ile Glu Glu Met Asn
 660 665 670
 Glu Lys Thr Leu Glu Lys Leu Asp Val Lys Gln Thr Glu Leu Glu Ser
 675 680 685
 Leu Ser Ser Glu Leu Ser Glu Val Leu Lys Ala Arg His Lys Leu Glu
 690 695 700
 Glu Glu Leu Ser Val Leu Lys Asp Gln Thr Asp Lys Met Lys Gln Glu
 705 710 715 720
 Leu Glu Ala Lys Met Asp Glu Gln Lys Asn His His Gln Gln Gln Val
 725 730 735
 Asp Ser Ile Ile Lys Glu His Glu Val Ser Ile Gln Arg Thr Glu Lys
 740 745 750
 Ala Leu Lys Asp Gln Ile Asn Gln Leu Glu Leu Leu Lys Glu Arg
 755 760 765
 Asp Lys His Leu Lys Glu His Gln Ala His Val Glu Asn Leu Glu Ala
 770 775 780

Asp Ile Lys Arg Ser Glu Gly Glu Leu Gln Gln Ala Ser Ala Lys Leu
 785 790 795 800
 Asp Val Phe Gln Ser Tyr Gln Ser Ala Thr His Glu Gln Thr Lys Ala
 805 810 815
 Tyr Glu Glu Gln Leu Ala Gln Leu Gln Gln Lys Leu Leu Asp Leu Glu
 820 825 830
 Thr Glu Arg Ile Leu Leu Thr Lys Gln Val Ala Glu Val Glu Ala Gln
 835 840 845
 Lys Lys Asp Val Cys Thr Glu Leu Asp Ala His Lys Ile Gln Val Gln
 850 855 860
 Asp Leu Met Gln Gln Leu Glu Lys Gln Asn Ser Glu Met Glu Gln Lys
 865 870 875 880
 Val Lys Ser Leu Thr Gln Val Tyr Glu Ser Lys Leu Glu Asp Gly Asn
 885 890 895
 Lys Glu Gln Glu Gln Thr Lys Gln Ile Leu Val Glu Lys Glu Asn Met
 900 905 910
 Ile Leu Gln Met Arg Glu Gly Gln Lys Lys Glu Ile Glu Ile Leu Thr
 915 920 925
 Gln Lys Leu Ser Ala Lys Glu Asp Ser Ile His Ile Leu Asn Glu Glu
 930 935 940
 Tyr Glu Thr Lys Phe Lys Asn Gln Glu Lys Lys Met Glu Lys Val Lys
 945 950 955 960
 Gln Lys Ala Lys Glu Met Gln Glu Thr Leu Lys Lys Lys Leu Leu Asp
 965 970 975
 Gln Glu Ala Lys Leu Lys Lys Glu Leu Glu Asn Thr Ala Leu Glu Leu
 980 985 990
 Ser Gln Lys Glu Lys Gln Phe Asn Ala Lys Met Leu Glu Met Ala Gln
 995 1000 1005
 Ala Asn Ser Ala Gly Ile Ser Asp Ala Val Ser Arg Leu Glu Thr
 1010 1015 1020
 Asn Gln Lys Glu Gln Ile Glu Ser Leu Thr Glu Val His Arg Arg
 1025 1030 1035
 Glu Leu Asn Asp Val Ile Ser Ile Trp Glu Lys Lys Leu Asn Gln
 1040 1045 1050
 Gln Ala Glu Glu Leu Gln Glu Ile His Glu Ile Gln Leu Gln Glu
 1055 1060 1065
 Lys Glu Gln Glu Val Ala Glu Leu Lys Gln Lys Ile Leu Leu Phe
 1070 1075 1080
 Gly Cys Glu Lys Glu Glu Met Asn Lys Glu Ile Thr Trp Leu Lys

1085	1090	1095
Glu Glu Gly Val Lys Gln Asp 1100	Thr Thr Leu Asn Glu 1105	Leu Gln Glu 1110
Gln Leu Lys Gln Lys Ser Ala 1115	His Val Asn Ser Leu 1120	Ala Gln Asp 1125
Glu Thr Lys Leu Lys Ala His 1130	Leu Glu Lys Leu Glu 1135	Val Asp Leu 1140
Asn Lys Ser Leu Lys Glu Asn 1145	Thr Phe Leu Gln Glu 1150	Gln Leu Val 1155
Glu Leu Lys Met Leu Ala Glu 1160	Glu Asp Lys Arg Lys 1165	Val Ser Glu 1170
Leu Thr Ser Lys Leu Lys Thr 1175	Thr Asp Glu Glu Phe 1180	Gln Ser Leu 1185
Lys Ser Ser His Glu Lys Ser 1190	Asn Lys Ser Leu Glu 1195	Asp Lys Ser 1200
Leu Glu Phe Lys Lys Leu Ser 1205	Glu Glu Leu Ala Ile 1210	Gln Leu Asp 1215
Ile Cys Cys Lys Lys Thr Glu 1220	Ala Leu Leu Glu Ala 1225	Lys Thr Asn 1230
Glu Leu Ile Asn Ile Ser Ser 1235	Ser Lys Thr Asn Ala 1240	Ile Leu Ser 1245
Arg Ile Ser His Cys Gln His 1250	Arg Thr Thr Lys Val 1255	Lys Glu Ala 1260
Leu Leu Ile Lys Thr Cys Thr 1265	Val Ser Glu Leu Glu 1270	Ala Gln Leu 1275
Arg Gln Leu Thr Glu Glu Gln 1280	Asn Thr Leu Asn Ile 1285	Ser Phe Gln 1290
Gln Ala Thr His Gln Leu Glu 1295	Glu Lys Glu Asn Gln 1300	Ile Lys Ser 1305
Met Lys Ala Asp Ile Glu Ser 1310	Leu Val Thr Glu Lys 1315	Glu Ala Leu 1320
Gln Lys Glu Gly Gly Asn Gln 1325	Gln Gln Ala Ala Ser 1330	Glu Lys Glu 1335
Ser Cys Ile Thr Gln Leu Lys 1340	Lys Glu Leu Ser Glu 1345	Asn Ile Asn 1350
Ala Val Thr Leu Met Lys Glu 1355	Glu Leu Lys Glu Lys 1360	Lys Val Glu 1365
Ile Ser Ser Leu Ser Lys Gln 1370	Leu Thr Asp Leu Asn 1375	Val Gln Leu 1380

Gln Asn Ser Ile Ser Leu Ser Glu Lys Glu Ala Ala Ile Ser Ser
 1385 1390 1395
 Leu Arg Lys Gln Tyr Asp Glu Glu Lys Cys Glu Leu Leu Asp Gln
 1400 1405 1410
 Val Gln Asp Leu Ser Phe Lys Val Asp Thr Leu Ser Lys Glu Lys
 1415 1420 1425
 Ile Ser Ala Leu Glu Gln Val Asp Asp Trp Ser Asn Lys Phe Ser
 1430 1435 1440
 Glu Trp Lys Lys Lys Ala Gln Ser Arg Phe Thr Gln His Gln Asn
 1445 1450 1455
 Thr Val Lys Glu Leu Gln Ile Gln Leu Glu Leu Lys Ser Lys Glu
 1460 1465 1470
 Ala Tyr Glu Lys Asp Glu Gln Ile Asn Leu Leu Lys Glu Glu Leu
 1475 1480 1485
 Asp Gln Gln Asn Lys Arg Phe Asp Cys Leu Lys Gly Glu Met Glu
 1490 1495 1500
 Asp Asp Lys Ser Lys Met Glu Lys Lys Glu Ser Asn Leu Glu Thr
 1505 1510 1515
 Glu Leu Lys Ser Gln Thr Ala Arg Ile Met Glu Leu Glu Asp His
 1520 1525 1530
 Ile Thr Gln Lys Thr Ile Glu Ile Glu Ser Leu Asn Glu Val Leu
 1535 1540 1545
 Lys Asn Tyr Asn Gln Gln Lys Asp Ile Glu His Lys Glu Leu Val
 1550 1555 1560
 Gln Lys Leu Gln His Phe Gln Glu Leu Gly Glu Glu Lys Asp Asn
 1565 1570 1575
 Arg Val Lys Glu Ala Glu Glu Lys Ile Leu Thr Leu Glu Asn Gln
 1580 1585 1590
 Val Tyr Ser Met Lys Ala Glu Leu Glu Thr Lys Lys Lys Glu Leu
 1595 1600 1605
 Glu His Val Asn Leu Ser Val Lys Ser Lys Glu Glu Glu Leu Lys
 1610 1615 1620
 Ala Leu Glu Asp Arg Leu Glu Ser Glu Ser Ala Ala Lys Leu Ala
 1625 1630 1635
 Glu Leu Lys Arg Lys Ala Glu Gln Lys Ile Ala Ala Ile Lys Lys
 1640 1645 1650
 Gln Leu Leu Ser Gln Met Glu Glu Lys Glu Glu Gln Tyr Lys Lys
 1655 1660 1665
 Gly Thr Glu Ser His Leu Ser Glu Leu Asn Thr Lys Leu Gln Glu
 1670 1675 1680

Arg Glu Arg Glu Val His Ile Leu Glu Glu Lys Leu Lys Ser Val
 1685 1690 1695
 Glu Ser Ser Gln Ser Glu Thr Leu Ile Val Pro Arg Ser Ala Lys
 1700 1705 1710
 Asn Val Ala Ala Tyr Thr Glu Gln Glu Glu Ala Asp Ser Gln Gly
 1715 1720 1725
 Cys Val Gln Lys Thr Tyr Glu Glu Lys Ile Ser Val Leu Gln Arg
 1730 1735 1740
 Asn Leu Thr Glu Lys Glu Lys Leu Leu Gln Arg Val Gly Gln Glu
 1745 1750 1755
 Lys Glu Glu Thr Val Ser Ser His Phe Glu Met Arg Cys Gln Tyr
 1760 1765 1770
 Gln Glu Arg Leu Ile Lys Leu Glu His Ala Glu Ala Lys Gln His
 1775 1780 1785
 Glu Asp Gln Ser Met Ile Gly His Leu Gln Glu Glu Leu Glu Glu
 1790 1795 1800
 Lys Asn Lys Lys Tyr Ser Leu Ile Val Ala Gln His Val Glu Lys
 1805 1810 1815
 Glu Gly Gly Lys Asn Asn Ile Gln Ala Lys Gln Asn Leu Glu Asn
 1820 1825 1830
 Val Phe Asp Asp Val Gln Lys Thr Leu Gln Glu Lys Glu Leu Thr
 1835 1840 1845
 Cys Gln Ile Leu Glu Gln Lys Ile Lys Glu Leu Asp Ser Cys Leu
 1850 1855 1860
 Val Arg Gln Lys Glu Val His Arg Val Glu Met Glu Glu Leu Thr
 1865 1870 1875
 Ser Lys Tyr Glu Lys Leu Gln Ala Leu Gln Gln Met Asp Gly Arg
 1880 1885 1890
 Asn Lys Pro Thr Glu Leu Leu Glu Glu Asn Thr Glu Glu Lys Ser
 1895 1900 1905
 Lys Ser His Leu Val Gln Pro Lys Leu Leu Ser Asn Met Glu Ala
 1910 1915 1920
 Gln His Asn Asp Leu Glu Phe Lys Leu Ala Gly Ala Glu Arg Glu
 1925 1930 1935
 Lys Gln Lys Leu Gly Lys Glu Ile Val Arg Leu Gln Lys Asp Leu
 1940 1945 1950
 Arg Met Leu Arg Lys Glu His Gln Gln Glu Leu Glu Ile Leu Lys
 1955 1960 1965
 Lys Glu Tyr Asp Gln Glu Arg Glu Glu Lys Ile Lys Gln Glu Gln
 1970 1975 1980

Glu Asp Leu Glu Leu Lys His Asn Ser Thr Leu Lys Gln Leu Met
1985 1990 1995

Arg Glu Phe Asn Thr Gln Leu Ala Gln Lys Glu Gln Glu Leu Glu
2000 2005 2010

Met Thr Ile Lys Glu Thr Ile Asn Lys Ala Gln Glu Val Glu Ala
2015 2020 2025

Glu Leu Leu Glu Ser His Gln Glu Glu Thr Asn Gln Leu Leu Lys
2030 2035 2040

Lys Ile Ala Glu Lys Asp Asp Asp Leu Lys Arg Thr Ala Lys Arg
2045 2050 2055

Tyr Glu Glu Ile Leu Asp Ala Arg Glu Glu Glu Met Thr Ala Lys
2060 2065 2070

Val Arg Asp Leu Gln Thr Gln Leu Glu Glu Leu Gln Lys Lys Tyr
2075 2080 2085

Gln Gln Lys Leu Glu Gln Glu Glu Asn Pro Gly Asn Asp Asn Val
2090 2095 2100

Thr Ile Met Glu Leu Gln Thr Gln Leu Ala Gln Lys Thr Thr Leu
2105 2110 2115

Ile Ser Asp Ser Lys Leu Lys Glu Gln Glu Phe Arg Glu Gln Ile
2120 2125 2130

His Asn Leu Glu Asp Arg Leu Lys Lys Tyr Glu Lys Asn Val Tyr
2135 2140 2145

Ala Thr Thr Val Gly Thr Pro Tyr Lys Gly Gly Asn Leu Tyr His
2150 2155 2160

Thr Asp Val Ser Leu Phe Gly Glu Pro Thr Glu Phe Glu Tyr Leu
2165 2170 2175

Arg Lys Val Leu Phe Glu Tyr Met Met Gly Arg Glu Thr Lys Thr
2180 2185 2190

Met Ala Lys Val Ile Thr Thr Val Leu Lys Phe Pro Asp Asp Gln
2195 2200 2205

Thr Gln Lys Ile Leu Glu Arg Glu Asp Ala Arg Leu Met Phe Thr
2210 2215 2220

Ser Pro Arg Ser Gly Ile Phe
2225 2230

<210> 156
<211> 719
<212> PRT
<213> Homo sapiens

<400> 156

Glu Ile Met Glu Glu Leu Arg Ser Leu Asp Pro Arg Arg Gln Glu Leu
1 5 10 15

Leu Glu Ala Arg Phe Thr Gly Val Gly Val Ser Lys Gly Pro Leu Asn
 20 25 30
 Ser Glu Ser Ser Asn Gln Ser Leu Cys Ser Val Gly Ser Leu Ser Asp
 35 40 45
 Lys Glu Val Glu Thr Pro Glu Lys Lys Gln Asn Asp Gln Arg Asn Arg
 50 55 60
 Lys Arg Lys Ala Glu Pro Tyr Glu Thr Ser Gln Gly Lys Gly Thr Pro
 65 70 75 80
 Arg Gly His Lys Ile Ser Asp Tyr Phe Glu Arg Arg Val Glu Gln Pro
 85 90 95
 Leu Tyr Gly Leu Asp Gly Ser Ala Ala Lys Glu Ala Thr Glu Glu Gln
 100 105 110
 Ser Ala Leu Pro Thr Leu Met Ser Val Met Leu Ala Lys Pro Arg Leu
 115 120 125
 Asp Pro Glu Gln Leu Ala Gln Arg Gly Ala Gly Leu Cys Phe Thr Phe
 130 135 140
 Val Ser Ala Gln Gln Asn Ser Pro Ser Ser Thr Gly Ser Gly Asn Thr
 145 150 155 160
 Glu His Ser Cys Ser Ser Gln Lys Gln Ile Ser Ile Gln His Arg Gln
 165 170 175
 Thr Gln Ser Asp Leu Thr Ile Glu Lys Ile Ser Ala Leu Glu Asn Ser
 180 185 190
 Lys Asn Ser Asp Leu Glu Lys Lys Glu Gly Arg Ile Asp Asp Leu Leu
 195 200 205
 Arg Ala Asn Cys Asp Leu Arg Arg Gln Ile Asp Glu Gln Gln Lys Met
 210 215 220
 Leu Glu Lys Tyr Lys Glu Arg Leu Asn Arg Cys Val Thr Met Ser Lys
 225 230 235 240
 Lys Leu Leu Ile Glu Lys Ser Lys Gln Glu Lys Met Ala Cys Arg Asp
 245 250 255
 Lys Ser Met Gln Asp Arg Leu Arg Leu Gly His Phe Thr Thr Val Arg
 260 265 270
 His Gly Ala Ser Phe Thr Glu Gln Trp Thr Asp Gly Tyr Ala Phe Gln
 275 280 285
 Asn Leu Ile Lys Gln Gln Glu Arg Ile Asn Ser Gln Arg Glu Glu Ile
 290 295 300
 Glu Arg Gln Arg Lys Met Leu Ala Lys Arg Lys Pro Pro Ala Met Gly
 305 310 315 320
 Gln Ala Pro Pro Ala Thr Asn Glu Gln Lys Gln Arg Lys Ser Lys Thr

325	330	335
Asn Gly Ala Glu Asn Glu Thr Leu Thr Leu Ala Glu Tyr His Glu Gln 340 345 350		
Glu Glu Ile Phe Lys Leu Arg Leu Gly His Leu Lys Lys Glu Glu Ala 355 360 365		
Glu Ile Gln Ala Glu Leu Glu Arg Leu Glu Arg Val Arg Asn Leu His 370 375 380		
Ile Arg Glu Leu Lys Arg Ile His Asn Glu Asp Asn Ser Gln Phe Lys 385 390 395 400		
Asp His Pro Thr Leu Asn Asp Arg Tyr Leu Leu Leu His Leu Leu Gly 405 410 415		
Arg Gly Gly Phe Ser Glu Val Tyr Lys Ala Phe Asp Leu Thr Glu Gln 420 425 430		
Arg Tyr Val Ala Val Lys Ile His Gln Leu Asn Lys Asn Trp Arg Asp 435 440 445		
Glu Lys Lys Glu Asn Tyr His Lys His Ala Cys Arg Glu Tyr Arg Ile 450 455 460		
His Lys Glu Leu Asp His Pro Arg Ile Val Lys Leu Tyr Asp Tyr Phe 465 470 475 480		
Ser Leu Asp Thr Asp Ser Phe Cys Thr Val Leu Glu Tyr Cys Glu Gly 485 490 495		
Asn Asp Leu Asp Phe Tyr Leu Lys Gln His Lys Leu Ile Ser Glu Lys 500 505 510		
Glu Ala Arg Ser Ile Ile Met Gln Ile Val Asn Ala Leu Lys Tyr Leu 515 520 525		
Asn Glu Ile Lys Pro Pro Ile Ile His Tyr Asp Leu Lys Pro Gly Asn 530 535 540		
Ile Leu Leu Val Asn Gly Thr Ala Cys Gly Glu Ile Lys Ile Thr Asp 545 550 555 560		
Phe Gly Leu Ser Lys Ile Met Asp Asp Asp Ser Tyr Asn Ser Val Asp 565 570 575		
Gly Met Glu Leu Thr Ser Gln Gly Ala Gly Thr Tyr Trp Tyr Leu Pro 580 585 590		
Pro Glu Cys Phe Val Val Gly Lys Glu Pro Pro Lys Ile Ser Asn Lys 595 600 605		
Val Asp Val Trp Ser Val Gly Val Ile Phe Tyr Gln Cys Leu Tyr Gly 610 615 620		
Arg Lys Pro Phe Gly His Asn Gln Ser Gln Gln Asp Ile Leu Gln Glu 625 630 635 640		

Asn Thr Ile Leu Lys Ala Thr Glu Val Gln Phe Pro Pro Lys Pro Val
645 650 655

Val Thr Pro Glu Ala Lys Ala Phe Ile Arg Arg Cys Leu Ala Tyr Arg
660 665 670

Lys Glu Asp Arg Ile Asp Val Gln Gln Leu Ala Cys Asp Pro Tyr Leu
675 680 685

Leu Pro His Ile Arg Lys Ser Val Ser Thr Ser Ser Pro Ala Gly Ala
690 695 700

Ala Ile Ala Ser Thr Ser Gly Ala Ser Asn Asn Ser Ser Ser Asn
705 710 715

<210> 157
<211> 1976
<212> PRT
<213> Homo sapiens

<400> 157

Met Ala Gln Arg Thr Gly Leu Glu Asp Pro Glu Arg Tyr Leu Phe Val
1 5 10 15

Asp Arg Ala Val Ile Tyr Asn Pro Ala Thr Gln Ala Asp Trp Thr Ala
20 25 30

Lys Lys Leu Val Trp Ile Pro Ser Glu Arg His Gly Phe Glu Ala Ala
35 40 45

Ser Ile Lys Glu Glu Arg Gly Asp Glu Val Met Val Glu Leu Ala Glu
50 55 60

Asn Gly Lys Lys Ala Met Val Asn Lys Asp Asp Ile Gln Lys Met Asn
65 70 75 80

Pro Pro Lys Phe Ser Lys Val Glu Asp Met Ala Glu Leu Thr Cys Leu
85 90 95

Asn Glu Ala Ser Val Leu His Asn Leu Lys Asp Arg Tyr Tyr Ser Gly
100 105 110

Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Val Ile Asn Pro Tyr
115 120 125

Lys Asn Leu Pro Ile Tyr Ser Glu Asn Ile Ile Glu Met Tyr Arg Gly
130 135 140

Lys Lys Arg His Glu Met Pro Pro His Ile Tyr Ala Ile Ser Glu Ser
145 150 155 160

Ala Tyr Arg Cys Met Leu Gln Asp Arg Glu Asp Gln Ser Ile Leu Cys
165 170 175

Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn Thr Lys Lys Val Ile
180 185 190

Gln Tyr Leu Ala His Val Ala Ser Ser His Lys Gly Arg Lys Asp His
195 200 205

Asn Ile Pro Gly Glu Leu Glu Arg Gln Leu Leu Gln Ala Asn Pro Ile
 210 215 220
 Leu Glu Ser Phe Gly Asn Ala Lys Thr Val Lys Asn Asp Asn Ser Ser
 225 230 235 240
 Arg Phe Gly Lys Phe Ile Arg Ile Asn Phe Asp Val Thr Gly Tyr Ile
 245 250 255
 Val Gly Ala Asn Ile Glu Thr Tyr Leu Leu Glu Lys Ser Arg Ala Val
 260 265 270
 Arg Gln Ala Lys Asp Glu Arg Thr Phe His Ile Phe Tyr Gln Leu Leu
 275 280 285
 Ser Gly Ala Gly Glu His Leu Lys Ser Asp Leu Leu Leu Glu Gly Phe
 290 295 300
 Asn Asn Tyr Arg Phe Leu Ser Asn Gly Tyr Ile Pro Ile Pro Gly Gln
 305 310 315 320
 Gln Asp Lys Asp Asn Phe Gln Glu Thr Met Glu Ala Met His Ile Met
 325 330 335
 Gly Phe Ser His Glu Glu Ile Leu Ser Met Leu Lys Val Val Ser Ser
 340 345 350
 Val Leu Gln Phe Gly Asn Ile Ser Phe Lys Lys Glu Arg Asn Thr Asp
 355 360 365
 Gln Ala Ser Met Pro Glu Asn Thr Val Ala Gln Lys Leu Cys His Leu
 370 375 380
 Leu Gly Met Asn Val Met Glu Phe Thr Arg Ala Ile Leu Thr Pro Arg
 385 390 395 400
 Ile Lys Val Gly Arg Asp Tyr Val Gln Lys Ala Gln Thr Lys Glu Gln
 405 410 415
 Ala Asp Phe Ala Val Glu Ala Leu Ala Lys Ala Thr Tyr Glu Arg Leu
 420 425 430
 Phe Arg Trp Leu Val His Arg Ile Asn Lys Ala Leu Asp Arg Thr Lys
 435 440 445
 Arg Gln Gly Ala Ser Phe Ile Gly Ile Leu Asp Ile Ala Gly Phe Glu
 450 455 460
 Ile Phe Glu Leu Asn Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn
 465 470 475 480
 Glu Lys Leu Gln Gln Leu Phe Asn His Thr Met Phe Ile Leu Glu Gln
 485 490 495
 Glu Glu Tyr Gln Arg Glu Gly Ile Glu Trp Asn Phe Ile Asp Phe Gly
 500 505 510
 Leu Asp Leu Gln Pro Cys Ile Asp Leu Ile Glu Arg Pro Ala Asn Pro
 515 520 525

Pro Gly Val Leu Ala Leu Leu Asp Glu Glu Cys Trp Phe Pro Lys Ala
 530 535 540
 Thr Asp Lys Thr Phe Val Glu Lys Leu Val Gln Glu Gln Gly Ser His
 545 550 555 560
 Ser Lys Phe Gln Lys Pro Arg Gln Leu Lys Asp Lys Ala Asp Phe Cys
 565 570 575
 Ile Ile His Tyr Ala Gly Lys Val Asp Tyr Lys Ala Asp Glu Trp Leu
 580 585 590
 Met Lys Asn Met Asp Pro Leu Asn Asp Asn Val Ala Thr Leu Leu His
 595 600 605
 Gln Ser, Ser Asp Arg Phe Val Ala Glu Leu Trp Lys Asp Val Asp Arg
 610 615 620
 Ile Val Gly Leu Asp Gln Val Thr Gly Met Thr Glu Thr Ala Phe Gly
 625 630 635 640
 Ser Ala Tyr Lys Thr Lys Lys Gly Met Phe Arg Thr Val Gly Gln Leu
 645 650 655
 Tyr Lys Glu Ser Leu Thr Lys Leu Met Ala Thr Leu Arg Asn Thr Asn
 660 665 670
 Pro Asn Phe Val Arg Cys Ile Ile Pro Asn His Glu Lys Arg Ala Gly
 675 680 685
 Lys Leu Asp Pro His Leu Val Leu Asp Gln Leu Arg Cys Asn Gly Val
 690 695 700
 Leu Glu Gly Ile Arg Ile Cys Arg Gln Gly Phe Pro Asn Arg Ile Val
 705 710 715 720
 Phe Gln Glu Phe Arg Gln Arg Tyr Glu Ile Leu Thr Pro Asn Ala Ile
 725 730 735
 Pro Lys Gly Phe Met Asp Gly Lys Gln Ala Cys Glu Arg Met Ile Arg
 740 745 750
 Ala Leu Glu Leu Asp Pro Asn Leu Tyr Arg Ile Gly Gln Ser Lys Ile
 755 760 765
 Phe Phe Arg Ala Gly Val Leu Ala His Leu Glu Glu Glu Arg Asp Leu
 770 775 780
 Lys Ile Thr Asp Ile Ile Ile Phe Phe Gln Ala Val Cys Arg Gly Cys
 785 790 795 800
 Leu Ala Arg Lys Ala Phe Ala Lys Lys Gln Gln Gln Leu Ser Ala Leu
 805 810 815
 Lys Val Leu Gln Arg Asn Cys Ala Ala Tyr Leu Lys Leu Arg His Trp
 820 825 830
 Gln Trp Trp Arg Val Phe Thr Lys Val Lys Pro Leu Leu Gln Val Thr
 835 840 845

Arg Gln Glu Glu Glu Leu Gln Ala Lys Asp Glu Glu Leu Leu Lys Val
 850 855 860
 Lys Glu Lys Gln Thr Lys Val Glu Gly Glu Leu Glu Glu Met Glu Arg
 865 870 875 880
 Lys His Gln Gln Leu Leu Glu Glu Lys Asn Ile Leu Ala Glu Gln Leu
 885 890 895
 Gln Ala Glu Thr Glu Leu Phe Ala Glu Ala Glu Glu Met Arg Ala Arg
 900 905 910
 Leu Ala Ala Lys Lys Gln Glu Leu Glu Glu Ile Leu His Asp Leu Glu
 915 920 925
 Ser Arg Val Glu Glu Glu Glu Glu Arg Asn Gln Ile Leu Gln Asn Glu
 930 935 940
 Lys Lys Lys Met Gln Ala His Ile Gln Asp Leu Glu Glu Gln Leu Asp
 945 950 955 960
 Glu Glu Glu Gly Ala Arg Gln Lys Leu Gln Leu Glu Lys Val Thr Ala
 965 970 975
 Glu Ala Lys Ile Lys Lys Met Glu Glu Glu Ile Leu Leu Leu Glu Asp
 980 985 990
 Gln Asn Ser Lys Phe Ile Lys Glu Lys Lys Leu Met Glu Asp Arg Ile
 995 1000 1005
 Ala Glu Cys Ser Ser Gln Leu Ala Glu Glu Glu Glu Lys Ala Lys
 1010 1015 1020
 Asn Leu Ala Lys Ile Arg Asn Lys Gln Glu Val Met Ile Ser Asp
 1025 1030 1035
 Leu Glu Glu Arg Leu Lys Lys Glu Glu Lys Thr Arg Gln Glu Leu
 1040 1045 1050
 Glu Lys Ala Lys Arg Lys Leu Asp Gly Glu Thr Thr Asp Leu Gln
 1055 1060 1065
 Asp Gln Ile Ala Glu Leu Gln Ala Gln Ile Asp Glu Leu Lys Leu
 1070 1075 1080
 Gln Leu Ala Lys Lys Glu Glu Glu Leu Gln Gly Ala Leu Ala Arg
 1085 1090 1095
 Gly Asp Asp Glu Thr Leu His Lys Asn Asn Ala Leu Lys Val Val
 1100 1105 1110
 Arg Glu Leu Gln Ala Gln Ile Ala Glu Leu Gln Glu Asp Phe Glu
 1115 1120 1125
 Ser Glu Lys Ala Ser Arg Asn Lys Ala Glu Lys Gln Lys Arg Asp
 1130 1135 1140
 Leu Ser Glu Glu Leu Glu Ala Leu Lys Thr Glu Leu Glu Asp Thr

1145	1150	1155
Leu Asp Thr Thr Ala Ala Gln 1160	Gln Gln Glu Leu Arg 1165	Thr Lys Arg Glu 1170
Gln Glu Val Ala Glu Leu Lys 1175	Lys Ala Leu Glu Glu 1180	Glu Thr Lys 1185
Asn His Glu Ala Gln Ile Lys 1190	Asp Met Arg Gln Arg 1195	His Ala Thr 1200
Ala Leu Glu Glu Leu Ser Glu 1205	Gln Leu Glu Gln Ala 1210	Lys Arg Phe 1215
Lys Ala Asn Leu Glu Lys Asn 1220	Lys Gln Gly Leu Glu 1225	Thr Asp Asn 1230
Lys Glu Leu Ala Cys Glu Val 1235	Lys Val Leu Gln Gln 1240	Val Lys Ala 1245
Glu Ser Glu His Lys Arg Lys 1250	Lys Leu Asp Ala Gln 1255	Val Gln Glu 1260
Leu His Ala Lys Val Ser Glu 1265	Gly Asp Arg Leu Arg 1270	Val Glu Leu 1275
Ala Glu Lys Ala Ser Lys Leu 1280	Gln Asn Glu Leu Asp 1285	Asn Val Ser 1290
Thr Leu Leu Glu Glu Ala Glu 1295	Lys Lys Gly Ile Lys 1300	Phe Ala Lys 1305
Asp Ala Ala Ser Leu Glu Ser 1310	Gln Leu Gln Asp Thr 1315	Gln Glu Leu 1320
Leu Gln Glu Glu Thr Arg Gln 1325	Lys Leu Asn Leu Ser 1330	Ser Arg Ile 1335
Arg Gln Leu Glu Glu Glu Lys 1340	Asn Ser Leu Gln Glu 1345	Gln Gln Glu 1350
Glu Glu Glu Glu Ala Arg Lys 1355	Asn Leu Glu Lys Gln 1360	Val Leu Ala 1365
Leu Gln Ser Gln Leu Ala Asp 1370	Thr Lys Lys Lys Val 1375	Asp Asp Asp 1380
Leu Gly Thr Ile Glu Ser Leu 1385	Glu Glu Ala Lys Lys 1390	Lys Leu Leu 1395
Lys Asp Ala Glu Ala Leu Ser 1400	Gln Arg Leu Glu Glu 1405	Lys Ala Leu 1410
Ala Tyr Asp Lys Leu Glu Lys 1415	Thr Lys Asn Arg Leu 1420	Gln Gln Glu 1425
Leu Asp Asp Leu Thr Val Asp 1430	Leu Asp His Gln Arg 1435	Gln Val Ala 1440

Ser Asn Leu Glu Lys Lys Gln Lys Lys Phe Asp Gln Leu Leu Ala
 1445 1450 1455
 Glu Glu Lys Ser Ile Ser Ala Arg Tyr Ala Glu Glu Arg Asp Arg
 1460 1465 1470
 Ala Glu Ala Glu Ala Arg Glu Lys Glu Thr Lys Ala Leu Ser Leu
 1475 1480 1485
 Ala Arg Ala Leu Glu Glu Ala Leu Glu Ala Lys Glu Glu Phe Glu
 1490 1495 1500
 Arg Gln Asn Lys Gln Leu Arg Ala Asp Met Glu Asp Leu Met Ser
 1505 1510 1515
 Ser Lys Asp Asp Val Gly Lys Asn Val His Glu Leu Glu Lys Ser
 1520 1525 1530
 Lys Arg Ala Leu Glu Gln Gln Val Glu Glu Met Arg Thr Gln Leu
 1535 1540 1545
 Glu Glu Leu Glu Asp Glu Leu Gln Ala Thr Glu Asp Ala Lys Leu
 1550 1555 1560
 Arg Leu Glu Val Asn Met Gln Ala Met Lys Ala Gln Phe Glu Arg
 1565 1570 1575
 Asp Leu Gln Thr Arg Asp Glu Gln Asn Glu Glu Lys Lys Arg Leu
 1580 1585 1590
 Leu Ile Lys Gln Val Arg Glu Leu Glu Ala Glu Leu Glu Asp Glu
 1595 1600 1605
 Arg Lys Gln Arg Ala Leu Ala Val Ala Ser Lys Lys Lys Met Glu
 1610 1615 1620
 Ile Asp Leu Lys Asp Leu Glu Ala Gln Ile Glu Ala Ala Asn Lys
 1625 1630 1635
 Ala Arg Asp Glu Val Ile Lys Gln Leu Arg Lys Leu Gln Ala Gln
 1640 1645 1650
 Met Lys Asp Tyr Gln Arg Glu Leu Glu Glu Ala Arg Ala Ser Arg
 1655 1660 1665
 Asp Glu Ile Phe Ala Gln Ser Lys Glu Ser Glu Lys Lys Leu Lys
 1670 1675 1680
 Ser Leu Glu Ala Glu Ile Leu Gln Leu Gln Glu Glu Leu Ala Ser
 1685 1690 1695
 Ser Glu Arg Ala Arg Arg His Ala Glu Gln Glu Arg Asp Glu Leu
 1700 1705 1710
 Ala Asp Glu Ile Thr Asn Ser Ala Ser Gly Lys Ser Ala Leu Leu
 1715 1720 1725
 Asp Glu Lys Arg Arg Leu Glu Ala Arg Ile Ala Gln Leu Glu Glu
 1730 1735 1740

Glu Leu Glu Glu Glu Gln Ser Asn Met Glu Leu Leu Asn Asp Arg
1745 1750 1755

Phe Arg Lys Thr Thr Leu Gln Val Asp Thr Leu Asn Ala Glu Leu
1760 1765 1770

Ala Ala Glu Arg Ser Ala Ala Gln Lys Ser Asp Asn Ala Arg Gln
1775 1780 1785

Gln Leu Glu Arg Gln Asn Lys Glu Leu Lys Ala Lys Leu Gln Glu
1790 1795 1800

Leu Glu Gly Ala Val Lys Ser Lys Phe Lys Ala Thr Ile Ser Ala
1805 1810 1815

Leu Glu Ala Lys Ile Gly Gln Leu Glu Glu Gln Leu Glu Gln Glu
1820 1825 1830

Ala Lys Glu Arg Ala Ala Ala Asn Lys Leu Val Arg Arg Thr Glu
1835 1840 1845

Lys Lys Leu Lys Glu Ile Phe Met Gln Val Glu Asp Glu Arg Arg
1850 1855 1860

His Ala Asp Gln Tyr Lys Glu Gln Met Glu Lys Ala Asn Ala Arg
1865 1870 1875

Met Lys Gln Leu Lys Arg Gln Leu Glu Glu Ala Glu Glu Glu Ala
1880 1885 1890

Thr Arg Ala Asn Ala Ser Arg Arg Lys Leu Gln Arg Glu Leu Asp
1895 1900 1905

Asp Ala Thr Glu Ala Asn Glu Gly Leu Ser Arg Glu Val Ser Thr
1910 1915 1920

Leu Lys Asn Arg Leu Arg Arg Gly Gly Pro Ile Ser Phe Ser Ser
1925 1930 1935

Ser Arg Ser Gly Arg Arg Gln Leu His Leu Glu Gly Ala Ser Leu
1940 1945 1950

Glu Leu Ser Asp Asp Asp Thr Glu Ser Lys Thr Ser Asp Val Asn
1955 1960 1965

Glu Thr Gln Pro Pro Gln Ser Glu
1970 1975

<210> 158
<211> 1064
<212> PRT
<213> Homo sapiens

<400> 158

Met Lys Ile Ala Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu
1 5 10 15

Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu
20 25 30

Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys
 35 40 45
 Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala
 50 55 60
 Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala
 65 70 75 80
 Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn
 85 90 95
 Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro
 100 105 110
 Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn
 115 120 125
 Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly
 130 135 140
 Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Asp Val
 145 150 155 160
 Cys Ser Ala Phe Arg Pro Phe Val Arg Asp Gly Arg Leu Gly Cys Thr
 165 170 175
 Arg Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn
 180 185 190
 Lys Cys Ala Met Cys Ala Glu Leu Phe Leu Lys Glu Ala Glu Asn Ala
 195 200 205
 Lys Arg Glu Gly Glu Thr Arg Ile Arg Arg Asn Ala Glu Lys Asp Phe
 210 215 220
 Cys Lys Glu Tyr Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr
 225 230 235 240
 Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn
 245 250 255
 Lys Cys Ala Leu Cys Ala Glu Ile Phe Lys Arg Arg Phe Ser Glu Glu
 260 265 270
 Asn Ser Lys Thr Asp Gln Asn Leu Gly Lys Ala Glu Glu Lys Thr Lys
 275 280 285
 Val Lys Arg Glu Ile Val Lys Leu Cys Ser Gln Tyr Gln Asn Gln Ala
 290 295 300
 Lys Asn Gly Ile Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly
 305 310 315 320
 Pro Asp Gly Lys Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr
 325 330 335
 Phe Gln Ala Glu Asn Glu Glu Lys Lys Lys Ala Glu Ala Arg Ala Arg
 340 345 350

Asn Lys Arg Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn
 355 360 365
 Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu
 370 375 380
 Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys
 385 390 395 400
 Ser Met Cys Glu Val Phe Phe Gln Ala Glu Glu Glu Lys Lys Lys
 405 410 415
 Lys Glu Gly Glu Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser
 420 425 430
 Phe Glu Glu Leu Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg
 435 440 445
 Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys
 450 455 460
 Met His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu
 465 470 475 480
 Glu Arg Ala Arg Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys
 485 490 495
 Ser Glu Phe Arg Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr Arg
 500 505 510
 Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly Asn Lys
 515 520 525
 Cys Ala Met Cys Ala Ser Val Phe Lys Leu Glu Glu Glu Glu Lys Lys
 530 535 540
 Asn Asp Lys Glu Glu Lys Gly Lys Val Glu Ala Glu Lys Val Lys Arg
 545 550 555 560
 Glu Ala Val Gln Glu Leu Cys Ser Glu Tyr Arg His Tyr Val Arg Asn
 565 570 575
 Gly Arg Leu Pro Cys Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp
 580 585 590
 Gly Lys Ile His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln
 595 600 605
 Gln Glu Ala Lys Glu Lys Glu Arg Ala Glu Pro Arg Ala Lys Val Lys
 610 615 620
 Arg Glu Ala Glu Lys Glu Thr Cys Asp Glu Phe Arg Arg Leu Leu Gln
 625 630 635 640
 Asn Gly Lys Leu Phe Cys Thr Arg Glu Asn Asp Pro Val Arg Gly Pro
 645 650 655
 Asp Gly Lys Thr His Gly Asn Lys Cys Ala Met Cys Lys Ala Val Phe

660	665	670
Gln Lys Glu Asn Glu Glu Arg Lys Arg Lys Glu Glu Glu Asp Gln Arg 675 680 685		
Asn Ala Ala Gly His Gly Ser Ser Gly Gly Gly Gly Gly Asn Thr Gln 690 695 700		
Asp Glu Cys Ala Glu Tyr Gln Glu Gln Met Lys Asn Gly Arg Leu Ser 705 710 715 720		
Cys Thr Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr 725 730 735		
Asn Asn Gln Cys Thr Met Cys Lys Ala Lys Leu Glu Arg Glu Ala Glu 740 745 750		
Arg Lys Asn Glu Tyr Ser Arg Ser Arg Ser Asn Gly Thr Gly Ser Glu 755 760 765		
Ser Gly Lys Asp Thr Cys Asp Glu Phe Arg Ser Gln Met Lys Asn Gly 770 775 780		
Lys Leu Ile Cys Thr Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly 785 790 795 800		
Lys Thr His Gly Asn Lys Cys Thr Met Cys Lys Glu Lys Leu Glu Arg 805 810 815		
Glu Ala Ala Glu Lys Lys Lys Lys Glu Asp Glu Asp Arg Ser Asn Thr 820 825 830		
Gly Glu Arg Ser Asn Thr Gly Glu Arg Ser Asn Asp Lys Glu Asp Leu 835 840 845		
Cys Arg Glu Phe Arg Ser Met Gln Arg Asn Gly Lys Leu Ile Cys Thr 850 855 860		
Arg Glu Asn Asn Pro Val Arg Gly Pro Tyr Gly Lys Met His Ile Asn 865 870 875 880		
Lys Cys Ala Met Cys Gln Ser Ile Phe Asp Arg Glu Ala Asn Glu Arg 885 890 895		
Lys Lys Lys Asp Glu Glu Lys Ser Ser Ser Lys Pro Ser Asn Asn Ala 900 905 910		
Lys Asp Glu Cys Ser Glu Phe Arg Asn Tyr Ile Arg Asn Asn Glu Leu 915 920 925		
Ile Cys Pro Arg Glu Asn Asp Pro Val His Gly Ala Asp Gly Lys Phe 930 935 940		
Tyr Thr Asn Lys Cys Tyr Met Cys Arg Ala Val Phe Leu Thr Glu Ala 945 950 955 960		
Leu Glu Arg Ala Lys Leu Gln Glu Lys Pro Ser His Val Arg Ala Ser 965 970 975		

Gln Glu Glu Asp Ser Pro Asp Ser Phe Ser Ser Leu Asp Ser Glu Met
 980 985 990

Cys Lys Asp Tyr Arg Val Leu Pro Arg Ile Gly Tyr Leu Cys Pro Lys
 995 1000 1005

Asp Leu Lys Pro Val Cys Gly Asp Asp Gly Gln Thr Tyr Asn Asn
 1010 1015 1020

Pro Cys Met Leu Cys His Glu Asn Leu Ile Arg Gln Thr Asn Thr
 1025 1030 1035

His Ile Arg Ser Thr Gly Lys Cys Glu Glu Ser Ser Thr Pro Gly
 1040 1045 1050

Thr Thr Ala Ala Ser Met Pro Pro Ser Asp Glu
 1055 1060

<210> 159
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 159

Met His Lys Glu Glu His Glu Val Ala Val Leu Gly Ala Pro Pro Ser
 1 5 10 15

Thr Ile Leu Pro Arg Ser Thr Val Ile Asn Ile His Ser Glu Thr Ser
 20 25 30

Val Pro Asp His Val Val Trp Ser Leu Phe Asn Thr Leu Phe Leu Asn
 35 40 45

Trp Cys Cys Leu Gly Phe Ile Ala Phe Ala Tyr Ser Val Lys Ser Arg
 50 55 60

Asp Arg Lys Met Val Gly Asp Val Thr Gly Ala Gln Ala Tyr Ala Ser
 65 70 75 80

Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu Ile Leu Gly Ile Leu Met
 85 90 95

Thr Ile Gly Phe Ile Leu Leu Leu Val Phe Gly Ser Val Thr Val Tyr
 100 105 110

His Ile Met Leu Gln Ile Ile Gln Glu Lys Arg Gly Tyr
 115 120 125

<210> 160
 <211> 400
 <212> PRT
 <213> Homo sapiens

<400> 160

Met Met Asp Leu Arg Asn Thr Pro Ala Lys Ser Leu Asp Lys Phe Ile
 1 5 10 15

Glu Asp Tyr Leu Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asp His
 20 25 30

Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly

```

          35              40              45
Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser
 50              55              60

Gly Lys Gly Thr Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val
65              70              75              80

Phe Leu Ser Pro Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly
      85              90              95

Glu Phe Ile Gln Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu
      100              105              110

Arg Ala Leu Ser Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn
      115              120              125

Pro Arg Ala Leu Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly
      130              135              140

Val Glu Phe Asp Val Leu Pro Ala Phe Asp Ala Leu Gly Gln Leu Thr
      145              150              155              160

Gly Ser Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu Glu
      165              170              175

Cys Thr Asp Leu Gln Lys Glu Gly Glu Phe Ser Thr Cys Phe Thr Glu
      180              185              190

Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser Leu
      195              200              205

Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu Gly
      210              215              220

Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala Trp
      225              230              235              240

Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe Arg
      245              250              255

Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr Trp
      260              265              270

Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu Arg
      275              280              285

Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro
      290              295              300

Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu Ala
      305              310              315              320

Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp Asp
      325              330              335

Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Ala Glu Ser Asn Ser Thr
      340              345              350

```

Asp Asp Glu Thr Asp Asp Pro Arg Thr Tyr Gln Lys Tyr Gly Tyr Ile
 355 360 365
 Gly Thr His Glu Tyr Pro His Phe Ser His Arg Pro Ser Thr Leu Gln
 370 375 380
 Ala Ala Ser Thr Pro Gln Ala Glu Glu Asp Trp Thr Cys Thr Ile Leu
 385 390 395 400
 <210> 161
 <211> 370
 <212> PRT
 <213> Homo sapiens
 <400> 161
 Met Glu Asn Gln Val Leu Thr Pro His Val Tyr Trp Ala Gln Arg His
 1 5 10 15
 Arg Glu Leu Tyr Leu Arg Val Glu Leu Ser Asp Val Gln Asn Pro Ala
 20 25 30
 Ile Ser Ile Thr Glu Asn Val Leu His Phe Lys Ala Gln Gly His Gly
 35 40 45
 Ala Lys Gly Asp Asn Val Tyr Glu Phe His Leu Glu Phe Leu Asp Leu
 50 55 60
 Val Lys Pro Glu Pro Val Tyr Lys Leu Thr Gln Arg Gln Val Asn Ile
 65 70 75 80
 Thr Val Gln Lys Lys Val Ser Gln Trp Trp Glu Arg Leu Thr Lys Gln
 85 90 95
 Glu Lys Arg Pro Leu Phe Leu Ala Pro Asp Phe Asp Arg Trp Leu Asp
 100 105 110
 Glu Ser Asp Ala Glu Met Glu Leu Arg Ala Lys Glu Glu Glu Arg Leu
 115 120 125
 Asn Lys Leu Arg Leu Glu Ser Glu Gly Ser Pro Glu Thr Leu Thr Asn
 130 135 140
 Leu Arg Lys Gly Tyr Leu Phe Met Tyr Asn Leu Val Gln Phe Leu Gly
 145 150 155 160
 Phe Ser Trp Ile Phe Val Asn Leu Thr Val Arg Phe Cys Ile Leu Gly
 165 170 175
 Lys Glu Ser Phe Tyr Asp Thr Phe His Thr Val Ala Asp Met Met Tyr
 180 185 190
 Phe Cys Gln Met Leu Ala Val Val Glu Thr Ile Asn Ala Ala Ile Gly
 195 200 205
 Val Thr Thr Ser Pro Val Leu Pro Ser Leu Ile Gln Leu Leu Gly Arg
 210 215 220
 Asn Phe Ile Leu Phe Ile Ile Phe Gly Thr Met Glu Glu Met Gln Asn
 225 230 235 240

Lys Ala Val Val Phe Phe Val Phe Tyr Leu Trp Ser Ala Ile Glu Ile
245 250 255

Phe Arg Tyr Ser Phe Tyr Met Leu Thr Cys Ile Asp Met Asp Trp Lys
260 265 270

Val Leu Thr Trp Leu Arg Tyr Thr Leu Trp Ile Pro Leu Tyr Pro Leu
275 280 285

Gly Cys Leu Ala Glu Ala Val Ser Val Ile Gln Ser Ile Pro Ile Phe
290 295 300

Asn Glu Thr Gly Arg Phe Ser Phe Thr Leu Pro Tyr Pro Val Lys Ile
305 310 315 320

Lys Val Arg Phe Ser Phe Phe Leu Gln Ile Tyr Leu Ile Met Ile Phe
325 330 335

Leu Gly Leu Tyr Ile Asn Phe Arg His Leu Tyr Lys Gln Arg Arg Leu
340 345 350

Lys Met Arg Ala Gly Ala Val Ala His Ala Cys Asp Pro Ser Ala Leu
355 360 365

Gly Gly
370

<210> 162

<211> 372

<212> PRT

<213> Homo sapiens

<400> 162

Met Leu Asp Gly Leu Gly Val Val Ala Ile Ser Ile Phe Gly Ile Gln
1 5 10 15

Leu Lys Thr Glu Gly Ser Leu Arg Thr Ala Val Pro Gly Ile Pro Thr
20 25 30

Gln Ser Ala Phe Asn Lys Cys Leu Gln Arg Tyr Ile Gly Ala Leu Gly
35 40 45

Ala Arg Val Ile Cys Asp Asn Ile Pro Gly Leu Val Ser Arg Gln Arg
50 55 60

Gln Leu Cys Gln Arg Tyr Pro Asp Ile Met Arg Ser Val Gly Glu Gly
65 70 75 80

Ala Arg Glu Trp Ile Arg Glu Cys Gln His Gln Phe Arg His His Arg
85 90 95

Trp Asn Cys Thr Thr Leu Asp Arg Asp His Thr Val Phe Gly Arg Val
100 105 110

Met Leu Arg Ser Ser Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser
115 120 125

Ala Gly Val Ile His Ala Ile Thr Arg Ala Cys Ser Gln Gly Glu Leu
130 135 140

Ser Val Cys Ser Cys Asp Pro Tyr Thr Arg Gly Arg His His Asp Gln
145 150 155 160

Arg Gly Thr Phe Asp Trp Gly Gly Cys Ser Asp Asn Ile His Tyr Gly
165 170 175

Val Arg Phe Ala Lys Ala Phe Val Asp Ala Lys Glu Lys Arg Leu Lys
180 185 190

Asp Ala Arg Ala Leu Met Asn Leu His Asn Asn Arg Cys Gly Arg Thr
195 200 205

Ala Val Arg Arg Phe Val Lys Leu Glu Cys Lys Cys His Gly Val Ser
210 215 220

Gly Ser Cys Thr Leu Arg Thr Cys Trp Arg Ala Leu Ser Asp Phe Arg
225 230 235 240

Arg Thr Gly Asp Tyr Leu Arg Arg Arg Tyr Asp Gly Ala Val Gln Val
245 250 255

Met Ala Thr Gln Asp Gly Ala Asn Phe Thr Ala Ala Arg Gln Gly Tyr
260 265 270

Arg Arg Ala Thr Arg Ser Asp Leu Val Tyr Phe Asp Asn Ser Pro Asp
275 280 285

Tyr Cys Val Leu Asp Lys Ala Ala Gly Ser Leu Gly Thr Ala Gly Arg
290 295 300

Val Cys Ser Lys Thr Ser Lys Gly Thr Asp Gly Cys Glu Ile Met Cys
305 310 315 320

Cys Gly Arg Gly Tyr Asp Thr Thr Arg Val Thr Arg Val Thr Gln Cys
325 330 335

Glu Cys Lys Phe His Trp Cys Cys Ala Val Arg Cys Lys Glu Cys Arg
340 345 350

Asn Thr Val Asp Val His Thr Cys Lys Ala Pro Lys Lys Ala Glu Trp
355 360 365

Leu Asp Gln Thr
370

<210> 163
<211> 249
<212> PRT
<213> Homo sapiens

<400> 163

Met Lys Leu Asn Ile Ser Phe Pro Ala Thr Gly Cys Gln Lys Leu Ile
1 5 10 15

Glu Val Asp Asp Glu Arg Thr Leu Arg Thr Phe Tyr Glu Lys Arg Met
20 25 30

Ala Thr Glu Val Ala Ala Asp Ala Leu Gly Glu Glu Trp Lys Gly Tyr
35 40 45

Val Val Arg Ile Ser Gly Gly Asn Asp Lys Gln Gly Phe Pro Met Lys
 50 55 60
 Gln Gly Val Leu Thr His Gly Arg Val Arg Leu Leu Leu Ser Lys Gly
 65 70 75 80
 His Ser Cys Tyr Arg Pro Arg Arg Thr Gly Glu Arg Lys Arg Lys Ser
 85 90 95
 Val Arg Gly Cys Ile Val Asp Ala Asn Leu Ser Val Leu Asn Leu Val
 100 105 110
 Ile Val Lys Lys Gly Glu Lys Asp Ile Pro Gly Leu Thr Asp Thr Thr
 115 120 125
 Val Pro Arg Arg Leu Gly Pro Lys Arg Ala Ser Arg Ile Arg Lys Arg
 130 135 140
 Phe Asn Leu Ser Lys Glu Asp Asp Val Arg Gln Tyr Val Val Arg Lys
 145 150 155 160
 Pro Leu Asn Lys Glu Gly Lys Lys Pro Arg Thr Lys Ala Pro Lys Ile
 165 170 175
 Gln Arg Leu Val Thr Pro Arg Val Leu Gln His Lys Arg Arg Arg Ile
 180 185 190
 Ala Leu Lys Gln Gln Arg Thr Lys Lys Asn Lys Glu Glu Ala Ala Glu
 195 200 205
 Tyr Ala Lys Leu Leu Ala Lys Arg Met Lys Glu Ala Lys Glu Lys Arg
 210 215 220
 Gln Glu Gln Ile Ala Lys Arg Arg Arg Leu Ser Ser Leu Arg Ala Ser
 225 230 235 240
 Thr Ser Lys Ser Glu Ser Ser Gln Lys
 245
 <210> 164
 <211> 469
 <212> PRT
 <213> Homo sapiens
 <400> 164
 Met His Ser Phe Pro Pro Leu Leu Leu Leu Leu Phe Trp Gly Val Val
 1 5 10 15
 Ser His Ser Phe Pro Ala Thr Leu Glu Thr Gln Glu Gln Asp Val Asp
 20 25 30
 Leu Val Gln Lys Tyr Leu Glu Lys Tyr Tyr Asn Leu Lys Asn Asp Gly
 35 40 45
 Arg Gln Val Glu Lys Arg Arg Asn Ser Gly Pro Val Val Glu Lys Leu
 50 55 60
 Lys Gln Met Gln Glu Phe Phe Gly Leu Lys Val Thr Gly Lys Pro Asp
 65 70 75 80

Ala Glu Thr Leu Lys Val Met Lys Gln Pro Arg Cys Gly Val Pro Asp
 85 90 95
 Val Ala Gln Phe Val Leu Thr Glu Gly Asn Pro Arg Trp Glu Gln Thr
 100 105 110
 His Leu Thr Tyr Arg Ile Glu Asn Tyr Thr Pro Asp Leu Pro Arg Ala
 115 120 125
 Asp Val Asp His Ala Ile Glu Lys Ala Phe Gln Leu Trp Ser Asn Val
 130 135 140
 Thr Pro Leu Thr Phe Thr Lys Val Ser Glu Gly Gln Ala Asp Ile Met
 145 150 155 160
 Ile Ser Phe Val Arg Gly Asp His Arg Asp Asn Ser Pro Phe Asp Gly
 165 170 175
 Pro Gly Gly Asn Leu Ala His Ala Phe Gln Pro Gly Pro Gly Ile Gly
 180 185 190
 Gly Asp Ala His Phe Asp Glu Asp Glu Arg Trp Thr Asn Asn Phe Arg
 195 200 205
 Glu Tyr Asn Leu His Arg Val Ala Ala His Glu Leu Gly His Ser Leu
 210 215 220
 Gly Leu Ser His Ser Thr Asp Ile Gly Ala Leu Met Tyr Pro Ser Tyr
 225 230 235 240
 Thr Phe Ser Gly Asp Val Gln Leu Ala Gln Asp Asp Ile Asp Gly Ile
 245 250 255
 Gln Ala Ile Tyr Gly Arg Ser Gln Asn Pro Val Gln Pro Ile Gly Pro
 260 265 270
 Gln Thr Pro Lys Ala Cys Asp Ser Lys Leu Thr Phe Asp Ala Ile Thr
 275 280 285
 Thr Ile Arg Gly Glu Val Met Phe Phe Lys Asp Arg Phe Tyr Met Arg
 290 295 300
 Thr Asn Pro Phe Tyr Pro Glu Val Glu Leu Asn Phe Ile Ser Val Phe
 305 310 315 320
 Trp Pro Gln Leu Pro Asn Gly Leu Glu Ala Ala Tyr Glu Phe Ala Asp
 325 330 335
 Arg Asp Glu Val Arg Phe Phe Lys Gly Asn Lys Tyr Trp Ala Val Gln
 340 345 350
 Gly Gln Asn Val Leu His Gly Tyr Pro Lys Asp Ile Tyr Ser Ser Phe
 355 360 365
 Gly Phe Pro Arg Thr Val Lys His Ile Asp Ala Ala Leu Ser Glu Glu
 370 375 380
 Asn Thr Gly Lys Thr Tyr Phe Phe Val Ala Asn Lys Tyr Trp Arg Tyr
 385 390 395 400

Asp Glu Tyr Lys Arg Ser Met Asp Pro Gly Tyr Pro Lys Met Ile Ala
405 410 415

His Asp Phe Pro Gly Ile Gly His Lys Val Asp Ala Val Phe Met Lys
420 425 430

Asp Gly Phe Phe Tyr Phe Phe His Gly Thr Arg Gln Tyr Lys Phe Asp
435 440 445

Pro Lys Thr Lys Arg Ile Leu Thr Leu Gln Lys Ala Asn Ser Trp Phe
450 455 460

Asn Cys Arg Lys Asn
465

<210> 165
<211> 156
<212> PRT
<213> Homo sapiens

<400> 165

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ala Lys Lys Arg
65 70 75 80

Lys Lys Lys Ser Tyr Thr Thr Pro Lys Lys Asn Lys His Lys Arg Lys
85 90 95

Lys Val Lys Leu Ala Val Leu Lys Tyr Tyr Lys Val Asp Glu Asn Gly
100 105 110

Lys Ile Ser Arg Leu Arg Arg Glu Cys Pro Ser Asp Glu Cys Gly Ala
115 120 125

Gly Val Phe Met Ala Ser His Phe Asp Arg His Tyr Cys Gly Lys Cys
130 135 140

Cys Leu Thr Tyr Cys Phe Asn Lys Pro Glu Asp Lys
145 150 155

<210> 166
<211> 783
<212> PRT
<213> Homo sapiens

<400> 166

Met Ala Lys Tyr Asn Thr Gly Gly Asn Pro Thr Glu Asp Val Ser Val
1 5 10 15

Asn Ser Arg Pro Phe Arg Val Thr Gly Pro Asn Ser Ser Ser Gly Ile
 20 25 30
 Gln Ala Arg Lys Asn Leu Phe Asn Asn Gln Gly Asn Ala Ser Pro Pro
 35 40 45
 Ala Gly Pro Ser Asn Val Pro Lys Phe Gly Ser Pro Lys Pro Pro Val
 50 55 60
 Ala Val Lys Pro Ser Ser Glu Glu Lys Pro Asp Lys Glu Pro Lys Pro
 65 70 75 80
 Pro Phe Leu Lys Pro Thr Gly Ala Gly Gln Arg Phe Gly Thr Pro Ala
 85 90 95
 Ser Leu Thr Thr Arg Asp Pro Glu Ala Lys Val Gly Phe Leu Lys Pro
 100 105 110
 Val Gly Pro Lys Pro Ile Asn Leu Pro Lys Glu Asp Ser Lys Pro Thr
 115 120 125
 Phe Pro Trp Pro Pro Gly Asn Lys Pro Ser Leu His Ser Val Asn Gln
 130 135 140
 Asp His Asp Leu Lys Pro Leu Gly Pro Lys Ser Gly Pro Thr Pro Pro
 145 150 155 160
 Thr Ser Glu Asn Glu Gln Lys Gln Ala Phe Pro Lys Leu Thr Gly Val
 165 170 175
 Lys Gly Lys Phe Met Ser Ala Ser Gln Asp Leu Glu Pro Lys Pro Leu
 180 185 190
 Phe Pro Lys Pro Ala Phe Gly Gln Lys Pro Pro Leu Ser Thr Glu Asn
 195 200 205
 Ser His Glu Asp Glu Ser Pro Met Lys Asn Val Ser Ser Ser Lys Gly
 210 215 220
 Ser Pro Ala Pro Leu Gly Val Arg Ser Lys Ser Gly Pro Leu Lys Pro
 225 230 235 240
 Ala Arg Glu Asp Ser Glu Asn Lys Asp His Ala Gly Glu Ile Ser Ser
 245 250 255
 Leu Pro Phe Pro Gly Val Val Leu Lys Pro Ala Ala Ser Arg Gly Gly
 260 265 270
 Leu Gly Leu Ser Lys Asn Gly Glu Glu Lys Lys Glu Asp Arg Lys Ile
 275 280 285
 Asp Ala Ala Lys Asn Thr Phe Gln Ser Lys Ile Asn Gln Glu Glu Leu
 290 295 300
 Ala Ser Gly Thr Pro Pro Ala Arg Phe Pro Lys Ala Pro Ser Lys Leu
 305 310 315 320
 Thr Val Gly Gly Pro Trp Gly Gln Ser Gln Glu Lys Glu Lys Gly Asp
 325 330 335

Lys Asn Ser Ala Thr Pro Lys Gln Lys Pro Leu Pro Pro Leu Phe Thr
 340 345 350
 Leu Gly Pro Pro Pro Pro Lys Pro Asn Arg Pro Pro Asn Val Asp Leu
 355 360 365
 Thr Lys Phe His Lys Thr Ser Ser Gly Asn Ser Thr Ser Lys Gly Gln
 370 375 380
 Thr Ser Tyr Ser Thr Thr Ser Leu Pro Pro Pro Pro Pro Ser His Pro
 385 390 395 400
 Ala Ser Gln Pro Pro Leu Pro Ala Ser His Pro Ser Gln Pro Pro Val
 405 410 415
 Pro Ser Leu Pro Pro Arg Asn Ile Lys Pro Pro Phe Asp Leu Lys Ser
 420 425 430
 Pro Val Asn Glu Asp Asn Gln Asp Gly Val Thr His Ser Asp Gly Ala
 435 440 445
 Gly Asn Leu Asp Glu Glu Gln Asp Ser Glu Gly Glu Thr Tyr Glu Asp
 450 455 460
 Ile Glu Ala Ser Lys Glu Arg Glu Lys Lys Arg Glu Lys Glu Glu Lys
 465 470 475 480
 Lys Arg Leu Glu Leu Glu Lys Lys Glu Gln Lys Glu Lys Glu Lys Lys
 485 490 495
 Glu Gln Glu Ile Lys Lys Lys Phe Lys Leu Thr Gly Pro Ile Gln Val
 500 505 510
 Ile His Leu Ala Lys Ala Cys Cys Asp Val Lys Gly Gly Lys Asn Glu
 515 520 525
 Leu Ser Phe Lys Gln Gly Glu Gln Ile Glu Ile Ile Arg Ile Thr Asp
 530 535 540
 Asn Pro Glu Gly Lys Trp Leu Gly Arg Thr Ala Arg Gly Ser Tyr Gly
 545 550 555 560
 Tyr Ile Lys Thr Thr Ala Val Glu Ile Asp Tyr Asp Ser Leu Lys Leu
 565 570 575
 Lys Lys Asp Ser Leu Gly Ala Pro Ser Arg Pro Ile Glu Asp Asp Gln
 580 585 590
 Glu Val Tyr Asp Asp Val Ala Glu Gln Asp Asp Ile Ser Ser His Ser
 595 600 605
 Gln Ser Gly Ser Gly Gly Ile Phe Pro Pro Pro Pro Asp Asp Asp Ile
 610 615 620
 Tyr Asp Gly Ile Glu Glu Glu Asp Ala Asp Asp Gly Phe Pro Ala Pro
 625 630 635 640
 Pro Lys Gln Leu Asp Met Gly Asp Glu Val Tyr Asp Asp Val Asp Thr
 645 650 655

Ser Asp Phe Pro Val Ser Ser Ala Glu Met Ser Gln Gly Thr Asn Phe
660 665 670

Gly Lys Ala Lys Thr Glu Glu Lys Asp Leu Lys Lys Leu Lys Lys Gln
675 680 685

Glu Lys Glu Glu Lys Asp Phe Arg Lys Lys Phe Lys Tyr Asp Gly Glu
690 695 700

Ile Arg Val Leu Tyr Ser Thr Lys Val Thr Thr Ser Ile Thr Ser Lys
705 710 715 720

Lys Trp Gly Thr Arg Asp Leu Gln Val Lys Pro Gly Glu Ser Leu Glu
725 730 735

Val Ile Gln Thr Thr Asp Asp Thr Lys Val Leu Cys Arg Asn Glu Glu
740 745 750

Gly Lys Tyr Gly Tyr Val Leu Arg Ser Tyr Leu Ala Asp Asn Asp Gly
755 760 765

Glu Ile Tyr Asp Asp Ile Ala Asp Gly Cys Ile Tyr Asp Asn Asp
770 775 780

<210> 167
<211> 117
<212> PRT
<213> Homo sapiens

<400> 167

Met Ala Ala Ala Ala Ala Ala Gly Ser Gly Thr Pro Arg Glu Glu Glu
1 5 10 15

Val Pro Ala Gly Glu Ala Ala Ala Ser Gln Pro Gln Ala Pro Thr Ser
20 25 30

Val Pro Gly Ala Arg Leu Ser Arg Leu Pro Leu Ala Arg Val Lys Ala
35 40 45

Leu Val Lys Ala Asp Pro Asp Val Thr Leu Ala Gly Gln Glu Ala Ile
50 55 60

Phe Ile Leu Ala Arg Ala Ala Glu Leu Phe Val Glu Thr Ile Ala Lys
65 70 75 80

Asp Ala Tyr Cys Cys Ala Gln Gln Gly Lys Arg Lys Thr Leu Gln Arg
85 90 95

Arg Asp Leu Asp Asn Ala Ile Glu Ala Val Asp Glu Phe Ala Phe Leu
100 105 110

Glu Gly Thr Leu Asp
115

<210> 168
<211> 243
<212> PRT
<213> Homo sapiens

<400> 168

Met Ala Val Gln Ile Ser Lys Arg Arg Lys Phe Val Ala Asp Gly Ile
1 5 10 15

Phe Lys Ala Glu Leu Asn Glu Phe Leu Thr Arg Glu Leu Ala Glu Asp
20 25 30

Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Thr Arg Thr Glu Ile
35 40 45

Ile Ile Leu Ala Thr Arg Thr Gln Asn Val Leu Gly Glu Lys Gly Arg
50 55 60

Arg Ile Arg Glu Leu Thr Ala Val Val Gln Lys Arg Phe Gly Phe Pro
65 70 75 80

Glu Gly Ser Val Glu Leu Tyr Ala Glu Lys Val Ala Thr Arg Gly Leu
85 90 95

Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr Lys Leu Leu Gly Gly
100 105 110

Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu Arg Phe Ile Met Glu
115 120 125

Ser Gly Ala Lys Gly Cys Glu Val Val Val Ser Gly Lys Leu Arg Gly
130 135 140

Gln Arg Ala Lys Ser Met Lys Phe Val Asp Gly Leu Met Ile His Ser
145 150 155 160

Gly Asp Pro Val Asn Tyr Tyr Val Asp Thr Ala Val Arg His Val Leu
165 170 175

Leu Arg Gln Gly Val Leu Gly Ile Lys Val Lys Ile Met Leu Pro Trp
180 185 190

Asp Pro Thr Gly Lys Ile Gly Pro Lys Lys Pro Leu Pro Asp His Val
195 200 205

Ser Ile Val Glu Pro Lys Asp Glu Ile Leu Pro Thr Thr Pro Ile Ser
210 215 220

Glu Gln Lys Gly Gly Lys Pro Glu Pro Pro Ala Met Pro Gln Pro Val
225 230 235 240

Pro Thr Ala

<210> 169
<211> 136
<212> PRT
<213> Homo sapiens

<400> 169

Met Val Leu Leu Glu Ser Glu Gln Phe Leu Thr Glu Leu Thr Arg Leu
1 5 10 15

Phe Gln Lys Cys Arg Thr Ser Gly Ser Val Tyr Ile Thr Leu Lys Lys
20 25 30

Tyr Asp Gly Arg Thr Lys Pro Ile Pro Lys Lys Gly Thr Val Glu Gly
35 40 45

Phe Glu Pro Ala Asp Asn Lys Cys Leu Leu Arg Ala Thr Asp Gly Lys
50 55 60

Lys Lys Ile Ser Thr Val Val Ser Ser Lys Glu Val Asn Lys Phe Gln
65 70 75 80

Met Ala Tyr Ser Asn Leu Leu Arg Ala Asn Met Asp Gly Leu Lys Lys
85 90 95

Arg Asp Lys Lys Asn Lys Thr Lys Lys Thr Lys Ala Ala Ala Ala Ala
100 105 110

Ala Ala Ala Ala Pro Ala Ala Ala Ala Thr Ala Ala Thr Thr Ala Ala
115 120 125

Thr Thr Ala Ala Thr Ala Ala Gln
130 135

<210> 170
<211> 409
<212> PRT
<213> Homo sapiens

<400> 170

Met Gln Val Thr Leu Lys Thr Leu Gln Gln Gln Thr Phe Lys Ile Asp
1 5 10 15

Ile Asp Pro Glu Glu Thr Val Lys Ala Leu Lys Glu Lys Ile Glu Ser
20 25 30

Glu Lys Gly Lys Asp Ala Phe Pro Val Ala Gly Gln Lys Leu Ile Tyr
35 40 45

Ala Gly Lys Ile Leu Asn Asp Asp Thr Ala Leu Lys Glu Tyr Lys Ile
50 55 60

Asp Glu Lys Asn Phe Val Val Val Met Val Thr Lys Pro Lys Ala Val
65 70 75 80

Ser Thr Pro Ala Pro Ala Thr Thr Gln Gln Ser Ala Pro Ala Ser Thr
85 90 95

Thr Ala Val Thr Ser Ser Thr Thr Thr Thr Val Ala Gln Ala Pro Thr
100 105 110

Pro Val Pro Ala Leu Ala Pro Thr Ser Thr Pro Ala Ser Ile Thr Pro
115 120 125

Ala Ser Ala Thr Ala Ser Ser Glu Pro Ala Pro Ala Ser Ala Ala Lys
130 135 140

Gln Glu Lys Pro Ala Glu Lys Pro Ala Glu Thr Pro Val Ala Thr Ser
145 150 155 160

Pro Thr Ala Thr Asp Ser Thr Ser Gly Asp Ser Ser Arg Ser Asn Leu
165 170 175

Phe Glu Asp Ala Thr Ser Ala Leu Val Thr Gly Gln Ser Tyr Glu Asn
180 185 190

Met Val Thr Glu Ile Met Ser Met Gly Tyr Glu Arg Glu Gln Val Ile
195 200 205

Ala Ala Leu Arg Ala Ser Phe Asn Asn Pro Asp Arg Ala Val Glu Tyr
210 215 220

Leu Leu Met Gly Ile Pro Gly Asp Arg Glu Ser Gln Ala Val Val Asp
225 230 235 240

Pro Pro Gln Ala Ala Ser Thr Gly Ala Pro Gln Ser Ser Ala Val Ala
245 250 255

Ala Ala Ala Ala Thr Thr Thr Ala Thr Thr Thr Thr Thr Ser Ser Gly
260 265 270

Gly His Pro Leu Glu Phe Leu Arg Asn Gln Pro Gln Phe Gln Gln Met
275 280 285

Arg Gln Ile Ile Gln Gln Asn Pro Ser Leu Leu Pro Ala Leu Leu Gln
290 295 300

Gln Ile Gly Arg Glu Asn Pro Gln Leu Leu Gln Gln Ile Ser Gln His
305 310 315 320

Gln Glu His Phe Ile Gln Met Leu Asn Glu Pro Val Gln Glu Ala Gly
325 330 335

Gly Gln Gly Gly Gly Gly Gly Gly Gly Ser Gly Gly Ile Ala Glu Ala
340 345 350

Gly Ser Gly His Met Asn Tyr Ile Gln Val Thr Pro Gln Glu Lys Glu
355 360 365

Ala Ile Glu Arg Leu Lys Ala Leu Gly Phe Pro Glu Gly Leu Val Ile
370 375 380

Gln Ala Tyr Phe Ala Cys Glu Lys Asn Glu Asn Leu Ala Ala Asn Phe
385 390 395 400

Leu Leu Gln Gln Asn Phe Asp Glu Asp
405

<210> 171

<211> 614

<212> PRT

<213> Homo sapiens

<400> 171

Met Ser Gly Ile Lys Lys Gln Lys Thr Glu Asn Gln Gln Lys Ser Thr
1 5 10 15

Asn Val Val Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln
20 25 30

Val Val Gly Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr
35 40 45

Gly Leu Ser Gly Ala Gly Lys Thr Thr Ile Ser Phe Ala Leu Glu Glu
 50 55 60
 Tyr Leu Val Ser His Ala Ile Pro Cys Tyr Ser Leu Asp Gly Asp Asn
 65 70 75 80
 Val Arg His Gly Leu Asn Arg Asn Leu Gly Phe Ser Pro Gly Asp Arg
 85 90 95
 Glu Glu Asn Ile Arg Arg Ile Ala Glu Val Ala Lys Leu Phe Ala Asp
 100 105 110
 Ala Gly Leu Val Cys Ile Thr Ser Phe Ile Ser Pro Phe Ala Lys Asp
 115 120 125
 Arg Glu Asn Ala Arg Lys Ile His Glu Ser Ala Gly Leu Pro Phe Phe
 130 135 140
 Glu Ile Phe Val Asp Ala Pro Leu Asn Ile Cys Glu Ser Arg Asp Val
 145 150 155 160
 Lys Gly Leu Tyr Lys Lys Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr
 165 170 175
 Gly Ile Asp Ser Asp Tyr Glu Lys Pro Glu Thr Pro Glu Arg Val Leu
 180 185 190
 Lys Thr Asn Leu Ser Thr Val Ser Asp Cys Val His Gln Val Val Glu
 195 200 205
 Leu Leu Gln Glu Gln Asn Ile Val Pro Tyr Thr Ile Ile Lys Asp Ile
 210 215 220
 His Glu Leu Phe Val Pro Glu Asn Lys Leu Asp His Val Arg Ala Glu
 225 230 235 240
 Ala Glu Thr Leu Pro Ser Leu Ser Ile Thr Lys Leu Asp Leu Gln Trp
 245 250 255
 Val Gln Val Leu Ser Glu Gly Trp Ala Thr Pro Leu Lys Gly Phe Met
 260 265 270
 Arg Glu Lys Glu Tyr Leu Gln Val Met His Phe Asp Thr Leu Leu Asp
 275 280 285
 Asp Gly Val Ile Asn Met Ser Ile Pro Ile Val Leu Pro Val Ser Ala
 290 295 300
 Glu Asp Lys Thr Arg Leu Glu Gly Cys Ser Lys Phe Val Leu Ala His
 305 310 315 320
 Gly Gly Arg Arg Val Ala Ile Leu Arg Asp Ala Glu Phe Tyr Glu His
 325 330 335
 Arg Lys Glu Glu Arg Cys Ser Arg Val Trp Gly Thr Thr Cys Thr Lys
 340 345 350
 His Pro His Ile Lys Met Val Met Glu Ser Gly Asp Trp Leu Val Gly
 355 360 365

Gly Asp Leu Gln Val Leu Glu Lys Ile Arg Trp Asn Asp Gly Leu Asp
370 375 380

Gln Tyr Arg Leu Thr Pro Leu Glu Leu Lys Gln Lys Cys Lys Glu Met
385 390 395 400

Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn
405 410 415

Gly His Ala Leu Leu Met Gln Asp Thr Arg Arg Arg Leu Leu Glu Arg
420 425 430

Gly Tyr Lys His Pro Val Leu Leu Leu His Pro Leu Gly Gly Trp Thr
435 440 445

Lys Asp Asp Asp Val Pro Leu Asp Trp Arg Met Lys Gln His Ala Ala
450 455 460

Val Leu Glu Glu Gly Val Leu Asp Pro Lys Ser Thr Ile Val Ala Ile
465 470 475 480

Phe Pro Ser Pro Met Leu Tyr Ala Gly Pro Thr Glu Val Gln Trp His
485 490 495

Cys Arg Ser Arg Met Ile Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg
500 505 510

Asp Pro Ala Gly Met Pro His Pro Glu Thr Lys Lys Asp Leu Tyr Glu
515 520 525

Pro Thr His Gly Gly Lys Val Leu Ser Met Ala Pro Gly Leu Thr Ser
530 535 540

Val Glu Ile Ile Pro Phe Arg Val Ala Ala Tyr Asn Lys Ala Lys Lys
545 550 555 560

Ala Met Asp Phe Tyr Asp Leu Ala Arg His Asn Glu Phe Asp Phe Ile
565 570 575

Ser Gly Thr Arg Met Arg Lys Leu Ala Arg Glu Gly Glu Asn Pro Pro
580 585 590

Asp Gly Phe Met Ala Pro Lys Ala Trp Lys Val Leu Thr Asp Tyr Tyr
595 600 605

Arg Ser Leu Glu Lys Asn
610

<210> 172
<211> 798
<212> PRT
<213> Homo sapiens

<400> 172

Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys
1 5 10 15

Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala
20 25 30

Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys
 35 40 45
 Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys
 50 55 60
 Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro Pro Asp Asp Ile
 65 70 75 80
 Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr
 85 90 95
 Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His
 100 105 110
 Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro
 115 120 125
 Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp
 130 135 140
 Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu
 145 150 155 160
 Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile
 165 170 175
 Thr Ser Asp Phe Arg Ile Gly Phe Gly Ser Phe Val Glu Lys Thr Val
 180 185 190
 Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr
 195 200 205
 Ser Glu Gln Asn Cys Thr Thr Pro Phe Ser Tyr Lys Asn Val Leu Ser
 210 215 220
 Leu Thr Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys Gln Arg
 225 230 235 240
 Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met
 245 250 255
 Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg
 260 265 270
 Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly
 275 280 285
 Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu
 290 295 300
 Asn Asn Met Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala
 305 310 315 320
 His Leu Val Gln Lys Leu Ser Glu Asn Asn Ile Gln Thr Ile Phe Ala
 325 330 335
 Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile

340	345	350
Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile 355 360 365		
Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu 370 375 380		
Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser Tyr 385 390 395 400		
Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser 405 410 415		
Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ser 420 425 430		
Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu 435 440 445		
Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys 450 455 460		
Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly 465 470 475 480		
Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val 485 490 495		
Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met 500 505 510		
Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn 515 520 525		
Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr 530 535 540		
Asn Glu Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys 545 550 555 560		
Asp Arg Ser Asn Gly Leu Ile Cys Gly Gly Asn Gly Val Cys Lys Cys 565 570 575		
Arg Val Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys 580 585 590		
Ser Leu Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn 595 600 605		
Gly Arg Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp Pro Lys 610 615 620		
Phe Gln Gly Gln Thr Cys Glu Met Cys Gln Thr Cys Leu Gly Val Cys 625 630 635 640		
Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu 645 650 655		

Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys
660 665 670

Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val
675 680 685

Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr
690 695 700

Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn
705 710 715 720

Pro Glu Cys Pro Thr Gly Pro Asp Ile Ile Pro Ile Val Ala Gly Val
725 730 735

Val Ala Gly Ile Val Leu Ile Gly Leu Ala Leu Leu Leu Ile Trp Lys
740 745 750

Leu Leu Met Ile Ile His Asp Arg Arg Glu Phe Ala Lys Phe Glu Lys
755 760 765

Glu Lys Met Asn Ala Lys Trp Asp Thr Gly Glu Asn Pro Ile Tyr Lys
770 775 780

Ser Ala Val Thr Thr Val Val Asn Pro Lys Tyr Glu Gly Lys
785 790 795

<210> 173
<211> 502
<212> PRT
<213> Homo sapiens

<400> 173

Met Ala Ser Lys Lys Leu Gly Ala Asp Phe His Gly Thr Phe Ser Tyr
1 5 10 15

Leu Asp Asp Val Pro Phe Lys Thr Gly Asp Lys Phe Lys Thr Pro Ala
20 25 30

Lys Val Gly Leu Pro Ile Gly Phe Ser Leu Pro Asp Cys Leu Gln Val
35 40 45

Val Arg Glu Val Gln Tyr Asp Phe Ser Leu Glu Lys Lys Thr Ile Glu
50 55 60

Trp Ala Glu Glu Ile Lys Lys Ile Glu Glu Ala Glu Arg Glu Ala Glu
65 70 75 80

Cys Lys Ile Ala Glu Ala Glu Ala Lys Val Asn Ser Lys Ser Gly Pro
85 90 95

Glu Gly Asp Ser Lys Met Ser Phe Ser Lys Thr His Ser Thr Ala Thr
100 105 110

Met Pro Pro Pro Ile Asn Pro Ile Leu Ala Ser Leu Gln His Asn Ser
115 120 125

Ile Leu Thr Pro Thr Arg Val Ser Ser Ser Ala Thr Lys Gln Lys Val
130 135 140

Leu Ser Pro Pro His Ile Lys Ala Asp Phe Asn Leu Ala Asp Phe Glu
 145 150 155 160
 Cys Glu Glu Asp Pro Phe Asp Asn Leu Glu Leu Lys Thr Ile Asp Glu
 165 170 175
 Lys Glu Glu Leu Arg Asn Ile Leu Val Gly Thr Thr Gly Pro Ile Met
 180 185 190
 Ala Gln Leu Leu Asp Asn Asn Leu Pro Arg Gly Gly Ser Gly Ser Val
 195 200 205
 Leu Gln Asp Glu Glu Val Leu Ala Ser Leu Glu Arg Ala Thr Leu Asp
 210 215 220
 Phe Lys Pro Leu His Lys Pro Asn Gly Phe Ile Thr Leu Pro Gln Leu
 225 230 235 240
 Gly Asn Cys Glu Lys Met Ser Leu Ser Ser Lys Val Ser Leu Pro Pro
 245 250 255
 Ile Pro Ala Val Ser Asn Ile Lys Ser Leu Ser Phe Pro Lys Leu Asp
 260 265 270
 Ser Asp Asp Ser Asn Gln Lys Thr Ala Lys Leu Ala Ser Thr Phe His
 275 280 285
 Ser Thr Ser Cys Leu Arg Asn Gly Thr Phe Gln Asn Ser Leu Lys Pro
 290 295 300
 Ser Thr Gln Ser Ser Ala Ser Glu Leu Asn Gly His His Thr Leu Gly
 305 310 315 320
 Leu Ser Ala Leu Asn Leu Asp Ser Gly Thr Glu Met Pro Ala Leu Thr
 325 330 335
 Ser Ser Gln Met Pro Ser Leu Ser Val Leu Ser Val Cys Thr Glu Glu
 340 345 350
 Ser Ser Pro Pro Asn Thr Gly Pro Thr Val Thr Pro Pro Asn Phe Ser
 355 360 365
 Val Ser Gln Val Pro Asn Met Pro Ser Cys Pro Gln Ala Tyr Ser Glu
 370 375 380
 Leu Gln Met Leu Ser Pro Ser Glu Arg Gln Cys Val Glu Thr Val Val
 385 390 395 400
 Asn Met Gly Tyr Ser Tyr Glu Cys Val Leu Arg Ala Met Lys Lys Lys
 405 410 415
 Gly Glu Asn Ile Glu Gln Ile Leu Asp Tyr Leu Phe Ala His Gly Gln
 420 425 430
 Leu Cys Glu Lys Gly Phe Asp Pro Leu Leu Val Glu Glu Ala Leu Glu
 435 440 445
 Met His Gln Cys Ser Glu Glu Lys Met Met Glu Phe Leu Gln Leu Met
 450 455 460

Ser Lys Phe Lys Glu Met Gly Phe Glu Leu Lys Asp Ile Lys Glu Val
465 470 475 480

Leu Leu Leu His Asn Asn Asp Gln Asp Asn Ala Leu Glu Asp Leu Met
485 490 495

Ala Arg Ala Gly Ala Ser
500

<210> 174
<211> 545
<212> PRT
<213> Homo sapiens

<400> 174

Met Ser Asn Asn Gly Leu Asp Ile Gln Asp Lys Pro Pro Ala Pro Pro
1 5 10 15

Met Arg Asn Thr Ser Thr Met Ile Gly Val Gly Ser Lys Asp Ala Gly
20 25 30

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
35 40 45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
50 55 60

Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
65 70 75 80

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
85 90 95

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
100 105 110

Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
115 120 125

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
130 135 140

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Ala Leu Asn
145 150 155 160

Val Lys Ala Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
165 170 175

Glu Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
180 185 190

Arg Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro
195 200 205

Leu Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro
210 215 220

Thr Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Arg Asn Thr Glu
225 230 235 240

Lys Gln Lys Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys
 245 250 255
 Leu Arg Ser Ile Val Ser Val Gly Asp Pro Lys Lys Lys Tyr Thr Arg
 260 265 270
 Phe Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met
 275 280 285
 Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln
 290 295 300
 Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
 305 310 315 320
 Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
 325 330 335
 Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
 340 345 350
 Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
 355 360 365
 Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
 370 375 380
 Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
 385 390 395 400
 Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro
 405 410 415
 Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala
 420 425 430
 Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp
 435 440 445
 Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr
 450 455 460
 Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly
 465 470 475 480
 Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp
 485 490 495
 Phe Leu Asn Arg Cys Leu Asp Met Asp Val Glu Lys Arg Gly Ser Ala
 500 505 510
 Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser
 515 520 525
 Ser Leu Thr Pro Leu Ile Ala Ala Ala Lys Glu Ala Thr Lys Asn Asn
 530 535 540
 His
 545

<210> 175
 <211> 1360
 <212> PRT
 <213> Homo sapiens

<400> 175

Met Ser Arg Gln Ser Thr Leu Tyr Ser Phe Phe Pro Lys Ser Pro Ala
 1 5 10 15

Leu Ser Asp Ala Asn Lys Ala Ser Ala Arg Ala Ser Arg Glu Gly Gly
 20 25 30

Arg Ala Ala Ala Ala Pro Gly Ala Ser Pro Ser Pro Gly Gly Asp Ala
 35 40 45

Ala Trp Ser Glu Ala Gly Pro Gly Pro Arg Pro Leu Ala Arg Ser Ala
 50 55 60

Ser Pro Pro Lys Ala Lys Asn Leu Asn Gly Gly Leu Arg Arg Ser Val
 65 70 75 80

Ala Pro Ala Ala Pro Thr Ser Cys Asp Phe Ser Pro Gly Asp Leu Val
 85 90 95

Trp Ala Lys Met Glu Gly Tyr Pro Trp Trp Pro Cys Leu Val Tyr Asn
 100 105 110

His Pro Phe Asp Gly Thr Phe Ile Arg Glu Lys Gly Lys Ser Val Arg
 115 120 125

Val His Val Gln Phe Phe Asp Asp Ser Pro Thr Arg Gly Trp Val Ser
 130 135 140

Lys Arg Leu Leu Lys Pro Tyr Thr Gly Ser Lys Ser Lys Glu Ala Gln
 145 150 155 160

Lys Gly Gly His Phe Tyr Ser Ala Lys Pro Glu Ile Leu Arg Ala Met
 165 170 175

Gln Arg Ala Asp Glu Ala Leu Asn Lys Asp Lys Ile Lys Arg Leu Glu
 180 185 190

Leu Ala Val Cys Asp Glu Pro Ser Glu Pro Glu Glu Glu Glu Glu Met
 195 200 205

Glu Val Gly Thr Thr Tyr Val Thr Asp Lys Ser Glu Glu Asp Asn Glu
 210 215 220

Ile Glu Ser Glu Glu Glu Val Gln Pro Lys Thr Gln Gly Ser Arg Arg
 225 230 235 240

Ser Ser Arg Gln Ile Lys Lys Arg Arg Val Ile Ser Asp Ser Glu Ser
 245 250 255

Asp Ile Gly Gly Ser Asp Val Glu Phe Lys Pro Asp Thr Lys Glu Glu
 260 265 270

Gly Ser Ser Asp Glu Ile Ser Ser Gly Val Gly Asp Ser Glu Ser Glu
 275 280 285

Gly Leu Asn Ser Pro Val Lys Val Ala Arg Lys Arg Lys Arg Met Val
 290 295 300
 Thr Gly Asn Gly Ser Leu Lys Arg Lys Ser Ser Arg Lys Glu Thr Pro
 305 310 315 320
 Ser Ala Thr Lys Gln Ala Thr Ser Ile Ser Ser Glu Thr Lys Asn Thr
 325 330 335
 Leu Arg Ala Phe Ser Ala Pro Gln Asn Ser Glu Ser Gln Ala His Val
 340 345 350
 Ser Gly Gly Gly Asp Asp Ser Ser Arg Pro Thr Val Trp Tyr His Glu
 355 360 365
 Thr Leu Glu Trp Leu Lys Glu Glu Lys Arg Arg Asp Glu His Arg Arg
 370 375 380
 Arg Pro Asp His Pro Asp Phe Asp Ala Ser Thr Leu Tyr Val Pro Glu
 385 390 395 400
 Asp Phe Leu Asn Ser Cys Thr Pro Gly Met Arg Lys Trp Trp Gln Ile
 405 410 415
 Lys Ser Gln Asn Phe Asp Leu Val Ile Cys Tyr Lys Val Gly Lys Phe
 420 425 430
 Tyr Glu Leu Tyr His Met Asp Ala Leu Ile Gly Val Ser Glu Leu Gly
 435 440 445
 Leu Val Phe Met Lys Gly Asn Trp Ala His Ser Gly Phe Pro Glu Ile
 450 455 460
 Ala Phe Gly Arg Tyr Ser Asp Ser Leu Val Gln Lys Gly Tyr Lys Val
 465 470 475 480
 Ala Arg Val Glu Gln Thr Glu Thr Pro Glu Met Met Glu Ala Arg Cys
 485 490 495
 Arg Lys Met Ala His Ile Ser Lys Tyr Asp Arg Val Val Arg Arg Glu
 500 505 510
 Ile Cys Arg Ile Ile Thr Lys Gly Thr Gln Thr Tyr Ser Val Leu Glu
 515 520 525
 Gly Asp Pro Ser Glu Asn Tyr Ser Lys Tyr Leu Leu Ser Leu Lys Glu
 530 535 540
 Lys Glu Glu Asp Ser Ser Gly His Thr Arg Ala Tyr Gly Val Cys Phe
 545 550 555 560
 Val Asp Thr Ser Leu Gly Lys Phe Phe Ile Gly Gln Phe Ser Asp Asp
 565 570 575
 Arg His Cys Ser Arg Phe Arg Thr Leu Val Ala His Tyr Pro Pro Val
 580 585 590
 Gln Val Leu Phe Glu Lys Gly Asn Leu Ser Lys Glu Thr Lys Thr Ile

595	600	605
Leu Lys Ser Ser Leu Ser Cys Ser Leu Gln Glu Gly Leu Ile Pro Gly 610 615 620		
Ser Gln Phe Trp Asp Ala Ser Lys Thr Leu Arg Thr Leu Leu Glu Glu 625 630 635 640		
Glu Tyr Phe Arg Glu Lys Leu Ser Asp Gly Ile Gly Val Met Leu Pro 645 650 655		
Gln Val Leu Lys Gly Met Thr Ser Glu Ser Asp Ser Ile Gly Leu Thr 660 665 670		
Pro Gly Glu Lys Ser Glu Leu Ala Leu Ser Ala Leu Gly Gly Cys Val 675 680 685		
Phe Tyr Leu Lys Lys Cys Leu Ile Asp Gln Glu Leu Leu Ser Met Ala 690 695 700		
Asn Phe Glu Glu Tyr Ile Pro Leu Asp Ser Asp Thr Val Ser Thr Thr 705 710 715 720		
Arg Ser Gly Ala Ile Phe Thr Lys Ala Tyr Gln Arg Met Val Leu Asp 725 730 735		
Ala Val Thr Leu Asn Asn Leu Glu Ile Phe Leu Asn Gly Thr Asn Gly 740 745 750		
Ser Thr Glu Gly Thr Leu Leu Glu Arg Val Asp Thr Cys His Thr Pro 755 760 765		
Phe Gly Lys Arg Leu Leu Lys Gln Trp Leu Cys Ala Pro Leu Cys Asn 770 775 780		
His Tyr Ala Ile Asn Asp Arg Leu Asp Ala Ile Glu Asp Leu Met Val 785 790 795 800		
Val Pro Asp Lys Ile Ser Glu Val Val Glu Leu Leu Lys Lys Leu Pro 805 810 815		
Asp Leu Glu Arg Leu Leu Ser Lys Ile His Asn Val Gly Ser Pro Leu 820 825 830		
Lys Ser Gln Asn His Pro Asp Ser Arg Ala Ile Met Tyr Glu Glu Thr 835 840 845		
Thr Tyr Ser Lys Lys Lys Ile Ile Asp Phe Leu Ser Ala Leu Glu Gly 850 855 860		
Phe Lys Val Met Cys Lys Ile Ile Gly Ile Met Glu Glu Val Ala Asp 865 870 875 880		
Gly Phe Lys Ser Lys Ile Leu Lys Gln Val Ile Ser Leu Gln Thr Lys 885 890 895		
Asn Pro Glu Gly Arg Phe Pro Asp Leu Thr Val Glu Leu Asn Arg Trp 900 905 910		

Asp Thr Ala Phe Asp His Glu Lys Ala Arg Lys Thr Gly Leu Ile Thr
 915 920 925
 Pro Lys Ala Gly Phe Asp Ser Asp Tyr Asp Gln Ala Leu Ala Asp Ile
 930 935 940
 Arg Glu Asn Glu Gln Ser Leu Leu Glu Tyr Leu Glu Lys Gln Arg Asn
 945 950 955 960
 Arg Ile Gly Cys Arg Thr Ile Val Tyr Trp Gly Ile Gly Arg Asn Arg
 965 970 975
 Tyr Gln Leu Glu Ile Pro Glu Asn Phe Thr Thr Arg Asn Leu Pro Glu
 980 985 990
 Glu Tyr Glu Leu Lys Ser Thr Lys Lys Gly Cys Lys Arg Tyr Trp Thr
 995 1000 1005
 Lys Thr Ile Glu Lys Lys Leu Ala Asn Leu Ile Asn Ala Glu Glu
 1010 1015 1020
 Arg Arg Asp Val Ser Leu Lys Asp Cys Met Arg Arg Leu Phe Tyr
 1025 1030 1035
 Asn Phe Asp Lys Asn Tyr Lys Asp Trp Gln Ser Ala Val Glu Cys
 1040 1045 1050
 Ile Ala Val Leu Asp Val Leu Leu Cys Leu Ala Asn Tyr Ser Arg
 1055 1060 1065
 Gly Gly Asp Gly Pro Met Cys Arg Pro Val Ile Leu Leu Pro Glu
 1070 1075 1080
 Asp Thr Pro Pro Phe Leu Glu Leu Lys Gly Ser Arg His Pro Cys
 1085 1090 1095
 Ile Thr Lys Thr Phe Phe Gly Asp Asp Phe Ile Pro Asn Asp Ile
 1100 1105 1110
 Leu Ile Gly Cys Glu Glu Glu Glu Gln Glu Asn Gly Lys Ala Tyr
 1115 1120 1125
 Cys Val Leu Val Thr Gly Pro Asn Met Gly Gly Lys Ser Thr Leu
 1130 1135 1140
 Met Arg Gln Ala Gly Leu Leu Ala Val Met Ala Gln Met Gly Cys
 1145 1150 1155
 Tyr Val Pro Ala Glu Val Cys Arg Leu Thr Pro Ile Asp Arg Val
 1160 1165 1170
 Phe Thr Arg Leu Gly Ala Ser Asp Arg Ile Met Ser Gly Glu Ser
 1175 1180 1185
 Thr Phe Phe Val Glu Leu Ser Glu Thr Ala Ser Ile Leu Met His
 1190 1195 1200
 Ala Thr Ala His Ser Leu Val Leu Val Asp Glu Leu Gly Arg Gly
 1205 1210 1215

Thr Ala Thr Phe Asp Gly Thr Ala Ile Ala Asn Ala Val Val Lys
 1220 1225 1230
 Glu Leu Ala Glu Thr Ile Lys Cys Arg Thr Leu Phe Ser Thr His
 1235 1240 1245
 Tyr His Ser Leu Val Glu Asp Tyr Ser Gln Asn Val Ala Val Arg
 1250 1255 1260
 Leu Gly His Met Ala Cys Met Val Glu Asn Glu Cys Glu Asp Pro
 1265 1270 1275
 Ser Gln Glu Thr Ile Thr Phe Leu Tyr Lys Phe Ile Lys Gly Ala
 1280 1285 1290
 Cys Pro Lys Ser Tyr Gly Phe Asn Ala Ala Arg Leu Ala Asn Leu
 1295 1300 1305
 Pro Glu Glu Val Ile Gln Lys Gly His Arg Lys Ala Arg Glu Phe
 1310 1315 1320
 Glu Lys Met Asn Gln Ser Leu Arg Leu Phe Arg Glu Val Cys Leu
 1325 1330 1335
 Ala Ser Glu Arg Ser Thr Val Asp Ala Glu Ala Val His Lys Leu
 1340 1345 1350
 Leu Thr Leu Ile Lys Glu Leu
 1355 1360
 <210> 176
 <211> 398
 <212> PRT
 <213> Homo sapiens
 <400> 176
 Met Gln Ser Glu Arg Gly Ile Thr Ile Asp Ile Ser Leu Trp Lys Phe
 1 5 10 15
 Glu Thr Ser Lys Tyr Tyr Val Thr Ile Ile Asp Ala Pro Gly His Arg
 20 25 30
 Asp Phe Ile Gln Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
 35 40 45
 Val Leu Ile Val Ala Ala Gly Val Gly Glu Phe Glu Ala Gly Ile Ser
 50 55 60
 Lys Asn Gly Gln Thr Arg Glu His Ala Leu Leu Ala Tyr Thr Leu Gly
 65 70 75 80
 Val Lys Gln Leu Ile Val Gly Val Asn Lys Met Asp Ser Thr Glu Pro
 85 90 95
 Pro Tyr Ser Gln Lys Arg Tyr Glu Glu Ile Val Lys Glu Val Ser Thr
 100 105 110
 Tyr Ile Lys Lys Ile Gly Tyr Asn Pro Asp Thr Val Ala Phe Val Pro
 115 120 125

Ile Ser Gly Trp Asn Gly Asp Asn Met Leu Glu Pro Ser Ala Asn Met
130 135 140

Pro Trp Phe Lys Gly Trp Lys Val Thr Arg Lys Asp Gly Asn Ala Ser
145 150 155 160

Gly Thr Thr Leu Leu Glu Ala Leu Asp Cys Ile Leu Pro Pro Thr Arg
165 170 175

Pro Thr Asp Lys Pro Leu Gly Leu Pro Leu Gln Asp Val Tyr Lys Ile
180 185 190

Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu
195 200 205

Lys Pro Gly Met Val Val Thr Phe Gly Pro Val Asn Val Thr Thr Glu
210 215 220

Val Lys Ser Val Glu Met His His Glu Ala Leu Gly Glu Ala Leu Pro
225 230 235 240

Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Val
245 250 255

Arg Arg Gly Asn Val Ala Gly Asp Ser Lys Asn Asp Pro Pro Met Glu
260 265 270

Ala Ala Gly Phe Pro Ala Gln Val Ile Ile Leu Asn His Pro Gly Gln
275 280 285

Ile Ser Ala Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ala His Ile
290 295 300

Ala Cys Lys Phe Ala Glu Leu Lys Glu Lys Ile Asp Arg Arg Ser Gly
305 310 315 320

Lys Lys Leu Glu Asp Gly Pro Lys Phe Leu Lys Ser Gly Asp Ala Ala
325 330 335

Ile Val Asp Met Val Pro Gly Lys Pro Met Cys Val Glu Ser Phe Ser
340 345 350

Asp Tyr Pro Pro Leu Gly Cys Phe Ala Val Arg Asp Met Arg Gln Thr
355 360 365

Val Ala Val Gly Val Ile Lys Ala Val Asp Lys Lys Ala Ala Gly Ala
370 375 380

Gly Lys Val Thr Lys Ser Ala Gln Lys Ala Gln Lys Ala Lys
385 390 395

<210> 177
<211> 334
<212> PRT
<213> Homo sapiens

<400> 177

Met Ala Thr Leu Lys Glu Lys Leu Ile Ala Pro Val Ala Glu Glu Glu
1 5 10 15

Ala Thr Val Pro Asn Asn Lys Ile Thr Val Val Gly Val Gly Gln Val
 20 25 30
 Gly Met Ala Cys Ala Ile Ser Ile Leu Gly Lys Ser Leu Ala Asp Glu
 35 40 45
 Leu Ala Leu Val Asp Val Leu Glu Asp Lys Leu Lys Gly Glu Met Met
 50 55 60
 Asp Leu Gln His Gly Ser Leu Phe Leu Gln Thr Pro Lys Ile Val Ala
 65 70 75 80
 Asp Lys Asp Tyr Ser Val Thr Ala Asn Ser Lys Ile Val Val Val Thr
 85 90 95
 Ala Gly Val Arg Gln Gln Glu Gly Glu Ser Arg Leu Asn Leu Val Gln
 100 105 110
 Arg Asn Val Asn Val Phe Lys Phe Ile Ile Pro Gln Ile Val Lys Tyr
 115 120 125
 Ser Pro Asp Cys Ile Ile Ile Val Val Ser Asn Pro Val Asp Ile Leu
 130 135 140
 Thr Tyr Val Thr Trp Lys Leu Ser Gly Leu Pro Lys His Arg Val Ile
 145 150 155 160
 Gly Ser Gly Cys Asn Leu Asp Ser Ala Arg Phe Arg Tyr Leu Met Ala
 165 170 175
 Glu Lys Leu Gly Ile His Pro Ser Ser Cys His Gly Trp Ile Leu Gly
 180 185 190
 Glu His Gly Asp Ser Ser Val Ala Val Trp Ser Gly Val Asn Val Ala
 195 200 205
 Gly Val Ser Leu Gln Glu Leu Asn Pro Glu Met Gly Thr Asp Asn Asp
 210 215 220
 Ser Glu Asn Trp Lys Glu Val His Lys Met Val Val Glu Ser Ala Tyr
 225 230 235 240
 Glu Val Ile Lys Leu Lys Gly Tyr Thr Asn Trp Ala Ile Gly Leu Ser
 245 250 255
 Val Ala Asp Leu Ile Glu Ser Met Leu Lys Asn Leu Ser Arg Ile His
 260 265 270
 Pro Val Ser Thr Met Val Lys Gly Met Tyr Gly Ile Glu Asn Glu Val
 275 280 285
 Phe Leu Ser Leu Pro Cys Ile Leu Asn Ala Arg Gly Leu Thr Ser Val
 290 295 300
 Ile Asn Gln Lys Leu Lys Asp Asp Glu Val Ala Gln Leu Lys Lys Ser
 305 310 315 320
 Ala Asp Thr Leu Trp Asp Ile Gln Lys Asp Leu Lys Asp Leu
 325 330

<210> 178
 <211> 364
 <212> PRT
 <213> Homo sapiens
 <400> 178
 Met Tyr Leu Ser Arg Phe Leu Ser Ile His Ala Leu Trp Val Thr Val
 1 5 10 15
 Ser Ser Val Met Gln Pro Tyr Pro Leu Val Trp Gly His Tyr Asp Leu
 20 25 30
 Cys Lys Thr Gln Ile Tyr Thr Glu Glu Gly Lys Val Trp Asp Tyr Met
 35 40 45
 Ala Cys Gln Pro Glu Ser Thr Asp Met Thr Lys Tyr Leu Lys Val Lys
 50 55 60
 Leu Asp Pro Pro Asp Ile Thr Cys Gly Asp Pro Pro Glu Thr Phe Cys
 65 70 75 80
 Ala Met Gly Asn Pro Tyr Met Cys Asn Asn Glu Cys Asp Ala Ser Thr
 85 90 95
 Pro Glu Leu Ala His Pro Pro Glu Leu Met Phe Asp Phe Glu Gly Arg
 100 105 110
 His Pro Ser Thr Phe Trp Gln Ser Ala Thr Trp Lys Glu Tyr Pro Lys
 115 120 125
 Pro Leu Gln Val Asn Ile Thr Leu Ser Trp Ser Lys Thr Ile Glu Leu
 130 135 140
 Thr Asp Asn Ile Val Ile Thr Phe Glu Ser Gly Arg Pro Asp Gln Met
 145 150 155 160
 Ile Leu Glu Lys Ser Leu Asp Tyr Gly Arg Thr Trp Gln Pro Tyr Gln
 165 170 175
 Tyr Tyr Ala Thr Asp Cys Leu Asp Ala Phe His Met Asp Pro Lys Ser
 180 185 190
 Val Lys Asp Leu Ser Gln His Thr Val Leu Glu Ile Ile Cys Thr Glu
 195 200 205
 Glu Tyr Ser Thr Gly Tyr Thr Thr Asn Ser Lys Ile Ile His Phe Glu
 210 215 220
 Ile Lys Asp Arg Phe Ala Phe Phe Ala Gly Pro Arg Leu Arg Asn Met
 225 230 235 240
 Ala Ser Leu Tyr Gly Gln Leu Asp Thr Thr Lys Lys Leu Arg Asp Phe
 245 250 255
 Phe Thr Val Thr Asp Leu Arg Ile Arg Leu Leu Arg Pro Ala Val Gly
 260 265 270
 Glu Ile Phe Val Asp Glu Leu His Leu Ala Arg Tyr Phe Tyr Ala Ile
 275 280 285

Ser Asp Ile Lys Val Arg Gly Arg Cys Lys Cys Asn Leu His Ala Thr
290 295 300

Val Cys Val Tyr Asp Asn Ser Lys Leu Thr Cys Glu Cys Glu His Asn
305 310 315 320

Thr Thr Gly Pro Asp Cys Gly Lys Cys Lys Lys Asn Tyr Gln Gly Arg
325 330 335

Pro Trp Ser Pro Gly Ser Tyr Leu Pro Ile Pro Lys Gly Thr Ala Asn
340 345 350

Thr Cys Ile Pro Ser Ile Ser Ser Ile Gly Ser Lys
355 360

<210> 179

<211> 416

<212> PRT

<213> Homo sapiens

<400> 179

Met His Thr Asp Pro Asp Tyr Ser Ala Ala Tyr Val Val Ile Glu Thr
1 5 10 15

Asp Ala Glu Asp Gly Ile Lys Gly Cys Gly Ile Thr Phe Thr Leu Gly
20 25 30

Lys Gly Thr Glu Val Val Val Cys Ala Val Asn Ala Leu Ala His His
35 40 45

Val Leu Asn Lys Asp Leu Lys Asp Ile Val Gly Asp Phe Arg Gly Phe
50 55 60

Tyr Arg Gln Leu Thr Ser Asp Gly Gln Leu Arg Trp Ile Gly Pro Glu
65 70 75 80

Lys Gly Val Val His Leu Ala Thr Ala Ala Val Leu Asn Ala Val Trp
85 90 95

Asp Leu Trp Ala Lys Gln Glu Gly Lys Pro Val Trp Lys Leu Leu Val
100 105 110

Asp Met Asp Pro Arg Met Leu Val Ser Cys Ile Asp Phe Arg Tyr Ile
115 120 125

Thr Asp Val Leu Thr Glu Glu Asp Ala Leu Glu Ile Leu Gln Lys Gly
130 135 140

Gln Ile Gly Lys Lys Glu Arg Glu Lys Gln Met Leu Ala Gln Gly Tyr
145 150 155 160

Pro Ala Tyr Thr Thr Ser Cys Ala Trp Leu Gly Tyr Ser Asp Asp Thr
165 170 175

Leu Lys Gln Leu Cys Ala Gln Ala Leu Lys Asp Gly Trp Thr Arg Phe
180 185 190

Lys Val Lys Val Gly Ala Asp Leu Gln Asp Asp Met Arg Arg Cys Gln
195 200 205

Ile Ile Arg Asp Met Ile Gly Pro Glu Lys Thr Leu Met Met Asp Ala
210 215 220

Asn Gln Arg Trp Asp Val Pro Glu Ala Val Glu Trp Met Ser Lys Leu
225 230 235 240

Ala Lys Phe Lys Pro Leu Trp Ile Glu Glu Pro Thr Ser Pro Asp Asp
245 250 255

Ile Leu Gly His Ala Thr Ile Ser Lys Ala Leu Val Pro Leu Gly Ile
260 265 270

Gly Ile Ala Thr Gly Glu Gln Cys His Asn Arg Val Ile Phe Lys Gln
275 280 285

Leu Leu Gln Ala Lys Ala Leu Gln Phe Leu Gln Ile Asp Ser Cys Arg
290 295 300

Leu Gly Ser Val Asn Glu Asn Leu Ser Val Leu Leu Met Ala Lys Lys
305 310 315 320

Phe Glu Ile Pro Val Cys Pro His Ala Gly Gly Val Gly Leu Cys Glu
325 330 335

Leu Val Gln His Leu Ile Ile Phe Asp Tyr Ile Ser Val Ser Ala Ser
340 345 350

Leu Glu Asn Arg Val Cys Glu Tyr Val Asp His Leu His Glu His Phe
355 360 365

Lys Tyr Pro Val Met Ile Gln Arg Ala Ser Tyr Met Pro Pro Lys Asp
370 375 380

Pro Gly Tyr Ser Thr Glu Met Lys Glu Glu Ser Val Lys Lys His Gln
385 390 395 400

Tyr Pro Asp Gly Glu Val Trp Lys Lys Leu Leu Pro Ala Gln Glu Asn
405 410 415

<210> 180

<211> 89

<212> PRT

<213> Homo sapiens

<400> 180

Met Ser Ser Gln Gln Gln Lys Gln Pro Cys Ile Pro Pro Pro Gln Leu
1 5 10 15

Gln Gln Gln Gln Val Lys Gln Pro Cys Gln Pro Pro Pro Gln Glu Pro
20 25 30

Cys Ile Pro Lys Thr Lys Glu Pro Cys His Pro Lys Val Pro Glu Pro
35 40 45

Cys His Pro Lys Val Pro Glu Pro Cys Gln Pro Lys Leu Pro Glu Pro
50 55 60

Cys His Pro Lys Val Pro Glu Pro Cys Pro Ser Ile Val Thr Pro Ala
65 70 75 80

Pro Ala Gln Gln Lys Thr Lys Gln Lys
85

<210> 181
<211> 253
<212> PRT
<213> Homo sapiens

<400> 181

Met Ala Arg Ser Leu Leu Leu Pro Leu Gln Ile Leu Leu Leu Ser Leu
1 5 10 15

Ala Leu Glu Thr Ala Gly Glu Glu Ala Gln Gly Asp Lys Ile Ile Asp
20 25 30

Gly Ala Pro Cys Ala Arg Gly Ser His Pro Trp Gln Val Ala Leu Leu
35 40 45

Ser Gly Asn Gln Leu His Cys Gly Gly Val Leu Val Asn Glu Arg Trp
50 55 60

Val Leu Thr Ala Ala His Cys Lys Met Asn Glu Tyr Thr Val His Leu
65 70 75 80

Gly Ser Asp Thr Leu Gly Asp Arg Arg Ala Gln Arg Ile Lys Ala Ser
85 90 95

Lys Ser Phe Arg His Pro Gly Tyr Ser Thr Gln Thr His Val Asn Asp
100 105 110

Leu Met Leu Val Lys Leu Asn Ser Gln Ala Arg Leu Ser Ser Met Val
115 120 125

Lys Lys Val Arg Leu Pro Ser Arg Cys Glu Pro Pro Gly Thr Thr Cys
130 135 140

Thr Val Ser Gly Trp Gly Thr Thr Thr Ser Pro Asp Val Thr Phe Pro
145 150 155 160

Ser Asp Leu Met Cys Val Asp Val Lys Leu Ile Ser Pro Gln Asp Cys
165 170 175

Thr Lys Val Tyr Lys Asp Leu Leu Glu Asn Ser Met Leu Cys Ala Gly
180 185 190

Ile Pro Asp Ser Lys Lys Asn Ala Cys Asn Gly Asp Ser Gly Gly Pro
195 200 205

Leu Val Cys Arg Gly Thr Leu Gln Gly Leu Val Ser Trp Gly Thr Phe
210 215 220

Pro Cys Gly Gln Pro Asn Asp Pro Gly Val Tyr Thr Gln Val Cys Lys
225 230 235 240

Phe Thr Lys Trp Ile Asn Asp Thr Met Lys Lys His Arg
245 250

<210> 182
<211> 169

<212> PRT

<213> Homo sapiens

<400> 182

Met Leu Ala Thr Arg Val Phe Ser Leu Val Gly Lys Arg Ala Ile Ser
 1 5 10 15

Thr Ser Val Cys Val Arg Ala His Glu Ser Val Val Lys Ser Glu Asp
 20 25 30

Phe Ser Leu Pro Ala Tyr Met Asp Arg Arg Asp His Pro Leu Pro Glu
 35 40 45

Val Ala His Val Lys His Leu Ser Ala Ser Gln Lys Ala Leu Lys Glu
 50 55 60

Lys Glu Lys Ala Ser Trp Ser Ser Leu Ser Met Asp Glu Lys Val Glu
 65 70 75 80

Leu Tyr Arg Ile Lys Phe Lys Glu Ser Phe Ala Glu Met Asn Arg Gly
 85 90 95

Ser Asn Glu Trp Lys Thr Val Val Gly Gly Ala Met Phe Phe Ile Gly
 100 105 110

Phe Thr Ala Leu Val Ile Met Trp Gln Lys His Tyr Val Tyr Gly Pro
 115 120 125

Leu Pro Gln Ser Phe Asp Lys Glu Trp Val Ala Lys Gln Thr Lys Arg
 130 135 140

Met Leu Asp Met Lys Val Asn Pro Ile Gln Gly Leu Ala Ser Lys Trp
 145 150 155 160

Asp Tyr Glu Lys Asn Glu Trp Lys Lys
 165

<210> 183

<211> 879

<212> PRT

<213> Homo sapiens

<400> 183

Met Ala Gly Gly Gly Gly Asp Leu Ser Thr Arg Arg Leu Asn Glu Cys
 1 5 10 15

Ile Ser Pro Val Ala Asn Glu Met Asn His Leu Pro Ala His Ser His
 20 25 30

Asp Leu Gln Arg Met Phe Thr Glu Asp Gln Gly Val Asp Asp Arg Leu
 35 40 45

Leu Tyr Asp Ile Val Phe Lys His Phe Lys Arg Asn Lys Val Glu Ile
 50 55 60

Ser Asn Ala Ile Lys Lys Thr Phe Pro Phe Leu Glu Gly Leu Arg Asp
 65 70 75 80

Arg Asp Leu Ile Thr Asn Lys Met Phe Glu Asp Ser Gln Asp Ser Cys
 85 90 95

Arg Asn Leu Val Pro Val Gln Arg Val Val Tyr Asn Val Leu Ser Glu
 100 105 110
 Leu Glu Lys Thr Phe Asn Leu Pro Val Leu Glu Ala Leu Phe Ser Asp
 115 120 125
 Val Asn Met Gln Glu Tyr Pro Asp Leu Ile His Ile Tyr Lys Gly Phe
 130 135 140
 Glu Asn Val Ile His Asp Lys Leu Pro Leu Gln Glu Ser Glu Glu Glu
 145 150 155 160
 Glu Arg Glu Glu Arg Ser Gly Leu Gln Leu Ser Leu Glu Gln Gly Thr
 165 170 175
 Gly Glu Asn Ser Phe Arg Ser Leu Thr Trp Pro Pro Ser Gly Ser Pro
 180 185 190
 Ser His Ala Gly Thr Thr Pro Pro Glu Asn Gly Leu Ser Glu His Pro
 195 200 205
 Cys Glu Thr Glu Gln Ile Asn Ala Lys Arg Lys Asp Thr Thr Ser Asp
 210 215 220
 Lys Asp Asp Ser Leu Gly Ser Gln Gln Thr Asn Glu Gln Cys Ala Gln
 225 230 235 240
 Lys Ala Glu Pro Thr Glu Ser Cys Glu Gln Ile Ala Val Gln Val Asn
 245 250 255
 Asn Gly Asp Ala Gly Arg Glu Met Pro Cys Pro Leu Pro Cys Asp Glu
 260 265 270
 Glu Ser Pro Glu Ala Glu Leu His Asn His Gly Ile Gln Ile Asn Ser
 275 280 285
 Cys Ser Val Arg Leu Val Asp Ile Lys Lys Glu Lys Pro Phe Ser Asn
 290 295 300
 Ser Lys Val Glu Cys Gln Ala Gln Ala Arg Thr His His Asn Gln Ala
 305 310 315 320
 Ser Asp Ile Ile Val Ile Ser Ser Glu Asp Ser Glu Gly Ser Thr Asp
 325 330 335
 Val Asp Glu Pro Leu Glu Val Phe Ile Ser Ala Pro Arg Ser Glu Pro
 340 345 350
 Val Ile Asn Asn Asp Asn Pro Leu Glu Ser Asn Asp Glu Lys Glu Gly
 355 360 365
 Gln Glu Ala Thr Cys Ser Arg Pro Gln Ile Val Pro Glu Pro Met Asp
 370 375 380
 Phe Arg Lys Leu Ser Thr Phe Arg Glu Ser Phe Lys Lys Arg Val Ile
 385 390 395 400
 Gly Gln Asp His Asp Phe Ser Glu Ser Ser Glu Glu Glu Ala Pro Ala
 405 410 415

Glu Ala Ser Ser Gly Ala Leu Arg Ser Lys His Gly Glu Lys Ala Pro
 420 425 430
 Met Thr Ser Arg Ser Thr Ser Thr Trp Arg Ile Pro Ser Arg Lys Arg
 435 440 445
 Arg Phe Ser Ser Ser Asp Phe Ser Asp Leu Ser Asn Gly Glu Glu Leu
 450 455 460
 Gln Glu Thr Cys Ser Ser Ser Leu Arg Arg Gly Ser Gly Ser Gln Pro
 465 470 475 480
 Gln Glu Pro Glu Asn Lys Lys Cys Ser Cys Val Met Cys Phe Pro Lys
 485 490 495
 Gly Val Pro Arg Ser Gln Glu Ala Arg Thr Glu Ser Ser Gln Ala Ser
 500 505 510
 Asp Met Met Asp Thr Met Asp Val Glu Asn Asn Ser Thr Leu Glu Lys
 515 520 525
 His Ser Gly Lys Arg Arg Lys Lys Arg Arg His Arg Ser Lys Val Asn
 530 535 540
 Gly Leu Gln Arg Gly Arg Lys Lys Asp Arg Pro Arg Lys His Leu Thr
 545 550 555 560
 Leu Asn Asn Lys Val Gln Lys Lys Arg Trp Gln Gln Arg Gly Arg Lys
 565 570 575
 Ala Asn Thr Arg Pro Leu Lys Arg Arg Arg Lys Arg Gly Pro Arg Ile
 580 585 590
 Pro Lys Asp Glu Asn Ile Asn Phe Lys Gln Ser Glu Leu Pro Val Thr
 595 600 605
 Cys Gly Glu Val Lys Gly Thr Leu Tyr Lys Glu Arg Phe Lys Gln Gly
 610 615 620
 Thr Ser Lys Lys Cys Ile Gln Ser Glu Asp Lys Lys Trp Phe Thr Pro
 625 630 635 640
 Arg Glu Phe Glu Ile Glu Gly Asp Arg Gly Ala Ser Lys Asn Trp Lys
 645 650 655
 Leu Ser Ile Arg Cys Gly Gly Tyr Thr Leu Lys Val Leu Met Glu Asn
 660 665 670
 Lys Phe Leu Pro Glu Pro Pro Ser Thr Arg Lys Lys Arg Ile Leu Glu
 675 680 685
 Ser His Asn Asn Thr Leu Val Asp Pro Cys Glu Glu His Lys Lys Lys
 690 695 700
 Asn Pro Asp Ala Ser Val Lys Phe Ser Glu Phe Leu Lys Lys Cys Ser
 705 710 715 720
 Glu Thr Trp Lys Thr Ile Phe Ala Lys Glu Lys Gly Lys Phe Glu Asp

725										730					735				
Met	Ala	Lys	Ala	Asp	Lys	Ala	His	Tyr	Glu	Arg	Glu	Met	Lys	Thr	Tyr				
			740					745					750						
Ile	Pro	Pro	Lys	Gly	Glu	Lys	Lys	Lys	Lys	Phe	Lys	Asp	Pro	Asn	Ala				
			755				760					765							
Pro	Lys	Arg	Pro	Pro	Leu	Ala	Phe	Phe	Leu	Phe	Cys	Ser	Glu	Tyr	Arg				
			770			775					780								
Pro	Lys	Ile	Lys	Gly	Glu	His	Pro	Gly	Leu	Ser	Ile	Asp	Asp	Val	Val				
785					790					795					800				
Lys	Lys	Leu	Ala	Gly	Met	Trp	Asn	Asn	Thr	Ala	Ala	Ala	Asp	Lys	Gln				
				805					810					815					
Phe	Tyr	Glu	Lys	Lys	Ala	Ala	Lys	Leu	Lys	Glu	Lys	Tyr	Lys	Lys	Asp				
			820					825					830						
Ile	Ala	Ala	Tyr	Arg	Ala	Lys	Gly	Lys	Pro	Asn	Ser	Ala	Lys	Lys	Arg				
			835				840					845							
Val	Val	Lys	Ala	Glu	Lys	Ser	Lys	Lys	Lys	Lys	Glu	Glu	Glu	Glu	Asp				
			850			855						860							
Glu	Glu	Asp	Glu	Gln	Glu	Glu	Glu	Asn	Glu	Glu	Asp	Asp	Asp	Lys					
865					870						875								
<210> 184																			
<211> 316																			
<212> PRT																			
<213> Homo sapiens																			
<400> 184																			
Met	Ala	Ser	Thr	Ser	Arg	Leu	Asp	Ala	Leu	Pro	Arg	Val	Thr	Cys	Pro				
1				5					10					15					
Asn	His	Pro	Asp	Ala	Ile	Leu	Val	Glu	Asp	Tyr	Arg	Ala	Gly	Asp	Met				
			20					25					30						
Ile	Cys	Pro	Glu	Cys	Gly	Leu	Val	Val	Gly	Asp	Arg	Val	Ile	Asp	Val				
		35					40					45							
Gly	Ser	Glu	Trp	Arg	Thr	Phe	Ser	Asn	Asp	Lys	Ala	Thr	Lys	Asp	Pro				
	50					55					60								
Ser	Arg	Val	Gly	Asp	Ser	Gln	Asn	Pro	Leu	Leu	Ser	Asp	Gly	Asp	Leu				
65					70					75					80				
Ser	Thr	Met	Ile	Gly	Lys	Gly	Thr	Gly	Ala	Ala	Ser	Phe	Asp	Glu	Phe				
				85					90					95					
Gly	Asn	Ser	Lys	Tyr	Gln	Asn	Arg	Arg	Thr	Met	Ser	Ser	Ser	Asp	Arg				
			100					105					110						
Ala	Met	Met	Asn	Ala	Phe	Lys	Glu	Ile	Thr	Thr	Met	Ala	Asp	Arg	Ile				
			115				120					125							
Asn	Leu	Pro	Arg	Asn	Ile	Val	Asp	Arg	Thr	Asn	Asn	Leu	Phe	Lys	Gln				

130 135 140
 Val Tyr Glu Gln Lys Ser Leu Lys Gly Arg Ala Asn Asp Ala Ile Ala
 145 150 155 160
 Ser Ala Cys Leu Tyr Ile Ala Cys Arg Gln Glu Gly Val Pro Arg Thr
 165 170 175
 Phe Lys Glu Ile Cys Ala Val Ser Arg Ile Ser Lys Lys Glu Ile Gly
 180 185 190
 Arg Cys Phe Lys Leu Ile Leu Lys Ala Leu Glu Thr Ser Val Asp Leu
 195 200 205
 Ile Thr Thr Gly Asp Phe Met Ser Arg Phe Cys Ser Asn Leu Cys Leu
 210 215 220
 Pro Lys Gln Val Gln Met Ala Ala Thr His Ile Ala Arg Lys Ala Val
 225 230 235 240
 Glu Leu Asp Leu Val Pro Gly Arg Ser Pro Ile Ser Val Ala Ala Ala
 245 250 255
 Ala Ile Tyr Met Ala Ser Gln Ala Ser Ala Glu Lys Arg Thr Gln Lys
 260 265 270
 Glu Ile Gly Asp Ile Ala Gly Val Ala Asp Val Thr Ile Arg Gln Ser
 275 280 285
 Tyr Arg Leu Ile Tyr Pro Arg Ala Pro Asp Leu Phe Pro Thr Asp Phe
 290 295 300
 Lys Phe Asp Thr Pro Val Asp Lys Leu Pro Gln Leu
 305 310 315
 <210> 185
 <211> 628
 <212> PRT
 <213> Homo sapiens
 <400> 185
 Ala Asp Phe Leu Asp Ala Leu Ile Val Ser Met Asp Val Ile Gln His
 1 5 10 15
 Glu Thr Ile Gly Lys Lys Phe Glu Lys Arg His Ile Glu Ile Phe Thr
 20 25 30
 Asp Leu Ser Ser Arg Phe Ser Lys Ser Gln Leu Asp Ile Ile Ile His
 35 40 45
 Ser Leu Lys Lys Cys Asp Ile Ser Leu Gln Phe Phe Leu Pro Phe Ser
 50 55 60
 Leu Gly Lys Glu Asp Gly Ser Gly Asp Arg Gly Asp Gly Pro Phe Arg
 65 70 75 80
 Leu Gly Gly His Gly Pro Ser Phe Pro Leu Lys Gly Ile Thr Glu Gln
 85 90 95
 Gln Lys Glu Gly Leu Glu Ile Val Lys Met Val Met Ile Ser Leu Glu

100	105	110
Gly Glu Asp Gly Leu Asp Glu Ile Tyr Ser Phe Ser Glu Ser Leu Arg 115 120 125		
Lys Leu Cys Val Phe Lys Lys Ile Glu Arg His Ser Ile His Trp Pro 130 135 140		
Cys Arg Leu Thr Ile Gly Ser Asn Leu Ser Ile Arg Ile Ala Ala Tyr 145 150 155 160		
Lys Ser Ile Leu Gln Glu Arg Val Lys Lys Thr Trp Thr Val Val Asp 165 170 175		
Ala Lys Thr Leu Lys Lys Glu Asp Ile Gln Lys Glu Thr Val Tyr Cys 180 185 190		
Leu Asn Asp Asp Asp Glu Thr Glu Val Leu Lys Glu Asp Ile Ile Gln 195 200 205		
Gly Phe Leu Tyr Gly Ser Asp Ile Val Pro Phe Ser Lys Val Asp Glu 210 215 220		
Glu Gln Met Lys Tyr Lys Ser Glu Gly Lys Cys Phe Ser Val Leu Gly 225 230 235 240		
Phe Cys Lys Ser Ser Gln Val Gln Arg Arg Phe Phe Met Gly Asn Gln 245 250 255		
Val Leu Lys Val Phe Ala Ala Arg Asp Asp Glu Ala Ala Val Ala 260 265 270		
Leu Ser Ser Leu Ile His Ala Leu Asp Asp Leu Asp Met Val Ala Ile 275 280 285		
Val Arg Tyr Ala Tyr Asp Lys Arg Ala Asn Pro Gln Val Gly Val Ala 290 295 300		
Phe Pro His Ile Lys His Asn Tyr Glu Cys Leu Val Tyr Val Gln Leu 305 310 315 320		
Pro Phe Met Glu Asp Leu Arg Gln Tyr Met Phe Ser Ser Leu Lys Asn 325 330 335		
Ser Lys Lys Tyr Ala Pro Thr Glu Ala Gln Leu Asn Ala Val Asp Ala 340 345 350		
Leu Ile Asp Ser Met Ser Leu Ala Lys Lys Asp Glu Lys Thr Asp Thr 355 360 365		
Leu Glu Asp Leu Phe Pro Thr Thr Lys Ile Pro Asn Pro Arg Phe Gln 370 375 380		
Arg Leu Phe Gln Cys Leu Leu His Arg Ala Leu His Pro Arg Glu Pro 385 390 395 400		
Leu Pro Pro Ile Gln Gln His Ile Trp Asn Met Leu Asn Pro Pro Ala 405 410 415		

Glu Val Thr Thr Lys Ser Gln Ile Pro Leu Ser Lys Ile Lys Thr Leu
420 425 430

Phe Pro Leu Ile Glu Ala Lys Lys Lys Asp Gln Val Thr Ala Gln Glu
435 440 445

Ile Phe Gln Asp Asn His Glu Asp Gly Pro Thr Ala Lys Lys Leu Lys
450 455 460

Thr Glu Gln Gly Gly Ala His Phe Ser Val Ser Ser Leu Ala Glu Gly
465 470 475 480

Ser Val Thr Ser Val Gly Ser Val Asn Pro Ala Glu Asn Phe Arg Val
485 490 495

Leu Val Lys Gln Lys Lys Ala Ser Phe Glu Glu Ala Ser Asn Gln Leu
500 505 510

Ile Asn His Ile Glu Gln Phe Leu Asp Thr Asn Glu Thr Pro Tyr Phe
515 520 525

Met Lys Ser Ile Asp Cys Ile Arg Ala Phe Arg Glu Glu Ala Ile Lys
530 535 540

Phe Ser Glu Glu Gln Arg Phe Asn Asn Phe Leu Lys Ala Leu Gln Glu
545 550 555 560

Lys Val Glu Ile Lys Gln Leu Asn His Phe Trp Glu Ile Val Val Gln
565 570 575

Asp Gly Ile Thr Leu Ile Thr Lys Glu Glu Ala Ser Gly Ser Ser Val
580 585 590

Thr Ala Glu Glu Ala Lys Lys Phe Leu Ala Pro Lys Asp Lys Pro Ser
595 600 605

Gly Asp Thr Ala Ala Val Phe Glu Glu Gly Gly Asp Val Asp Asp Leu
610 615 620

Leu Asp Met Ile
625

<210> 186

<211> 420

<212> PRT

<213> Homo sapiens

<400> 186

Met Gly Ser Gly Trp Lys Lys Ile Lys Leu Gln Met Lys Cys Asp Gly
1 5 10 15

Cys Ser Glu Gln Gly Ser His Pro Cys Ala Phe Ile Gly Ile Gly Asn
20 25 30

Ser Asp Gln Glu Met Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys
35 40 45

Thr Ala Lys Thr Leu Tyr Ile Ser Asp Ser Asp Lys Gln Lys His Phe
50 55 60

Met Leu Ser Val Lys Val Phe Tyr Gly Asn Gly Asp Asp Ile Gly Val
 65 70 75 80
 Phe Leu Ser Lys Ser Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys
 85 90 95
 Asn Ala Asp Leu Cys Ile Gly Ser Gly Thr Lys Val Ala Leu Phe Asn
 100 105 110
 Arg Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly
 115 120 125
 Gly Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Thr Leu Phe
 130 135 140
 Leu Asp Asp Asp Gly Ser Glu Gly Glu Glu Phe Thr Val Arg Asp Gly
 145 150 155 160
 Tyr Ile His Tyr Gly Gln Thr Val Lys Leu Val Cys Ser Val Thr Gly
 165 170 175
 Met Ala Leu Pro Arg Leu Ile Ile Arg Lys Val Asp Lys Gln Thr Thr
 180 185 190
 Leu Leu Asp Ala Asp Asp Pro Val Ser Gln Leu His Lys Cys Ala Phe
 195 200 205
 Asp Leu Glu Asp Thr Glu Arg Met Tyr Leu Cys Leu Ser Gln Glu Arg
 210 215 220
 Ile Ile Gln Phe Gln Ala Thr Pro Cys Pro Thr Glu Pro Asn Lys Glu
 225 230 235 240
 Met Ile Asn Asp Gly Ala Ser Trp Ala Ile Ile Ser Thr His Lys Ala
 245 250 255
 Lys Tyr Thr Phe Tyr Glu Arg Met Gly Pro Val Leu Ala Leu Val Met
 260 265 270
 Pro Met Pro Val Val Glu Ser Leu Lys Leu Asn Gly Gly Gly Asp Glu
 275 280 285
 Ala Met Leu Glu Leu Thr Gly Gln Asn Phe Thr Pro Asn Leu Arg Val
 290 295 300
 Trp Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly Glu Ser
 305 310 315 320
 Met Leu Arg Val Val Pro Asp Val Leu His Ser Glu Lys Val Gly Asp
 325 330 335
 Ser Ser Gln Gln Pro Val Gln Val Ser Val Thr Leu Val Arg Asn Asp
 340 345 350
 Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Ala
 355 360 365
 Gly Pro Arg Pro His Cys Ser Val Ala Gly Ala Ile Leu Lys Ala Ser
 370 375 380

Ser Ser His Val Pro Pro Asn Glu Leu Asn Thr Asn Ser Asp Gly Ser
385 390 395 400

Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser Thr Pro
405 410 415

Thr Val Val Ser
420

<210> 187
<211> 103
<212> PRT
<213> Homo sapiens

<400> 187

Met Glu Thr Val Gln Glu Leu Ile Pro Leu Ala Lys Glu Met Met Ala
1 5 10 15

Gln Lys Arg Lys Gly Lys Met Val Lys Leu Tyr Val Leu Gly Ser Val
20 25 30

Leu Ala Leu Phe Gly Val Val Leu Gly Leu Met Glu Thr Val Cys Ser
35 40 45

Pro Phe Thr Ala Ala Arg Arg Leu Arg Asp Gln Glu Ala Ala Val Ala
50 55 60

Glu Leu Gln Ala Ala Leu Glu Arg Gln Ala Leu Gln Lys Gln Ala Leu
65 70 75 80

Gln Glu Lys Gly Lys Gln Gln Asp Thr Val Leu Gly Gly Arg Ala Leu
85 90 95

Ser Asn Arg Gln His Ala Ser
100

<210> 188
<211> 1306
<212> PRT
<213> Homo sapiens

<400> 188

Met Gly Ala Ala Ser Gly Arg Arg Gly Pro Gly Leu Leu Leu Pro Leu
1 5 10 15

Pro Leu Leu Leu Leu Leu Pro Pro Gln Pro Ala Leu Ala Leu Asp Pro
20 25 30

Gly Leu Gln Pro Gly Asn Phe Ser Ala Asp Glu Ala Gly Ala Gln Leu
35 40 45

Phe Ala Gln Ser Tyr Asn Ser Ser Ala Glu Gln Val Leu Phe Gln Ser
50 55 60

Val Ala Ala Ser Trp Ala His Asp Thr Asn Ile Thr Ala Glu Asn Ala
65 70 75 80

Arg Arg Gln Glu Glu Ala Ala Leu Leu Ser Gln Glu Phe Ala Glu Ala
85 90 95

Trp Gly Gln Lys Ala Lys Glu Leu Tyr Glu Pro Ile Trp Gln Asn Phe
 100 105 110
 Thr Asp Pro Gln Leu Arg Arg Ile Ile Gly Ala Val Arg Thr Leu Gly
 115 120 125
 Ser Ala Asn Leu Pro Leu Ala Lys Arg Gln Gln Tyr Asn Ala Leu Leu
 130 135 140
 Ser Asn Met Ser Arg Ile Tyr Ser Thr Ala Lys Val Cys Leu Pro Asn
 145 150 155 160
 Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro Asp Leu Thr Asn Ile Leu
 165 170 175
 Ala Ser Ser Arg Ser Tyr Ala Met Leu Leu Phe Ala Trp Glu Gly Trp
 180 185 190
 His Asn Ala Ala Gly Ile Pro Leu Lys Pro Leu Tyr Glu Asp Phe Thr
 195 200 205
 Ala Leu Ser Asn Glu Ala Tyr Lys Gln Asp Gly Phe Thr Asp Thr Gly
 210 215 220
 Ala Tyr Trp Arg Ser Trp Tyr Asn Ser Pro Thr Phe Glu Asp Asp Leu
 225 230 235 240
 Glu His Leu Tyr Gln Gln Leu Glu Pro Leu Tyr Leu Asn Leu His Ala
 245 250 255
 Phe Val Arg Arg Ala Leu His Arg Arg Tyr Gly Asp Arg Tyr Ile Asn
 260 265 270
 Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly Asp Met Trp Ala Gln
 275 280 285
 Ser Trp Glu Asn Ile Tyr Asp Met Val Val Pro Phe Pro Asp Lys Pro
 290 295 300
 Asn Leu Asp Val Thr Ser Thr Met Leu Gln Gln Gly Trp Asn Ala Thr
 305 310 315 320
 His Met Phe Arg Val Ala Glu Glu Phe Phe Thr Ser Leu Glu Leu Ser
 325 330 335
 Pro Met Pro Pro Glu Phe Trp Glu Gly Ser Met Leu Glu Lys Pro Ala
 340 345 350
 Asp Gly Arg Glu Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn
 355 360 365
 Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Arg Val Thr Met Asp Gln
 370 375 380
 Leu Ser Thr Val His His Glu Met Gly His Ile Gln Tyr Tyr Leu Gln
 385 390 395 400
 Tyr Lys Asp Leu Pro Val Ser Leu Arg Arg Gly Ala Asn Pro Gly Phe
 405 410 415

His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser Val Ser Thr Pro Glu
 420 425 430
 His Leu His Lys Ile Gly Leu Leu Asp Arg Val Thr Asn Asp Thr Glu
 435 440 445
 Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu Glu Lys Ile Ala Phe
 450 455 460
 Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg Trp Gly Val Phe Ser
 465 470 475 480
 Gly Arg Thr Pro Pro Ser Arg Tyr Asn Phe Asp Trp Trp Tyr Leu Arg
 485 490 495
 Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Thr Arg Asn Glu Thr His
 500 505 510
 Phe Asp Ala Gly Ala Lys Phe His Val Pro Asn Val Thr Pro Tyr Ile
 515 520 525
 Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln Phe His Glu Ala Leu
 530 535 540
 Cys Lys Glu Ala Gly Tyr Glu Gly Pro Leu His Gln Cys Asp Ile Tyr
 545 550 555 560
 Arg Ser Thr Lys Ala Gly Ala Lys Leu Arg Lys Val Leu Gln Ala Gly
 565 570 575
 Ser Ser Arg Pro Trp Gln Glu Val Leu Lys Asp Met Val Gly Leu Asp
 580 585 590
 Ala Leu Asp Ala Gln Pro Leu Leu Lys Tyr Phe Gln Pro Val Thr Gln
 595 600 605
 Trp Leu Gln Glu Gln Asn Gln Gln Asn Gly Glu Val Leu Gly Trp Pro
 610 615 620
 Glu Tyr Gln Trp His Pro Pro Leu Pro Asp Asn Tyr Pro Glu Gly Ile
 625 630 635 640
 Asp Leu Val Thr Asp Glu Ala Glu Ala Ser Lys Phe Val Glu Glu Tyr
 645 650 655
 Asp Arg Thr Ser Gln Val Val Trp Asn Glu Tyr Ala Glu Ala Asn Trp
 660 665 670
 Asn Tyr Asn Thr Asn Ile Thr Thr Glu Thr Ser Lys Ile Leu Leu Gln
 675 680 685
 Lys Asn Met Gln Ile Ala Asn His Thr Leu Lys Tyr Gly Thr Gln Ala
 690 695 700
 Arg Lys Phe Asp Val Asn Gln Leu Gln Asn Thr Thr Ile Lys Arg Ile
 705 710 715 720
 Ile Lys Lys Val Gln Asp Leu Glu Arg Ala Ala Leu Pro Ala Gln Glu
 725 730 735

Leu Glu Glu Tyr Asn Lys Ile Leu Leu Asp Met Glu Thr Thr Tyr Ser
 740 745 750
 Val Ala Thr Val Cys His Pro Asn Gly Ser Cys Leu Gln Leu Glu Pro
 755 760 765
 Asp Leu Thr Asn Val Met Ala Thr Ser Arg Lys Tyr Glu Asp Leu Leu
 770 775 780
 Trp Ala Trp Glu Gly Trp Arg Asp Lys Ala Gly Arg Ala Ile Leu Gln
 785 790 795 800
 Phe Tyr Pro Lys Tyr Val Glu Leu Ile Asn Gln Ala Ala Arg Leu Asn
 805 810 815
 Gly Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met Tyr Glu Thr Pro
 820 825 830
 Ser Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu Leu Gln Pro Leu
 835 840 845
 Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg His Tyr
 850 855 860
 Gly Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro Ala His Leu Leu
 865 870 875 880
 Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr Asp Leu Val Val
 885 890 895
 Pro Phe Pro Ser Ala Pro Ser Met Asp Thr Thr Glu Ala Met Leu Lys
 900 905 910
 Gln Gly Trp Thr Pro Arg Arg Met Phe Lys Glu Ala Asp Asp Phe Phe
 915 920 925
 Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn Lys Ser
 930 935 940
 Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser
 945 950 955 960
 Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln Cys Thr
 965 970 975
 Thr Val Asn Leu Glu Asp Leu Val Val Ala His His Glu Met Gly His
 980 985 990
 Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Ala Leu Arg Glu
 995 1000 1005
 Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala
 1010 1015 1020
 Leu Ser Val Ser Thr Pro Lys His Leu His Ser Leu Asn Leu Leu
 1025 1030 1035
 Ser Ser Glu Gly Gly Ser Asp Glu His Asp Ile Asn Phe Leu Met

1040	1045	1050
Lys Met 1055	Ala Leu Asp Lys Ile 1060	Ala Phe Ile Pro Phe Ser Tyr Leu 1065
Val Asp 1070	Gln Trp Arg Trp Arg 1075	Val Phe Asp Gly Ser Ile Thr Lys 1080
Glu Asn 1085	Tyr Asn Gln Glu Trp 1090	Trp Ser Leu Arg Leu Lys Tyr Gln 1095
Gly Leu 1100	Cys Pro Pro Val Pro 1105	Arg Thr Gln Gly Asp Phe Asp Pro 1110
Gly Ala 1115	Lys Phe His Ile Pro 1120	Ser Ser Val Pro Tyr Ile Arg Tyr 1125
Phe Val 1130	Ser Phe Ile Ile Gln 1135	Phe Gln Phe His Glu Ala Leu Cys 1140
Gln Ala 1145	Ala Gly His Thr Gly 1150	Pro Leu His Lys Cys Asp Ile Tyr 1155
Gln Ser 1160	Lys Glu Ala Gly Gln 1165	Arg Leu Ala Thr Ala Met Lys Leu 1170
Gly Phe 1175	Ser Arg Pro Trp Pro 1180	Glu Ala Met Gln Leu Ile Thr Gly 1185
Gln Pro 1190	Asn Met Ser Ala Ser 1195	Ala Met Leu Ser Tyr Phe Lys Pro 1200
Leu Leu 1205	Asp Trp Leu Arg Thr 1210	Glu Asn Glu Leu His Gly Glu Lys 1215
Leu Gly 1220	Trp Pro Gln Tyr Asn 1225	Trp Thr Pro Asn Ser Ala Arg Ser 1230
Glu Gly 1235	Pro Leu Pro Asp Ser 1240	Gly Arg Val Ser Phe Leu Gly Leu 1245
Asp Leu 1250	Asp Ala Gln Gln Ala 1255	Arg Val Gly Gln Trp Leu Leu Leu 1260
Phe Leu 1265	Gly Ile Ala Leu Leu 1270	Val Ala Thr Leu Gly Leu Ser Gln 1275
Arg Leu 1280	Phe Ser Ile Arg His 1285	Arg Ser Leu His Arg His Ser His 1290
Gly Pro 1295	Gln Phe Gly Ser Glu 1300	Val Glu Leu Arg His Ser 1305

<210> 189
 <211> 1461
 <212> PRT
 <213> Homo sapiens

<400> 189

Met Ala Ala Glu Arg Gly Ala Arg Arg Leu Leu Ser Thr Pro Ser Phe

1	5	10	15												
Trp	Leu	Tyr	Cys	Leu	Leu	Leu	Leu	Gly	Arg	Arg	Ala	Pro	Gly	Ala	Ala
	20							25				30			
Ala	Ala	Arg	Ser	Gly	Ser	Ala	Pro	Gln	Ser	Pro	Gly	Ala	Ser	Ile	Arg
	35						40					45			
Thr	Phe	Thr	Pro	Phe	Tyr	Phe	Leu	Val	Glu	Pro	Val	Asp	Thr	Leu	Ser
	50					55					60				
Val	Arg	Gly	Ser	Ser	Val	Ile	Leu	Asn	Cys	Ser	Ala	Tyr	Ser	Glu	Pro
65				70				75						80	
Ser	Pro	Lys	Ile	Glu	Trp	Lys	Lys	Asp	Gly	Thr	Phe	Leu	Asn	Leu	Val
			85					90					95		
Ser	Asp	Asp	Arg	Arg	Gln	Leu	Leu	Pro	Asp	Gly	Ser	Leu	Phe	Ile	Ser
	100							105				110			
Asn	Val	Val	His	Ser	Lys	His	Asn	Lys	Pro	Asp	Glu	Gly	Tyr	Tyr	Gln
	115						120					125			
Cys	Val	Ala	Thr	Val	Glu	Ser	Leu	Gly	Thr	Ile	Ile	Ser	Arg	Thr	Ala
	130					135					140				
Lys	Leu	Ile	Val	Ala	Gly	Leu	Pro	Arg	Phe	Thr	Ser	Gln	Pro	Glu	Pro
145				150				155						160	
Ser	Ser	Val	Tyr	Ala	Gly	Asn	Gly	Ala	Ile	Leu	Asn	Cys	Glu	Val	Asn
			165					170						175	
Ala	Asp	Leu	Val	Pro	Phe	Val	Arg	Trp	Glu	Gln	Asn	Arg	Gln	Pro	Leu
		180						185					190		
Leu	Leu	Asp	Asp	Arg	Val	Ile	Lys	Leu	Pro	Ser	Gly	Met	Leu	Val	Ile
	195						200					205			
Ser	Asn	Ala	Thr	Glu	Gly	Asp	Gly	Gly	Leu	Tyr	Arg	Cys	Val	Val	Glu
	210					215					220				
Ser	Gly	Gly	Pro	Pro	Lys	Tyr	Ser	Asp	Glu	Val	Glu	Leu	Lys	Val	Leu
225				230					235					240	
Pro	Asp	Pro	Glu	Val	Ile	Ser	Asp	Leu	Val	Phe	Leu	Lys	Gln	Pro	Ser
			245					250						255	
Pro	Leu	Val	Arg	Val	Ile	Gly	Gln	Asp	Val	Val	Leu	Pro	Cys	Val	Ala
		260						265					270		
Ser	Gly	Leu	Pro	Thr	Pro	Thr	Ile	Lys	Trp	Met	Lys	Asn	Glu	Glu	Ala
	275						280					285			
Leu	Asp	Thr	Glu	Ser	Ser	Glu	Arg	Leu	Val	Leu	Leu	Ala	Gly	Gly	Ser
	290					295					300				
Leu	Glu	Ile	Ser	Asp	Val	Thr	Glu	Asp	Asp	Ala	Gly	Thr	Tyr	Phe	Cys
305				310					315					320	

Ile Ala Asp Asn Gly Asn Glu Thr Ile Glu Ala Gln Ala Glu Leu Thr
 325 330 335
 Val Gln Ala Gln Pro Glu Phe Leu Lys Gln Pro Thr Asn Ile Tyr Ala
 340 345 350
 His Glu Ser Met Asp Ile Val Phe Glu Cys Glu Val Thr Gly Lys Pro
 355 360 365
 Thr Pro Thr Val Lys Trp Val Lys Asn Gly Asp Met Val Ile Pro Ser
 370 375 380
 Asp Tyr Phe Lys Ile Val Lys Glu His Asn Leu Gln Val Leu Gly Leu
 385 390 395 400
 Val Lys Ser Asp Glu Gly Phe Tyr Gln Cys Ile Ala Glu Asn Asp Val
 405 410 415
 Gly Asn Ala Gln Ala Gly Ala Gln Leu Ile Ile Leu Glu His Ala Pro
 420 425 430
 Ala Thr Thr Gly Pro Leu Pro Ser Ala Pro Arg Asp Val Val Ala Ser
 435 440 445
 Leu Val Ser Thr Arg Phe Ile Lys Leu Thr Trp Arg Thr Pro Ala Ser
 450 455 460
 Asp Pro His Gly Asp Asn Leu Thr Tyr Ser Val Phe Tyr Thr Lys Glu
 465 470 475 480
 Gly Ile Ala Arg Glu Arg Val Glu Asn Thr Ser His Pro Gly Glu Met
 485 490 495
 Gln Val Thr Ile Gln Asn Leu Met Pro Ala Thr Val Tyr Ile Phe Arg
 500 505 510
 Val Met Ala Gln Asn Lys His Gly Ser Gly Glu Ser Ser Ala Pro Leu
 515 520 525
 Arg Val Glu Thr Gln Pro Glu Val Gln Leu Pro Gly Pro Ala Pro Asn
 530 535 540
 Leu Arg Ala Tyr Ala Ala Ser Pro Thr Ser Ile Thr Val Thr Trp Glu
 545 550 555 560
 Thr Pro Val Ser Gly Asn Gly Glu Ile Gln Asn Tyr Lys Leu Tyr Tyr
 565 570 575
 Met Glu Lys Gly Thr Asp Lys Glu Gln Asp Val Asp Val Ser Ser His
 580 585 590
 Ser Tyr Thr Ile Asn Gly Leu Lys Lys Tyr Thr Glu Tyr Ser Phe Arg
 595 600 605
 Val Val Ala Tyr Asn Lys His Gly Pro Gly Val Ser Thr Pro Asp Val
 610 615 620
 Ala Val Arg Thr Leu Ser Asp Val Pro Ser Ala Ala Pro Gln Asn Leu
 625 630 635 640

Ser Leu Glu Val Arg Asn Ser Lys Ser Ile Met Ile His Trp Gln Pro
 645 650 655
 Pro Ala Pro Ala Thr Gln Asn Gly Gln Ile Thr Gly Tyr Lys Ile Arg
 660 665 670
 Tyr Arg Lys Ala Ser Arg Lys Ser Asp Val Thr Glu Thr Leu Val Ser
 675 680 685
 Gly Thr Gln Leu Ser Gln Leu Ile Glu Gly Leu Asp Arg Gly Thr Glu
 690 695 700
 Tyr Asn Phe Arg Val Ala Ala Leu Thr Ile Asn Gly Thr Gly Pro Ala
 705 710 715 720
 Thr Asp Trp Leu Ser Ala Glu Thr Phe Glu Ser Asp Leu Asp Glu Thr
 725 730 735
 Arg Val Pro Glu Val Pro Ser Ser Leu His Val Arg Pro Leu Val Thr
 740 745 750
 Ser Ile Val Val Ser Trp Thr Pro Pro Glu Asn Gln Asn Ile Val Val
 755 760 765
 Arg Gly Tyr Ala Ile Gly Tyr Gly Ile Gly Ser Pro His Ala Gln Thr
 770 775 780
 Ile Lys Val Asp Tyr Lys Gln Arg Tyr Tyr Thr Ile Glu Asn Leu Asp
 785 790 795 800
 Pro Ser Ser His Tyr Val Ile Thr Leu Lys Ala Phe Asn Asn Val Gly
 805 810 815
 Glu Gly Ile Pro Leu Tyr Glu Ser Ala Val Thr Arg Pro His Thr Asp
 820 825 830
 Thr Ser Glu Val Asp Leu Phe Val Ile Asn Ala Pro Tyr Thr Pro Val
 835 840 845
 Pro Asp Pro Thr Pro Met Met Pro Pro Val Gly Val Gln Ala Ser Ile
 850 855 860
 Leu Ser His Asp Thr Ile Arg Ile Thr Trp Ala Asp Asn Ser Leu Pro
 865 870 875 880
 Lys His Gln Lys Ile Thr Asp Ser Arg Tyr Tyr Thr Val Arg Trp Lys
 885 890 895
 Thr Asn Ile Pro Ala Asn Thr Lys Tyr Lys Asn Ala Asn Ala Thr Thr
 900 905 910
 Leu Ser Tyr Leu Val Thr Gly Leu Lys Pro Asn Thr Leu Tyr Glu Phe
 915 920 925
 Ser Val Met Val Thr Lys Gly Arg Arg Ser Ser Thr Trp Ser Met Thr
 930 935 940
 Ala His Gly Thr Thr Phe Glu Leu Val Pro Thr Ser Pro Pro Lys Asp
 945 950 955 960

Val Thr Val Val Ser Lys Glu Gly Lys Pro Lys Thr Ile Ile Val Asn
 965 970 975
 Trp Gln Pro Pro Ser Glu Ala Asn Gly Lys Ile Thr Gly Tyr Ile Ile
 980 985 990
 Tyr Tyr Ser Thr Asp Val Asn Ala Glu Ile His Asp Trp Val Ile Glu
 995 1000 1005
 Pro Val Val Gly Asn Arg Leu Thr His Gln Ile Gln Glu Leu Thr
 1010 1015 1020
 Leu Asp Thr Pro Tyr Tyr Phe Lys Ile Gln Ala Arg Asn Ser Lys
 1025 1030 1035
 Gly Met Gly Pro Met Ser Glu Ala Val Gln Phe Arg Thr Pro Lys
 1040 1045 1050
 Ala Asp Ser Ser Asp Lys Met Pro Asn Asp Gln Ala Ser Gly Ser
 1055 1060 1065
 Gly Gly Lys Gly Ser Arg Leu Pro Asp Leu Gly Ser Asp Tyr Lys
 1070 1075 1080
 Pro Pro Met Ser Gly Ser Asn Ser Pro His Gly Ser Pro Thr Ser
 1085 1090 1095
 Pro Leu Asp Ser Asn Met Leu Leu Val Ile Ile Val Ser Val Gly
 1100 1105 1110
 Val Ile Thr Ile Val Val Val Val Ile Ile Ala Val Phe Cys Thr
 1115 1120 1125
 Arg Arg Thr Thr Ser His Gln Lys Lys Lys Arg Ala Ala Cys Lys
 1130 1135 1140
 Ser Val Asn Gly Ser His Lys Tyr Lys Gly Asn Ser Lys Asp Val
 1145 1150 1155
 Lys Pro Pro Asp Leu Trp Ile His His Glu Arg Leu Glu Leu Lys
 1160 1165 1170
 Pro Ile Asp Lys Ser Pro Asp Pro Asn Pro Ile Met Thr Asp Thr
 1175 1180 1185
 Pro Ile Pro Arg Asn Ser Gln Asp Ile Thr Pro Val Asp Asn Ser
 1190 1195 1200
 Met Asp Ser Asn Ile His Gln Arg Arg Asn Ser Tyr Arg Gly His
 1205 1210 1215
 Glu Ser Glu Asp Ser Met Ser Thr Leu Ala Gly Arg Arg Gly Met
 1220 1225 1230
 Arg Pro Lys Met Met Met Pro Phe Asp Ser Gln Pro Pro Gln Pro
 1235 1240 1245
 Val Ile Ser Ala His Pro Ile His Ser Leu Asp Asn Pro His His

1250 1255 1260
 His Phe His Ser Ser Ser Leu Ala Ser Pro Ala Arg Ser His Leu
 1265 1270 1275
 Tyr His Pro Gly Ser Pro Trp Pro Ile Gly Thr Ser Met Ser Leu
 1280 1285 1290
 Ser Asp Arg Ala Asn Ser Thr Glu Ser Val Arg Asn Thr Pro Ser
 1295 1300 1305
 Thr Asp Thr Met Pro Ala Ser Ser Ser Gln Thr Cys Cys Thr Asp
 1310 1315 1320
 His Gln Asp Pro Glu Gly Ala Thr Ser Ser Ser Tyr Leu Ala Ser
 1325 1330 1335
 Ser Gln Glu Glu Asp Ser Gly Gln Ser Leu Pro Thr Ala His Val
 1340 1345 1350
 Arg Pro Ser His Pro Leu Lys Ser Phe Ala Val Pro Ala Ile Pro
 1355 1360 1365
 Pro Pro Gly Pro Pro Thr Tyr Asp Pro Ala Leu Pro Ser Thr Pro
 1370 1375 1380
 Leu Leu Ser Gln Gln Ala Leu Asn His His Ile His Ser Val Lys
 1385 1390 1395
 Thr Ala Ser Ile Gly Thr Leu Gly Arg Ser Arg Pro Pro Met Pro
 1400 1405 1410
 Val Val Val Pro Ser Ala Pro Glu Val Gln Glu Thr Thr Arg Met
 1415 1420 1425
 Leu Glu Asp Ser Glu Ser Ser Tyr Glu Pro Asp Glu Leu Thr Lys
 1430 1435 1440
 Glu Met Ala His Leu Glu Gly Leu Met Lys Asp Leu Asn Ala Ile
 1445 1450 1455
 Thr Thr Ala
 1460
 <210> 190
 <211> 736
 <212> PRT
 <213> Homo sapiens
 <400> 190
 Met Val Val Thr Arg Ser Ala Arg Ala Lys Ala Ser Ile Gln Ala Ala
 1 5 10 15
 Ser Ala Glu Ser Ser Gly Gln Lys Ser Phe Ala Ala Asn Gly Ile Gln
 20 25 30
 Ala His Pro Glu Ser Ser Thr Gly Ser Asp Ala Arg Thr Thr Asp Glu
 35 40 45
 Ser Gln Thr Thr Gly Lys Gln Ser Leu Ile Pro Arg Thr Pro Lys Ala

50	55	60
Arg Lys Ser Lys Ser 65	Arg Thr Thr Gly Ser 70	Leu Pro Lys Gly Thr Glu 75 80
Pro Ser Thr Asp 85	Gly Glu Thr Ser 90	Glu Ser Asn Tyr Ser Val 95
Ser Glu His His 100	Asp Thr Ile Leu Arg 105	Val Thr Arg Arg Arg Gln Ile 110
Leu Ile Ala Cys Ser 115	Pro Val Ser Ser 120	Val Arg Lys Lys Pro Lys Val 125
Thr Pro Thr Lys Glu 130	Ser Tyr Thr Glu Glu 135	Ile Val Ser Glu Ala Glu 140
Ser His Val Ser 145	Gly Ile Ser Arg Ile 150	Val Leu Pro Thr Glu Lys Thr 155 160
Thr Gly Ala Arg 165	Arg Ser Lys Ala Lys 170	Ser Leu Thr Asp Pro Ser Gln 175
Glu Ser His Thr 180	Glu Ala Ile Ser 185	Asp Ala Glu Thr Ser Ser Ser Asp 190
Ile Ser Phe Ser 195	Gly Ile Ala Thr 200	Arg Arg Thr Arg Ser Met Gln Arg 205
Lys Leu Lys Ala Gln 210	Thr Glu Lys Lys 215	Asp Ser Lys Ile Val Pro Gly 220
Asn Glu Lys Gln 225	Ile Val Gly Thr 230	Pro Val Asn Ser Glu Asp Ser Asp 235 240
Thr Arg Gln Thr 245	Ser His Leu Gln Ala 250	Arg Ser Leu Ser Glu Ile Asn 255
Lys Pro Asn Phe 260	Tyr Asn Asn Asp 265	Phe Asp Asp Asp Phe Ser His Arg 270
Ser Ser Glu Asn 275	Ile Leu Thr Val 280	His Glu Gln Ala Asn Val Glu Ser 285
Leu Lys Glu Thr 290	Lys Gln Asn Cys 295	Lys Asp Leu Asp Glu Asp Ala Asn 300
Gly Ile Thr Asp 305	Glu Gly Lys Glu 310	Ile Asn Glu Lys Ser Ser Gln Leu 315 320
Lys Asn Leu Ser 325	Glu Leu Gln Asp 330	Thr Ser Leu Gln Gln Leu Val Ser 335
Gln Arg His Ser 340	Thr Pro Gln Asn 345	Lys Asn Ala Val Ser Val His Ser 350
Asn Leu Asn Ser 355	Glu Ala Val Met 360	Lys Ser Leu Thr Gln Thr Phe Ala 365

Thr Val Glu Val Gly Arg Trp Asn Asn Asn Lys Lys Ser Pro Ile Lys
 370 375 380
 Ala Ser Asp Leu Thr Lys Phe Gly Asp Cys Gly Gly Ser Asp Asp Glu
 385 390 395 400
 Glu Glu Ser Thr Val Ile Ser Val Ser Glu Asp Met Asn Ser Glu Gly
 405 410 415
 Asn Val Asp Phe Glu Cys Asp Thr Lys Leu Tyr Thr Ser Ala Pro Asn
 420 425 430
 Thr Ser Gln Gly Lys Asp Asn Ser Val Leu Leu Val Leu Ser Ser Asp
 435 440 445
 Glu Ser Gln Gln Ser Glu Asn Ser Glu Asn Glu Glu Asp Thr Leu Cys
 450 455 460
 Phe Val Glu Asn Ser Gly Gln Arg Glu Ser Leu Ser Gly Asp Thr Gly
 465 470 475 480
 Ser Leu Ser Cys Asp Asn Ala Leu Phe Val Ile Asp Thr Thr Pro Gly
 485 490 495
 Met Ser Ala Asp Lys Asn Phe Tyr Leu Glu Glu Glu Asp Lys Ala Ser
 500 505 510
 Glu Val Ala Ile Glu Glu Glu Lys Glu Glu Glu Glu Asp Glu Lys Ser
 515 520 525
 Glu Glu Asp Ser Ser Asp His Asp Glu Asn Glu Asp Glu Phe Ser Asp
 530 535 540
 Glu Glu Asp Phe Leu Asn Ser Thr Lys Ala Lys Leu Leu Lys Leu Thr
 545 550 555 560
 Ser Ser Ser Ile Asp Pro Gly Leu Ser Ile Lys Gln Leu Gly Gly Leu
 565 570 575
 Tyr Ile Asn Phe Asn Ala Asp Lys Leu Gln Ser Asn Lys Arg Thr Leu
 580 585 590
 Thr Gln Ile Lys Glu Lys Lys Lys Asn Glu Leu Leu Gln Lys Ala Val
 595 600 605
 Ile Thr Pro Asp Phe Glu Lys Asn His Cys Val Pro Pro Tyr Ser Glu
 610 615 620
 Ser Lys Tyr Gln Leu Gln Lys Lys Arg Arg Lys Glu Arg Gln Lys Thr
 625 630 635 640
 Ala Gly Asp Gly Trp Phe Gly Met Lys Ala Pro Glu Met Thr Asn Glu
 645 650 655
 Leu Lys Asn Asp Leu Lys Ala Leu Lys Met Arg Ala Ser Met Asp Pro
 660 665 670
 Lys Arg Phe Tyr Lys Lys Asn Asp Arg Asp Gly Phe Pro Lys Tyr Phe
 675 680 685

Gln Ile Gly Thr Ile Val Asp Asn Pro Ala Asp Phe Tyr His Ser Arg
690 695 700

Ile Pro Lys Lys Gln Arg Lys Arg Thr Ile Val Glu Asp Cys Trp Leu
705 710 715 720

Ile Leu Asn Ser Glu Ile Gln Pro Lys Glu Val Leu Arg Asp His Gly
725 730 735

<210> 191
<211> 465
<212> PRT
<213> Homo sapiens

<400> 191

Met Ala Met Thr Gly Ser Thr Pro Cys Ser Ser Met Ser Asn His Thr
1 5 10 15

Lys Glu Arg Val Thr Met Thr Lys Val Thr Leu Glu Asn Phe Tyr Ser
20 25 30

Asn Leu Ile Ala Gln His Glu Glu Arg Glu Met Arg Gln Lys Lys Leu
35 40 45

Glu Lys Val Met Glu Glu Glu Gly Leu Lys Asp Glu Glu Lys Arg Leu
50 55 60

Arg Arg Ser Ala His Ala Arg Lys Glu Thr Glu Phe Leu Arg Leu Lys
65 70 75 80

Arg Thr Arg Leu Gly Leu Glu Asp Phe Glu Ser Leu Lys Val Ile Gly
85 90 95

Arg Gly Ala Phe Gly Glu Val Arg Leu Val Gln Lys Lys Asp Thr Gly
100 105 110

His Val Tyr Ala Met Lys Ile Leu Arg Lys Ala Asp Met Leu Glu Lys
115 120 125

Glu Gln Val Gly His Ile Arg Ala Glu Arg Asp Ile Leu Val Glu Ala
130 135 140

Asp Ser Leu Trp Val Val Lys Met Phe Tyr Ser Phe Gln Asp Lys Leu
145 150 155 160

Asn Leu Tyr Leu Ile Met Glu Phe Leu Pro Gly Gly Asp Met Met Thr
165 170 175

Leu Leu Met Lys Lys Asp Thr Leu Thr Glu Glu Glu Thr Gln Phe Tyr
180 185 190

Ile Ala Glu Thr Val Leu Ala Ile Asp Ser Ile His Gln Leu Gly Phe
195 200 205

Ile His Arg Asp Ile Lys Pro Asp Asn Leu Leu Leu Asp Ser Lys Gly
210 215 220

His Val Lys Leu Ser Asp Phe Gly Leu Cys Thr Gly Leu Lys Lys Ala
225 230 235 240

His Arg Thr Glu Phe Tyr Arg Asn Leu Asn His Ser Leu Pro Ser Asp
 245 250 255
 Phe Thr Phe Gln Asn Met Asn Ser Lys Arg Lys Ala Glu Thr Trp Lys
 260 265 270
 Arg Asn Arg Arg Gln Leu Ala Phe Ser Thr Val Gly Thr Pro Asp Tyr
 275 280 285
 Ile Ala Pro Glu Val Phe Met Gln Thr Gly Tyr Asn Lys Leu Cys Asp
 290 295 300
 Trp Trp Ser Leu Gly Val Ile Met Tyr Glu Met Leu Ile Gly Tyr Pro
 305 310 315 320
 Pro Phe Cys Ser Glu Thr Pro Gln Glu Thr Tyr Lys Lys Val Met Asn
 325 330 335
 Trp Lys Glu Thr Leu Thr Phe Pro Pro Glu Val Pro Ile Ser Glu Lys
 340 345 350
 Ala Lys Asp Leu Ile Leu Arg Phe Cys Cys Glu Trp Glu His Arg Ile
 355 360 365
 Gly Ala Pro Gly Val Glu Glu Ile Lys Ser Asn Ser Phe Phe Glu Gly
 370 375 380
 Val Asp Trp Glu His Ile Arg Glu Arg Pro Ala Ala Ile Ser Ile Glu
 385 390 395 400
 Ile Lys Ser Ile Asp Asp Thr Ser Asn Phe Asp Glu Phe Pro Glu Ser
 405 410 415
 Asp Ile Leu Lys Pro Thr Val Ala Thr Ser Asn His Pro Glu Thr Asp
 420 425 430
 Tyr Lys Asn Lys Asp Trp Val Phe Ile Asn Tyr Thr Tyr Lys Arg Phe
 435 440 445
 Glu Gly Leu Thr Ala Arg Gly Ala Ile Pro Ser Tyr Met Lys Ala Ala
 450 455 460

Lys
 465

<210> 192
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 192

Met Thr Tyr Phe Pro Leu Gly Arg Tyr Pro Val Val Gly Leu Leu Asp
 1 5 10 15
 Gln Met Val Val Leu Ser Thr Phe Ser Ser Leu Lys Asn Leu His Ile
 20 25 30
 Val Phe His Ser Gly Cys Thr Ser Leu His Ser His Gln Leu Cys Lys
 35 40 45

Arg Val Pro Phe Ser Pro His Pro Arg Gln His Leu Leu Phe Phe Asp
50 55 60

Phe Trp Ile Lys Ala Ile Leu Ala Glu
65 70

<210> 193
<211> 410
<212> PRT
<213> Homo sapiens

<400> 193

Met Val Cys Phe Arg Leu Phe Pro Val Pro Gly Ser Gly Leu Val Leu
1 5 10 15

Val Cys Leu Val Leu Gly Ala Val Arg Ser Tyr Ala Leu Glu Leu Asn
20 25 30

Leu Thr Asp Ser Glu Asn Ala Thr Cys Leu Tyr Ala Lys Trp Gln Met
35 40 45

Asn Phe Thr Val Arg Tyr Glu Thr Thr Asn Lys Thr Tyr Lys Thr Val
50 55 60

Thr Ile Ser Asp His Gly Thr Val Thr Tyr Asn Gly Ser Ile Cys Gly
65 70 75 80

Asp Asp Gln Asn Gly Pro Lys Ile Ala Val Gln Phe Gly Pro Gly Phe
85 90 95

Ser Trp Ile Ala Asn Phe Thr Lys Ala Ala Ser Thr Tyr Ser Ile Asp
100 105 110

Ser Val Ser Phe Ser Tyr Asn Thr Gly Asp Asn Thr Thr Phe Pro Asp
115 120 125

Ala Glu Asp Lys Gly Ile Leu Thr Val Asp Glu Leu Leu Ala Ile Arg
130 135 140

Ile Pro Leu Asn Asp Leu Phe Arg Cys Asn Ser Leu Ser Thr Leu Glu
145 150 155 160

Lys Asn Asp Val Val Gln His Tyr Trp Asp Val Leu Val Gln Ala Phe
165 170 175

Val Gln Asn Gly Thr Val Ser Thr Asn Glu Phe Leu Cys Asp Lys Asp
180 185 190

Lys Thr Ser Thr Val Ala Pro Thr Ile His Thr Thr Val Pro Ser Pro
195 200 205

Thr Thr Thr Pro Thr Pro Lys Glu Lys Pro Glu Ala Gly Thr Tyr Ser
210 215 220

Val Asn Asn Gly Asn Asp Thr Cys Leu Leu Ala Thr Met Gly Leu Gln
225 230 235 240

Leu Asn Ile Thr Gln Asp Lys Val Ala Ser Val Ile Asn Ile Asn Pro
245 250 255

Asn Thr Thr His Ser Thr Gly Ser Cys Arg Ser His Thr Ala Leu Leu
260 265 270

Arg Leu Asn Ser Ser Thr Ile Lys Tyr Leu Asp Phe Val Phe Ala Val
275 280 285

Lys Asn Glu Asn Arg Phe Tyr Leu Lys Glu Val Asn Ile Ser Met Tyr
290 295 300

Leu Val Asn Gly Ser Val Phe Ser Ile Ala Asn Asn Asn Leu Ser Tyr
305 310 315 320

Trp Asp Ala Pro Leu Gly Ser Ser Tyr Met Cys Asn Lys Glu Gln Thr
325 330 335

Val Ser Val Ser Gly Ala Phe Gln Ile Asn Thr Phe Asp Leu Arg Val
340 345 350

Gln Pro Phe Asn Val Thr Gln Gly Lys Tyr Ser Thr Ala Gln Glu Cys
355 360 365

Ser Leu Asp Asp Asp Thr Ile Leu Ile Pro Ile Ile Val Gly Ala Gly
370 375 380

Leu Ser Gly Leu Ile Ile Val Ile Val Ile Ala Tyr Val Ile Gly Arg
385 390 395 400

Arg Lys Ser Tyr Ala Gly Tyr Gln Thr Leu
405 410

<210> 194
<211> 480
<212> PRT
<213> Homo sapiens

<400> 194

Met Ala Gly Gly Gly Gly Asp Leu Ser Thr Arg Arg Leu Asn Glu Cys
1 5 10 15

Ile Ser Pro Val Ala Asn Glu Met Asn His Leu Pro Ala His Ser His
20 25 30

Asp Leu Gln Arg Met Phe Thr Glu Asp Gln Gly Val Asp Asp Arg Leu
35 40 45

Leu Tyr Asp Ile Val Phe Lys His Phe Lys Arg Asn Lys Val Glu Ile
50 55 60

Ser Asn Ala Ile Lys Lys Thr Phe Pro Phe Leu Glu Gly Leu Arg Asp
65 70 75 80

Arg Asp Leu Ile Thr Asn Lys Met Phe Glu Asp Ser Gln Asp Ser Cys
85 90 95

Arg Asn Leu Val Pro Val Gln Arg Val Val Tyr Asn Val Leu Ser Glu
100 105 110

Leu Glu Lys Thr Phe Asn Leu Pro Val Leu Glu Ala Leu Phe Ser Asp
115 120 125

Val Asn Met Gln Glu Tyr Pro Asp Leu Ile His Ile Tyr Lys Gly Phe
 130 135 140
 Glu Asn Val Ile His Asp Lys Leu Pro Leu Gln Glu Ser Glu Glu Glu
 145 150 155 160
 Glu Arg Glu Glu Arg Ser Gly Leu Gln Leu Ser Leu Glu Gln Gly Thr
 165 170 175
 Gly Glu Asn Ser Phe Arg Ser Leu Thr Trp Pro Pro Ser Gly Ser Pro
 180 185 190
 Ser His Ala Gly Thr Thr Pro Pro Glu Asn Gly Leu Ser Glu His Pro
 195 200 205
 Cys Glu Thr Glu Gln Ile Asn Ala Lys Arg Lys Asp Thr Thr Ser Asp
 210 215 220
 Lys Asp Asp Ser Leu Gly Ser Gln Gln Thr Asn Glu Gln Cys Ala Gln
 225 230 235 240
 Lys Ala Glu Pro Thr Glu Ser Cys Glu Gln Ile Ala Val Gln Val Asn
 245 250 255
 Asn Gly Asp Ala Gly Arg Glu Met Pro Cys Pro Leu Pro Cys Asp Glu
 260 265 270
 Glu Ser Pro Glu Ala Glu Leu His Asn His Gly Ile Gln Ile Asn Ser
 275 280 285
 Cys Ser Val Arg Leu Val Asp Ile Lys Lys Glu Lys Pro Phe Ser Asn
 290 295 300
 Ser Lys Val Glu Cys Gln Ala Gln Ala Arg Thr His His Asn Gln Ala
 305 310 315 320
 Ser Asp Ile Ile Val Ile Ser Ser Glu Asp Ser Glu Gly Ser Thr Asp
 325 330 335
 Val Asp Glu Pro Leu Glu Val Phe Ile Ser Ala Pro Arg Ser Glu Pro
 340 345 350
 Val Ile Asn Asn Asp Asn Pro Leu Glu Ser Asn Asp Glu Lys Glu Gly
 355 360 365
 Gln Glu Ala Thr Cys Ser Arg Pro Gln Ile Val Pro Glu Pro Met Asp
 370 375 380
 Phe Arg Lys Leu Ser Thr Phe Arg Glu Ser Phe Lys Lys Arg Val Ile
 385 390 395 400
 Gly Gln Asp His Asp Phe Ser Glu Ser Ser Glu Glu Glu Ala Pro Ala
 405 410 415
 Glu Ala Ser Ser Gly Ala Leu Arg Ser Lys His Gly Glu Lys Ala Pro
 420 425 430
 Met Thr Ser Arg Ser Thr Ser Thr Trp Arg Ile Pro Ser Arg Lys Arg
 435 440 445

Arg Phe Ser Ser Ser Asp Phe Ser Asp Leu Ser Asn Gly Glu Glu Leu
450 455 460

Gln Glu Thr Cys Ser Ser Ser Leu Arg Arg Gly Ser Gly Lys Glu Asp
465 470 475 480

<210> 195
<211> 339
<212> PRT
<213> Homo sapiens

<400> 195

Met Trp Gln Leu Trp Ala Ser Leu Cys Cys Leu Leu Val Leu Ala Asn
1 5 10 15

Ala Arg Ser Arg Pro Ser Phe His Pro Leu Ser Asp Glu Leu Val Asn
20 25 30

Tyr Val Asn Lys Arg Asn Thr Thr Trp Gln Ala Gly His Asn Phe Tyr
35 40 45

Asn Val Asp Met Ser Tyr Leu Lys Arg Leu Cys Gly Thr Phe Leu Gly
50 55 60

Gly Pro Lys Pro Pro Gln Arg Val Met Phe Thr Glu Asp Leu Lys Leu
65 70 75 80

Pro Ala Ser Phe Asp Ala Arg Glu Gln Trp Pro Gln Cys Pro Thr Ile
85 90 95

Lys Glu Ile Arg Asp Gln Gly Ser Cys Gly Ser Cys Trp Ala Phe Gly
100 105 110

Ala Val Glu Ala Ile Ser Asp Arg Ile Cys Ile His Thr Asn Ala His
115 120 125

Val Ser Val Glu Val Ser Ala Glu Asp Leu Leu Thr Cys Cys Gly Ser
130 135 140

Met Cys Gly Asp Gly Cys Asn Gly Gly Tyr Pro Ala Glu Ala Trp Asn
145 150 155 160

Phe Trp Thr Arg Lys Gly Leu Val Ser Gly Gly Leu Tyr Glu Ser His
165 170 175

Val Gly Cys Arg Pro Tyr Ser Ile Pro Pro Cys Glu His His Val Asn
180 185 190

Gly Ser Arg Pro Pro Cys Thr Gly Glu Gly Asp Thr Pro Lys Cys Ser
195 200 205

Lys Ile Cys Glu Pro Gly Tyr Ser Pro Thr Tyr Lys Gln Asp Lys His
210 215 220

Tyr Gly Tyr Asn Ser Tyr Ser Val Ser Asn Ser Glu Lys Asp Ile Met
225 230 235 240

Ala Glu Ile Tyr Lys Asn Gly Pro Val Glu Gly Ala Phe Ser Val Tyr
245 250 255

Ser Asp Phe Leu Leu Tyr Lys Ser Gly Val Tyr Gln His Val Thr Gly
260 265 270

Glu Met Met Gly Gly His Ala Ile Arg Ile Leu Gly Trp Gly Val Glu
275 280 285

Asn Gly Thr Pro Tyr Trp Leu Val Ala Asn Ser Trp Asn Thr Asp Trp
290 295 300

Gly Asp Asn Gly Phe Phe Lys Ile Leu Arg Gly Gln Asp His Cys Gly
305 310 315 320

Ile Glu Ser Glu Val Val Ala Gly Ile Pro Arg Thr Asp Gln Tyr Trp
325 330 335

Glu Lys Ile

<210> 196
<211> 2328
<212> PRT
<213> Homo sapiens

<400> 196

Lys Ser Lys Arg Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val
1 5 10 15

Ala Val Ser Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr
20 25 30

Gln Ile Asn Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val
35 40 45

Cys Thr Cys Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro
50 55 60

Glu Ala Glu Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg
65 70 75 80

Val Gly Asp Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys
85 90 95

Thr Cys Ile Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn
100 105 110

Arg Cys His Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg
115 120 125

Arg Pro His Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly
130 135 140

Asn Gly Lys Gly Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe
145 150 155 160

Asp His Ala Ala Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys
165 170 175

Pro Tyr Gln Gly Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly
180 185 190

Ser Gly Arg Ile Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp
 195 200 205
 Thr Arg Thr Ser Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn
 210 215 220
 Arg Gly Asn Leu Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu
 225 230 235 240
 Trp Lys Cys Glu Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser
 245 250 255
 Gly Pro Phe Thr Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His
 260 265 270
 Pro Gln Pro Pro Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val
 275 280 285
 Tyr Ser Val Gly Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met
 290 295 300
 Leu Cys Thr Cys Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val
 305 310 315 320
 Thr Gln Thr Tyr Gly Gly Asn Leu Asn Gly Glu Pro Cys Val Leu Pro
 325 330 335
 Phe Thr Tyr Asn Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg
 340 345 350
 Gln Asp Gly His Leu Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp
 355 360 365
 Gln Lys Tyr Ser Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Gln
 370 375 380
 Gly Gly Asn Ser Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn
 385 390 395 400
 Asn His Asn Tyr Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met
 405 410 415
 Lys Trp Cys Gly Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly
 420 425 430
 Phe Cys Pro Met Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly
 435 440 445
 Val Met Tyr Arg Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly
 450 455 460
 His Met Met Arg Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr
 465 470 475 480
 Cys Ile Ala Tyr Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile
 485 490 495
 Thr Tyr Asn Val Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His

500					505					510					
Met	Leu	Asn	Cys	Thr	Cys	Phe	Gly	Gln	Gly	Arg	Gly	Arg	Trp	Lys	Cys
	515						520					525			
Asp	Pro	Val	Asp	Gln	Cys	Gln	Asp	Ser	Glu	Thr	Gly	Thr	Phe	Tyr	Gln
	530					535					540				
Ile	Gly	Asp	Ser	Trp	Glu	Lys	Tyr	Val	His	Gly	Val	Arg	Tyr	Gln	Cys
	545					550					555				560
Tyr	Cys	Tyr	Gly	Arg	Gly	Ile	Gly	Glu	Trp	His	Cys	Gln	Pro	Leu	Gln
				565					570					575	
Thr	Tyr	Pro	Ser	Ser	Ser	Gly	Pro	Val	Glu	Val	Phe	Ile	Thr	Glu	Thr
			580						585				590		
Pro	Ser	Gln	Pro	Asn	Ser	His	Pro	Ile	Gln	Trp	Asn	Ala	Pro	Gln	Pro
		595					600					605			
Ser	His	Ile	Ser	Lys	Tyr	Ile	Leu	Arg	Trp	Arg	Pro	Lys	Asn	Ser	Val
	610					615					620				
Gly	Arg	Trp	Lys	Glu	Ala	Thr	Ile	Pro	Gly	His	Leu	Asn	Ser	Tyr	Thr
	625					630					635				640
Ile	Lys	Gly	Leu	Lys	Pro	Gly	Val	Val	Tyr	Glu	Gly	Gln	Leu	Ile	Ser
			645						650					655	
Ile	Gln	Gln	Tyr	Gly	His	Gln	Glu	Val	Thr	Arg	Phe	Asp	Phe	Thr	Thr
			660						665				670		
Thr	Ser	Thr	Ser	Thr	Pro	Val	Thr	Ser	Asn	Thr	Val	Thr	Gly	Glu	Thr
		675					680						685		
Thr	Pro	Phe	Ser	Pro	Leu	Val	Ala	Thr	Ser	Glu	Ser	Val	Thr	Glu	Ile
	690					695						700			
Thr	Ala	Ser	Ser	Phe	Val	Val	Ser	Trp	Val	Ser	Ala	Ser	Asp	Thr	Val
	705					710					715				720
Ser	Gly	Phe	Arg	Val	Glu	Tyr	Glu	Leu	Ser	Glu	Glu	Gly	Asp	Glu	Pro
			725						730					735	
Gln	Tyr	Leu	Asp	Leu	Pro	Ser	Thr	Ala	Thr	Ser	Val	Asn	Ile	Pro	Asp
		740						745					750		
Leu	Leu	Pro	Gly	Arg	Lys	Tyr	Ile	Val	Asn	Val	Tyr	Gln	Ile	Ser	Glu
		755					760					765			
Asp	Gly	Glu	Gln	Ser	Leu	Ile	Leu	Ser	Thr	Ser	Gln	Thr	Thr	Ala	Pro
	770					775						780			
Asp	Ala	Pro	Pro	Asp	Pro	Thr	Val	Asp	Gln	Val	Asp	Asp	Thr	Ser	Ile
	785					790					795				800
Val	Val	Arg	Trp	Ser	Arg	Pro	Gln	Ala	Pro	Ile	Thr	Gly	Tyr	Arg	Ile
				805					810					815	

Val Tyr Ser Pro Ser Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro
 820 825 830
 Glu Thr Ala Asn Ser Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln
 835 840 845
 Tyr Asn Ile Thr Ile Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro
 850 855 860
 Val Val Ile Gln Gln Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val
 865 870 875 880
 Pro Ser Pro Arg Asp Leu Gln Phe Val Glu Val Thr Asp Val Lys Val
 885 890 895
 Thr Ile Met Trp Thr Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val
 900 905 910
 Asp Val Ile Pro Val Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro
 915 920 925
 Ile Ser Arg Asn Thr Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val
 930 935 940
 Thr Tyr Tyr Phe Lys Val Phe Ala Val Ser His Gly Arg Glu Ser Lys
 945 950 955 960
 Pro Leu Thr Ala Gln Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu
 965 970 975
 Gln Phe Val Asn Glu Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro
 980 985 990
 Pro Arg Ala Gln Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg
 995 1000 1005
 Arg Gly Gln Pro Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys
 1010 1015 1020
 Tyr Pro Leu Arg Asn Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser
 1025 1030 1035
 Leu Val Ala Ile Lys Gly Asn Gln Glu Ser Pro Lys Ala Thr Gly
 1040 1045 1050
 Val Phe Thr Thr Leu Gln Pro Gly Ser Ser Ile Pro Pro Tyr Asn
 1055 1060 1065
 Thr Glu Val Thr Glu Thr Thr Ile Val Ile Thr Trp Thr Pro Ala
 1070 1075 1080
 Pro Arg Ile Gly Phe Lys Leu Gly Val Arg Pro Ser Gln Gly Gly
 1085 1090 1095
 Glu Ala Pro Arg Glu Val Thr Ser Asp Ser Gly Ser Ile Val Val
 1100 1105 1110
 Ser Gly Leu Thr Pro Gly Val Glu Tyr Val Tyr Thr Ile Gln Val
 1115 1120 1125

Leu Arg Asp Gly Gln Glu Arg Asp Ala Pro Ile Val Asn Lys Val
 1130 1135 1140
 Val Thr Pro Leu Ser Pro Pro Thr Asn Leu His Leu Glu Ala Asn
 1145 1150 1155
 Pro Asp Thr Gly Val Leu Thr Val Ser Trp Glu Arg Ser Thr Thr
 1160 1165 1170
 Pro Asp Ile Thr Gly Tyr Arg Ile Thr Thr Thr Pro Thr Asn Gly
 1175 1180 1185
 Gln Gln Gly Asn Ser Leu Glu Glu Val Val His Ala Asp Gln Ser
 1190 1195 1200
 Ser Cys Thr Phe Asp Asn Leu Ser Pro Gly Leu Glu Tyr Asn Val
 1205 1210 1215
 Ser Val Tyr Thr Val Lys Asp Asp Lys Glu Ser Val Pro Ile Ser
 1220 1225 1230
 Asp Thr Ile Ile Pro Ala Val Pro Pro Pro Thr Asp Leu Arg Phe
 1235 1240 1245
 Thr Asn Ile Gly Pro Asp Thr Met Arg Val Thr Trp Ala Pro Pro
 1250 1255 1260
 Pro Ser Ile Asp Leu Thr Asn Phe Leu Val Arg Tyr Ser Pro Val
 1265 1270 1275
 Lys Asn Glu Glu Asp Val Ala Glu Leu Ser Ile Ser Pro Ser Asp
 1280 1285 1290
 Asn Ala Val Val Leu Thr Asn Leu Leu Pro Gly Thr Glu Tyr Val
 1295 1300 1305
 Val Ser Val Ser Ser Val Tyr Glu Gln His Glu Ser Thr Pro Leu
 1310 1315 1320
 Arg Gly Arg Gln Lys Thr Gly Leu Asp Ser Pro Thr Gly Ile Asp
 1325 1330 1335
 Phe Ser Asp Ile Thr Ala Asn Ser Phe Thr Val His Trp Ile Ala
 1340 1345 1350
 Pro Arg Ala Thr Ile Thr Gly Tyr Arg Ile Arg His His Pro Glu
 1355 1360 1365
 His Phe Ser Gly Arg Pro Arg Glu Asp Arg Val Pro His Ser Arg
 1370 1375 1380
 Asn Ser Ile Thr Leu Thr Asn Leu Thr Pro Gly Thr Glu Tyr Val
 1385 1390 1395
 Val Ser Ile Val Ala Leu Asn Gly Arg Glu Glu Ser Pro Leu Leu
 1400 1405 1410
 Ile Gly Gln Gln Ser Thr Val Ser Asp Val Pro Arg Asp Leu Glu
 1415 1420 1425

Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala
 1430 1435 1440
 Pro Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr
 1445 1450 1455
 Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys
 1460 1465 1470
 Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
 1475 1480 1485
 Ile Thr Val Tyr Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser
 1490 1495 1500
 Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
 1505 1510 1515
 Ser Gln Met Gln Val Thr Asp Val Gln Asp Asn Ser Ile Ser Val
 1520 1525 1530
 Lys Trp Leu Pro Ser Ser Ser Pro Val Thr Gly Tyr Arg Val Thr
 1535 1540 1545
 Thr Thr Pro Lys Asn Gly Pro Gly Pro Thr Lys Thr Lys Thr Ala
 1550 1555 1560
 Gly Pro Asp Gln Thr Glu Met Thr Ile Glu Gly Leu Gln Pro Thr
 1565 1570 1575
 Val Glu Tyr Val Val Ser Val Tyr Ala Gln Asn Pro Ser Gly Glu
 1580 1585 1590
 Ser Gln Pro Leu Val Gln Thr Ala Val Thr Asn Ile Asp Arg Pro
 1595 1600 1605
 Lys Gly Leu Ala Phe Thr Asp Val Asp Val Asp Ser Ile Lys Ile
 1610 1615 1620
 Ala Trp Glu Ser Pro Gln Gly Gln Val Ser Arg Tyr Arg Val Thr
 1625 1630 1635
 Tyr Ser Ser Pro Glu Asp Gly Ile His Glu Leu Phe Pro Ala Pro
 1640 1645 1650
 Asp Gly Glu Glu Asp Thr Ala Glu Leu Gln Gly Leu Arg Pro Gly
 1655 1660 1665
 Ser Glu Tyr Thr Val Ser Val Val Ala Leu His Asp Asp Met Glu
 1670 1675 1680
 Ser Gln Pro Leu Ile Gly Thr Gln Ser Thr Ala Ile Pro Ala Pro
 1685 1690 1695
 Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala
 1700 1705 1710
 Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg

1715	1720	1725
Val Thr 1730	Pro Lys Glu Lys Thr 1735	Gly Pro Met Lys Glu Ile Asn Leu 1740
Ala Pro 1745	Asp Ser Ser Ser Val 1750	Val Val Ser Gly Leu Met Val Ala 1755
Thr Lys 1760	Tyr Glu Val Ser Val 1765	Tyr Ala Leu Lys Asp Thr Leu Thr 1770
Ser Arg 1775	Pro Ala Gln Gly Val 1780	Val Thr Thr Leu Glu Asn Val Ser 1785
Pro Pro 1790	Arg Arg Ala Arg Val 1795	Thr Asp Ala Thr Glu Thr Thr Ile 1800
Thr Ile 1805	Ser Trp Arg Thr Lys 1810	Thr Glu Thr Ile Thr Gly Phe Gln 1815
Val Asp 1820	Ala Val Pro Ala Asn 1825	Gly Gln Thr Pro Ile Gln Arg Thr 1830
Ile Lys 1835	Pro Asp Val Arg Ser 1840	Tyr Thr Ile Thr Gly Leu Gln Pro 1845
Gly Thr 1850	Asp Tyr Lys Ile Tyr 1855	Leu Tyr Thr Leu Asn Asp Asn Ala 1860
Arg Ser 1865	Ser Pro Val Val Ile 1870	Asp Ala Ser Thr Ala Ile Asp Ala 1875
Pro Ser 1880	Asn Leu Arg Phe Leu 1885	Ala Thr Thr Pro Asn Ser Leu Leu 1890
Val Ser 1895	Trp Gln Pro Pro Arg 1900	Ala Arg Ile Thr Gly Tyr Ile Ile 1905
Lys Tyr 1910	Glu Lys Pro Gly Ser 1915	Pro Pro Arg Glu Val Val Pro Arg 1920
Pro Arg 1925	Pro Gly Val Thr Glu 1930	Ala Thr Ile Thr Gly Leu Glu Pro 1935
Gly Thr 1940	Glu Tyr Thr Ile Tyr 1945	Val Ile Ala Leu Lys Asn Asn Gln 1950
Lys Ser 1955	Glu Pro Leu Ile Gly 1960	Arg Lys Lys Thr Asp Glu Leu Pro 1965
Gln Leu 1970	Val Thr Leu Pro His 1975	Pro Asn Leu His Gly Pro Glu Ile 1980
Leu Asp 1985	Val Pro Ser Thr Val 1990	Gln Lys Thr Pro Phe Val Thr His 1995
Pro Gly 2000	Tyr Asp Thr Gly Asn 2005	Gly Ile Gln Leu Pro Gly Thr Ser 2010

Gly Gln Gln Pro Ser Val Gly Gln Gln Met Ile Phe Glu Glu His
 2015 2020 2025
 Gly Phe Arg Arg Thr Thr Pro Pro Thr Thr Ala Thr Pro Ile Arg
 2030 2035 2040
 His Arg Pro Arg Pro Tyr Pro Pro Asn Val Gly Gln Glu Ala Leu
 2045 2050 2055
 Ser Gln Thr Thr Ile Ser Trp Ala Pro Phe Gln Asp Thr Ser Glu
 2060 2065 2070
 Tyr Ile Ile Ser Cys His Pro Val Gly Thr Asp Glu Glu Pro Leu
 2075 2080 2085
 Gln Phe Arg Val Pro Gly Thr Ser Thr Ser Ala Thr Leu Thr Gly
 2090 2095 2100
 Leu Thr Arg Gly Ala Thr Tyr Asn Ile Ile Val Glu Ala Leu Lys
 2105 2110 2115
 Asp Gln Gln Arg His Lys Val Arg Glu Glu Val Val Thr Val Gly
 2120 2125 2130
 Asn Ser Val Asn Glu Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys
 2135 2140 2145
 Phe Asp Pro Tyr Thr Val Ser His Tyr Ala Val Gly Asp Glu Trp
 2150 2155 2160
 Glu Arg Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu
 2165 2170 2175
 Gly Phe Gly Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys
 2180 2185 2190
 His Asp Asn Gly Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg
 2195 2200 2205
 Gln Gly Glu Asn Gly Gln Met Met Ser Cys Thr Cys Leu Gly Asn
 2210 2215 2220
 Gly Lys Gly Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys Tyr
 2225 2230 2235
 Asp Asp Gly Lys Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu
 2240 2245 2250
 Tyr Leu Gly Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg
 2255 2260 2265
 Gly Trp Arg Cys Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser
 2270 2275 2280
 Pro Glu Gly Thr Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg
 2285 2290 2295
 Tyr His Gln Arg Thr Asn Thr Asn Val Asn Cys Pro Ile Glu Cys
 2300 2305 2310

Phe Met Pro Leu Asp Val Gln Ala Asp Arg Glu Asp Ser Arg Glu
2315 2320 2325

<210> 197
<211> 165
<212> PRT
<213> Homo sapiens

<400> 197

Met Leu Met Pro Lys Lys Asn Arg Ile Ala Ile Tyr Glu Leu Leu Phe
1 5 10 15

Lys Glu Gly Val Met Val Ala Lys Lys Asp Val His Met Pro Lys His
20 25 30

Pro Glu Leu Ala Asp Lys Asn Val Pro Asn Leu His Val Met Lys Ala
35 40 45

Met Gln Ser Leu Lys Ser Arg Gly Tyr Val Lys Glu Gln Phe Ala Trp
50 55 60

Arg His Phe Tyr Trp Tyr Leu Thr Asn Glu Gly Ile Gln Tyr Leu Arg
65 70 75 80

Asp Tyr Leu His Leu Pro Pro Glu Ile Val Pro Ala Thr Leu Arg Arg
85 90 95

Ser Arg Pro Glu Thr Gly Arg Pro Arg Pro Lys Gly Leu Glu Gly Glu
100 105 110

Arg Pro Ala Arg Leu Thr Arg Gly Glu Ala Asp Arg Asp Thr Tyr Arg
115 120 125

Arg Ser Ala Val Pro Pro Gly Ala Asp Lys Lys Ala Glu Ala Gly Ala
130 135 140

Gly Ser Ala Thr Glu Phe Gln Phe Arg Gly Gly Phe Gly Arg Gly Arg
145 150 155 160

Gly Gln Pro Pro Gln
165

<210> 198
<211> 154
<212> PRT
<213> Homo sapiens

<400> 198

Met Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln
1 5 10 15

Gly Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val
20 25 30

Trp Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val
35 40 45

His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His
50 55 60

Phe Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg
65 70 75 80

His Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala
85 90 95

Asp Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys
100 105 110

Ile Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly
115 120 125

Lys Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg
130 135 140

Leu Ala Cys Gly Val Ile Gly Ile Ala Gln
145 150

<210> 199
<211> 3256
<212> PRT
<213> Homo sapiens

<400> 199

Met Trp Pro Thr Arg Arg Leu Val Thr Ile Lys Arg Ser Gly Val Asp
1 5 10 15

Gly Pro His Phe Pro Leu Ser Leu Ser Thr Cys Leu Phe Gly Arg Gly
20 25 30

Ile Glu Cys Asp Ile Arg Ile Gln Leu Pro Val Val Ser Lys Gln His
35 40 45

Cys Lys Ile Glu Ile His Glu Gln Glu Ala Ile Leu His Asn Phe Ser
50 55 60

Ser Thr Asn Pro Thr Gln Val Asn Gly Ser Val Ile Asp Glu Pro Val
65 70 75 80

Arg Leu Lys His Gly Asp Val Ile Thr Ile Ile Asp Arg Ser Phe Arg
85 90 95

Tyr Glu Asn Glu Ser Leu Gln Asn Gly Arg Lys Ser Thr Glu Phe Pro
100 105 110

Arg Lys Ile Arg Glu Gln Glu Pro Ala Arg Arg Val Ser Arg Ser Ser
115 120 125

Phe Ser Ser Asp Pro Asp Glu Lys Ala Gln Asp Ser Lys Ala Tyr Ser
130 135 140

Lys Ile Thr Glu Gly Lys Val Ser Gly Asn Pro Gln Val His Ile Lys
145 150 155 160

Asn Val Lys Glu Asp Ser Thr Ala Asp Asp Ser Lys Asp Ser Val Ala
165 170 175

Gln Gly Thr Thr Asn Val His Ser Ser Glu His Ala Gly Arg Asn Gly
180 185 190

Arg Asn Ala Ala Asp Pro Ile Ser Gly Asp Phe Lys Glu Ile Ser Ser
 195 200 205
 Val Lys Leu Val Ser Arg Tyr Gly Glu Leu Lys Ser Val Pro Thr Thr
 210 215 220
 Gln Cys Leu Asp Asn Ser Lys Lys Asn Glu Ser Pro Phe Trp Lys Leu
 225 230 235 240
 Tyr Glu Ser Val Lys Lys Glu Leu Asp Val Lys Ser Gln Lys Glu Asn
 245 250 255
 Val Leu Gln Tyr Cys Arg Lys Ser Gly Leu Gln Thr Asp Tyr Ala Thr
 260 265 270
 Glu Lys Glu Ser Ala Asp Gly Leu Gln Gly Glu Thr Gln Leu Leu Val
 275 280 285
 Ser Arg Lys Ser Arg Pro Lys Ser Gly Gly Ser Gly His Ala Val Ala
 290 295 300
 Glu Pro Ala Ser Pro Glu Gln Glu Leu Asp Gln Asn Lys Gly Lys Gly
 305 310 315 320
 Arg Asp Val Glu Ser Val Gln Thr Pro Ser Lys Ala Val Gly Ala Ser
 325 330 335
 Phe Pro Leu Tyr Glu Pro Ala Lys Met Lys Thr Pro Val Gln Tyr Ser
 340 345 350
 Gln Gln Gln Asn Ser Pro Gln Lys His Lys Asn Lys Asp Leu Tyr Thr
 355 360 365
 Thr Gly Arg Arg Glu Ser Val Asn Leu Gly Lys Ser Glu Gly Phe Lys
 370 375 380
 Ala Gly Asp Lys Thr Leu Thr Pro Arg Lys Leu Ser Thr Arg Asn Arg
 385 390 395 400
 Thr Pro Ala Lys Val Glu Asp Ala Ala Asp Ser Ala Thr Lys Pro Glu
 405 410 415
 Asn Leu Ser Ser Lys Thr Arg Gly Ser Ile Pro Thr Asp Val Glu Val
 420 425 430
 Leu Pro Thr Glu Thr Glu Ile His Asn Glu Pro Phe Leu Thr Leu Trp
 435 440 445
 Leu Thr Gln Val Glu Arg Lys Ile Gln Lys Asp Ser Leu Ser Lys Pro
 450 455 460
 Glu Lys Leu Gly Thr Thr Ala Gly Gln Met Cys Ser Gly Leu Pro Gly
 465 470 475 480
 Leu Ser Ser Val Asp Ile Asn Asn Phe Gly Asp Ser Ile Asn Glu Ser
 485 490 495
 Glu Gly Ile Pro Leu Lys Arg Arg Arg Val Ser Phe Gly Gly His Leu
 500 505 510

Arg Pro Glu Leu Phe Asp Glu Asn Leu Pro Pro Asn Thr Pro Leu Lys
 515 520 525
 Arg Gly Glu Ala Pro Thr Lys Arg Lys Ser Leu Val Met His Thr Pro
 530 535 540
 Pro Val Leu Lys Lys Ile Ile Lys Glu Gln Pro Gln Pro Ser Gly Lys
 545 550 555 560
 Gln Glu Ser Gly Ser Glu Ile His Val Glu Val Lys Ala Gln Ser Leu
 565 570 575
 Val Ile Ser Pro Pro Ala Pro Ser Pro Arg Lys Thr Pro Val Ala Ser
 580 585 590
 Asp Gln Arg Arg Arg Ser Cys Lys Thr Ala Pro Ala Ser Ser Ser Lys
 595 600 605
 Ser Gln Thr Glu Val Pro Lys Arg Gly Gly Glu Arg Val Ala Thr Cys
 610 615 620
 Leu Gln Lys Arg Val Ser Ile Ser Arg Ser Gln His Asp Ile Leu Gln
 625 630 635 640
 Met Ile Cys Ser Lys Arg Arg Ser Gly Ala Ser Glu Ala Asn Leu Ile
 645 650 655
 Val Ala Lys Ser Trp Ala Asp Val Val Lys Leu Gly Ala Lys Gln Thr
 660 665 670
 Gln Thr Lys Val Ile Lys His Gly Pro Gln Arg Ser Met Asn Lys Arg
 675 680 685
 Gln Arg Arg Pro Ala Thr Pro Lys Lys Pro Val Gly Glu Val His Ser
 690 695 700
 Gln Phe Ser Thr Gly His Ala Asn Ser Pro Cys Thr Ile Ile Ile Gly
 705 710 715 720
 Lys Ala His Thr Glu Lys Val His Val Pro Ala Arg Pro Tyr Arg Val
 725 730 735
 Leu Asn Asn Phe Ile Ser Asn Gln Lys Met Asp Phe Lys Glu Asp Leu
 740 745 750
 Ser Gly Ile Ala Glu Met Phe Lys Thr Pro Val Lys Glu Gln Pro Gln
 755 760 765
 Leu Thr Ser Thr Cys His Ile Ala Ile Ser Asn Ser Glu Asn Leu Leu
 770 775 780
 Gly Lys Gln Phe Gln Gly Thr Asp Ser Gly Glu Glu Pro Leu Leu Pro
 785 790 795 800
 Thr Ser Glu Ser Phe Gly Gly Asn Val Phe Phe Ser Ala Gln Asn Ala
 805 810 815
 Ala Lys Gln Pro Ser Asp Lys Cys Ser Ala Ser Pro Pro Leu Arg Arg
 820 825 830

Gln Cys Ile Arg Glu Asn Gly Asn Val Ala Lys Thr Pro Arg Asn Thr
 835 840 845
 Tyr Lys Met Thr Ser Leu Glu Thr Lys Thr Ser Asp Thr Glu Thr Glu
 850 855 860
 Pro Ser Lys Thr Val Ser Thr Val Asn Arg Ser Gly Arg Ser Thr Glu
 865 870 875 880
 Phe Arg Asn Ile Gln Lys Leu Pro Val Glu Ser Lys Ser Glu Glu Thr
 885 890 895
 Asn Thr Glu Ile Val Glu Cys Ile Leu Lys Arg Gly Gln Lys Ala Thr
 900 905 910
 Leu Leu Gln Gln Arg Arg Glu Gly Glu Met Lys Glu Ile Glu Arg Pro
 915 920 925
 Phe Glu Thr Tyr Lys Glu Asn Ile Glu Leu Lys Glu Asn Asp Glu Lys
 930 935 940
 Met Lys Ala Met Lys Arg Ser Arg Thr Trp Gly Gln Lys Cys Ala Pro
 945 950 955 960
 Met Ser Asp Leu Thr Asp Leu Lys Ser Leu Pro Asp Thr Glu Leu Met
 965 970 975
 Lys Asp Thr Ala Arg Gly Gln Asn Leu Leu Gln Thr Gln Asp His Ala
 980 985 990
 Lys Ala Pro Lys Ser Glu Lys Gly Lys Ile Thr Lys Met Pro Cys Gln
 995 1000 1005
 Ser Leu Gln Pro Glu Pro Ile Asn Thr Pro Thr His Thr Lys Gln
 1010 1015 1020
 Gln Leu Lys Ala Ser Leu Gly Lys Val Gly Val Lys Glu Glu Leu
 1025 1030 1035
 Leu Ala Val Gly Lys Phe Thr Arg Thr Ser Gly Glu Thr Thr His
 1040 1045 1050
 Thr His Arg Glu Pro Ala Gly Asp Gly Lys Ser Ile Arg Thr Phe
 1055 1060 1065
 Lys Glu Ser Pro Lys Gln Ile Leu Asp Pro Ala Ala Arg Val Thr
 1070 1075 1080
 Gly Met Lys Lys Trp Pro Arg Thr Pro Lys Glu Glu Ala Gln Ser
 1085 1090 1095
 Leu Glu Asp Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly
 1100 1105 1110
 Pro Ser Glu Glu Ser Met Thr Asp Glu Lys Thr Thr Lys Ile Ala
 1115 1120 1125
 Cys Lys Ser Pro Pro Pro Glu Ser Val Asp Thr Pro Thr Ser Thr

1130	1135	1140
Lys Gln Trp Pro Lys Arg Ser 1145	Leu Arg Lys Ala Asp 1150	Val Glu Glu 1155
Glu Phe Leu Ala Leu Arg Lys 1160	Leu Thr Pro Ser Ala 1165	Gly Lys Ala 1170
Met Leu Thr Pro Lys Pro Ala 1175	Gly Gly Asp Glu Lys 1180	Asp Ile Lys 1185
Ala Phe Met Gly Thr Pro Val 1190	Gln Lys Leu Asp Leu 1195	Ala Gly Thr 1200
Leu Pro Gly Ser Lys Arg Gln 1205	Leu Gln Thr Pro Lys 1210	Glu Lys Ala 1215
Gln Ala Leu Glu Asp Leu Ala 1220	Gly Phe Lys Glu Leu 1225	Phe Gln Thr 1230
Pro Gly His Thr Glu Glu Leu 1235	Val Ala Ala Gly Lys 1240	Thr Thr Lys 1245
Ile Pro Cys Asp Ser Pro Gln 1250	Ser Asp Pro Val Asp 1255	Thr Pro Thr 1260
Ser Thr Lys Gln Arg Pro Lys 1265	Arg Ser Ile Arg Lys 1270	Ala Asp Val 1275
Glu Gly Glu Leu Leu Ala Cys 1280	Arg Asn Leu Met Pro 1285	Ser Ala Gly 1290
Lys Ala Met His Thr Pro Lys 1295	Pro Ser Val Gly Glu 1300	Glu Lys Asp 1305
Ile Ile Ile Phe Val Gly Thr 1310	Pro Val Gln Lys Leu 1315	Asp Leu Thr 1320
Glu Asn Leu Thr Gly Ser Lys 1325	Arg Arg Pro Gln Thr 1330	Pro Lys Glu 1335
Glu Ala Gln Ala Leu Glu Asp 1340	Leu Thr Gly Phe Lys 1345	Glu Leu Phe 1350
Gln Thr Pro Gly His Thr Glu 1355	Glu Ala Val Ala Ala 1360	Gly Lys Thr 1365
Thr Lys Met Pro Cys Glu Ser 1370	Ser Pro Pro Glu Ser 1375	Ala Asp Thr 1380
Pro Thr Ser Thr Arg Arg Gln 1385	Pro Lys Thr Pro Leu 1390	Glu Lys Arg 1395
Asp Val Gln Lys Glu Leu Ser 1400	Ala Leu Lys Lys Leu 1405	Thr Gln Thr 1410
Ser Gly Glu Thr Thr His Thr 1415	Asp Lys Val Pro Gly 1420	Gly Glu Asp 1425

Lys Ser Ile Asn Ala Phe Arg Glu Thr Ala Lys Gln Lys Leu Asp
 1430 1435 1440
 Pro Ala Ala Ser Val Thr Gly Ser Lys Arg His Pro Lys Thr Lys
 1445 1450 1455
 Glu Lys Ala Gln Pro Leu Glu Asp Leu Ala Gly Trp Lys Glu Leu
 1460 1465 1470
 Phe Gln Thr Pro Val Cys Thr Asp Lys Pro Thr Thr His Glu Lys
 1475 1480 1485
 Thr Thr Lys Ile Ala Cys Arg Ser Gln Pro Asp Pro Val Asp Thr
 1490 1495 1500
 Pro Thr Ser Ser Lys Pro Gln Ser Lys Arg Ser Leu Arg Lys Val
 1505 1510 1515
 Asp Val Glu Glu Glu Phe Phe Ala Leu Arg Lys Arg Thr Pro Ser
 1520 1525 1530
 Ala Gly Lys Ala Met His Thr Pro Lys Pro Ala Val Ser Gly Glu
 1535 1540 1545
 Lys Asn Ile Tyr Ala Phe Met Gly Thr Pro Val Gln Lys Leu Asp
 1550 1555 1560
 Leu Thr Glu Asn Leu Thr Gly Ser Lys Arg Arg Leu Gln Thr Pro
 1565 1570 1575
 Lys Glu Lys Ala Gln Ala Leu Glu Asp Leu Ala Gly Phe Lys Glu
 1580 1585 1590
 Leu Phe Gln Thr Arg Gly His Thr Glu Glu Ser Met Thr Asn Asp
 1595 1600 1605
 Lys Thr Ala Lys Val Ala Cys Lys Ser Ser Gln Pro Asp Leu Asp
 1610 1615 1620
 Lys Asn Pro Ala Ser Ser Lys Arg Arg Leu Lys Thr Ser Leu Gly
 1625 1630 1635
 Lys Val Gly Val Lys Glu Glu Leu Leu Ala Val Gly Lys Leu Thr
 1640 1645 1650
 Gln Thr Ser Gly Glu Thr Thr His Thr His Thr Glu Pro Thr Gly
 1655 1660 1665
 Asp Gly Lys Ser Met Lys Ala Phe Met Glu Ser Pro Lys Gln Ile
 1670 1675 1680
 Leu Asp Ser Ala Ala Ser Leu Thr Gly Ser Lys Arg Gln Leu Arg
 1685 1690 1695
 Thr Pro Lys Gly Lys Ser Glu Val Pro Glu Asp Leu Ala Gly Phe
 1700 1705 1710
 Ile Glu Leu Phe Gln Thr Pro Ser His Thr Lys Glu Ser Met Thr
 1715 1720 1725

Asn Glu Lys Thr Thr Lys Val Ser Tyr Arg Ala Ser Gln Pro Asp
 1730 1735 1740
 Leu Val Asp Thr Pro Thr Ser Ser Lys Pro Gln Pro Lys Arg Ser
 1745 1750 1755
 Leu Arg Lys Ala Asp Thr Glu Glu Glu Phe Leu Ala Phe Arg Lys
 1760 1765 1770
 Gln Thr Pro Ser Ala Gly Lys Ala Met His Thr Pro Lys Pro Ala
 1775 1780 1785
 Val Gly Glu Glu Lys Asp Ile Asn Thr Phe Leu Gly Thr Pro Val
 1790 1795 1800
 Gln Lys Leu Asp Gln Pro Gly Asn Leu Pro Gly Ser Asn Arg Arg
 1805 1810 1815
 Leu Gln Thr Arg Lys Glu Lys Ala Gln Ala Leu Glu Glu Leu Thr
 1820 1825 1830
 Gly Phe Arg Glu Leu Phe Gln Thr Pro Cys Thr Asp Asn Pro Thr
 1835 1840 1845
 Ala Asp Glu Lys Thr Thr Lys Lys Ile Leu Cys Lys Ser Pro Gln
 1850 1855 1860
 Ser Asp Pro Ala Asp Thr Pro Thr Asn Thr Lys Gln Arg Pro Lys
 1865 1870 1875
 Arg Ser Leu Lys Lys Ala Asp Val Glu Glu Glu Phe Leu Ala Phe
 1880 1885 1890
 Arg Lys Leu Thr Pro Ser Ala Gly Lys Ala Met His Thr Pro Lys
 1895 1900 1905
 Ala Ala Val Gly Glu Glu Lys Asp Ile Asn Thr Phe Val Gly Thr
 1910 1915 1920
 Pro Val Glu Lys Leu Asp Leu Leu Gly Asn Leu Pro Gly Ser Lys
 1925 1930 1935
 Arg Arg Pro Gln Thr Pro Lys Glu Lys Ala Lys Ala Leu Glu Asp
 1940 1945 1950
 Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly His Thr Glu
 1955 1960 1965
 Glu Ser Met Thr Asp Asp Lys Ile Thr Glu Val Ser Cys Lys Ser
 1970 1975 1980
 Pro Gln Pro Asp Pro Val Lys Thr Pro Thr Ser Ser Lys Gln Arg
 1985 1990 1995
 Leu Lys Ile Ser Leu Gly Lys Val Gly Val Lys Glu Glu Val Leu
 2000 2005 2010
 Pro Val Gly Lys Leu Thr Gln Thr Ser Gly Lys Thr Thr Gln Thr
 2015 2020 2025

His Arg Glu Thr Ala Gly Asp Gly Lys Ser Ile Lys Ala Phe Lys
 2030 2035 2040
 Glu Ser Ala Lys Gln Met Leu Asp Pro Ala Asn Tyr Gly Thr Gly
 2045 2050 2055
 Met Glu Arg Trp Pro Arg Thr Pro Lys Glu Glu Ala Gln Ser Leu
 2060 2065 2070
 Glu Asp Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Pro Asp His
 2075 2080 2085
 Thr Glu Glu Ser Thr Thr Asp Asp Lys Thr Thr Lys Ile Ala Cys
 2090 2095 2100
 Lys Ser Pro Pro Pro Glu Ser Met Asp Thr Pro Thr Ser Thr Arg
 2105 2110 2115
 Arg Arg Pro Lys Thr Pro Leu Gly Lys Arg Asp Ile Val Glu Glu
 2120 2125 2130
 Leu Ser Ala Leu Lys Gln Leu Thr Gln Thr Thr His Thr Asp Lys
 2135 2140 2145
 Val Pro Gly Asp Glu Asp Lys Gly Ile Asn Val Phe Arg Glu Thr
 2150 2155 2160
 Ala Lys Gln Lys Leu Asp Pro Ala Ala Ser Val Thr Gly Ser Lys
 2165 2170 2175
 Arg Gln Pro Arg Thr Pro Lys Gly Lys Ala Gln Pro Leu Glu Asp
 2180 2185 2190
 Leu Ala Gly Leu Lys Glu Leu Phe Gln Thr Pro Val Cys Thr Asp
 2195 2200 2205
 Lys Pro Thr Thr His Glu Lys Thr Thr Lys Ile Ala Cys Arg Ser
 2210 2215 2220
 Pro Gln Pro Asp Pro Val Gly Thr Pro Thr Ile Phe Lys Pro Gln
 2225 2230 2235
 Ser Lys Arg Ser Leu Arg Lys Ala Asp Val Glu Glu Glu Ser Leu
 2240 2245 2250
 Ala Leu Arg Lys Arg Thr Pro Ser Val Gly Lys Ala Met Asp Thr
 2255 2260 2265
 Pro Lys Pro Ala Gly Gly Asp Glu Lys Asp Met Lys Ala Phe Met
 2270 2275 2280
 Gly Thr Pro Val Gln Lys Leu Asp Leu Pro Gly Asn Leu Pro Gly
 2285 2290 2295
 Ser Lys Arg Trp Pro Gln Thr Pro Lys Glu Lys Ala Gln Ala Leu
 2300 2305 2310
 Glu Asp Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly Thr

2315	2320	2325
Asp Lys Pro Thr Thr Asp Glu Lys Thr Thr Lys Ile Ala Cys Lys 2330 2335 2340		
Ser Pro Gln Pro Asp Pro Val Asp Thr Pro Ala Ser Thr Lys Gln 2345 2350 2355		
Arg Pro Lys Arg Asn Leu Arg Lys Ala Asp Val Glu Glu Glu Phe 2360 2365 2370		
Leu Ala Leu Arg Lys Arg Thr Pro Ser Ala Gly Lys Ala Met Asp 2375 2380 2385		
Thr Pro Lys Pro Ala Val Ser Asp Glu Lys Asn Ile Asn Thr Phe 2390 2395 2400		
Val Glu Thr Pro Val Gln Lys Leu Asp Leu Leu Gly Asn Leu Pro 2405 2410 2415		
Gly Ser Lys Arg Gln Pro Gln Thr Pro Lys Glu Lys Ala Glu Ala 2420 2425 2430		
Leu Glu Asp Leu Val Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly 2435 2440 2445		
His Thr Glu Glu Ser Met Thr Asp Asp Lys Ile Thr Glu Val Ser 2450 2455 2460		
Cys Lys Ser Pro Gln Pro Glu Ser Phe Lys Thr Ser Arg Ser Ser 2465 2470 2475		
Lys Gln Arg Leu Lys Ile Pro Leu Val Lys Val Asp Met Lys Glu 2480 2485 2490		
Glu Pro Leu Ala Val Ser Lys Leu Thr Arg Thr Ser Gly Glu Thr 2495 2500 2505		
Thr Gln Thr His Thr Glu Pro Thr Gly Asp Ser Lys Ser Ile Lys 2510 2515 2520		
Ala Phe Lys Glu Ser Pro Lys Gln Ile Leu Asp Pro Ala Ala Ser 2525 2530 2535		
Val Thr Gly Ser Arg Arg Gln Leu Arg Thr Arg Lys Glu Lys Ala 2540 2545 2550		
Arg Ala Leu Glu Asp Leu Val Asp Phe Lys Glu Leu Phe Ser Ala 2555 2560 2565		
Pro Gly His Thr Glu Glu Ser Met Thr Ile Asp Lys Asn Thr Lys 2570 2575 2580		
Ile Pro Cys Lys Ser Pro Pro Pro Glu Leu Thr Asp Thr Ala Thr 2585 2590 2595		
Ser Thr Lys Arg Cys Pro Lys Thr Arg Pro Arg Lys Glu Val Lys 2600 2605 2610		

Glu Glu Leu Ser Ala Val Glu Arg Leu Thr Gln Thr Ser Gly Gln
 2615 2620 2625
 Ser Thr His Thr His Lys Glu Pro Ala Ser Gly Asp Glu Gly Ile
 2630 2635 2640
 Lys Val Leu Lys Gln Arg Ala Lys Lys Lys Pro Asn Pro Val Glu
 2645 2650 2655
 Glu Glu Pro Ser Arg Arg Arg Pro Arg Ala Pro Lys Glu Lys Ala
 2660 2665 2670
 Gln Pro Leu Glu Asp Leu Ala Gly Phe Thr Glu Leu Ser Glu Thr
 2675 2680 2685
 Ser Gly His Thr Gln Glu Ser Leu Thr Ala Gly Lys Ala Thr Lys
 2690 2695 2700
 Ile Pro Cys Glu Ser Pro Pro Leu Glu Val Val Asp Thr Thr Ala
 2705 2710 2715
 Ser Thr Lys Arg His Leu Arg Thr Arg Val Gln Lys Val Gln Val
 2720 2725 2730
 Lys Glu Glu Pro Ser Ala Val Lys Phe Thr Gln Thr Ser Gly Glu
 2735 2740 2745
 Thr Thr Asp Ala Asp Lys Glu Pro Ala Gly Glu Asp Lys Gly Ile
 2750 2755 2760
 Lys Ala Leu Lys Glu Ser Ala Lys Gln Thr Pro Ala Pro Ala Ala
 2765 2770 2775
 Ser Val Thr Gly Ser Arg Arg Arg Pro Arg Ala Pro Arg Glu Ser
 2780 2785 2790
 Ala Gln Ala Ile Glu Asp Leu Ala Gly Phe Lys Asp Pro Ala Ala
 2795 2800 2805
 Gly His Thr Glu Glu Ser Met Thr Asp Asp Lys Thr Thr Lys Ile
 2810 2815 2820
 Pro Cys Lys Ser Ser Pro Glu Leu Glu Asp Thr Ala Thr Ser Ser
 2825 2830 2835
 Lys Arg Arg Pro Arg Thr Arg Ala Gln Lys Val Glu Val Lys Glu
 2840 2845 2850
 Glu Leu Leu Ala Val Gly Lys Leu Thr Gln Thr Ser Gly Glu Thr
 2855 2860 2865
 Thr His Thr Asp Lys Glu Pro Val Gly Glu Gly Lys Gly Thr Lys
 2870 2875 2880
 Ala Phe Lys Gln Pro Ala Lys Arg Asn Val Asp Ala Glu Asp Val
 2885 2890 2895
 Ile Gly Ser Arg Arg Gln Pro Arg Ala Pro Lys Glu Lys Ala Gln
 2900 2905 2910

Pro Leu Glu Asp Leu Ala Ser Phe Gln Glu Leu Ser Gln Thr Pro
 2915 2920 2925
 Gly His Thr Glu Glu Leu Ala Asn Gly Ala Ala Asp Ser Phe Thr
 2930 2935 2940
 Ser Ala Pro Lys Gln Thr Pro Asp Ser Gly Lys Pro Leu Lys Ile
 2945 2950 2955
 Ser Arg Arg Val Leu Arg Ala Pro Lys Val Glu Pro Val Gly Asp
 2960 2965 2970
 Val Val Ser Thr Arg Asp Pro Val Lys Ser Gln Ser Lys Ser Asn
 2975 2980 2985
 Thr Ser Leu Pro Pro Leu Pro Phe Lys Arg Gly Gly Gly Lys Asp
 2990 2995 3000
 Gly Ser Val Thr Gly Thr Lys Arg Leu Arg Cys Met Pro Ala Pro
 3005 3010 3015
 Glu Glu Ile Val Glu Glu Leu Pro Ala Ser Lys Lys Gln Arg Val
 3020 3025 3030
 Ala Pro Arg Ala Arg Gly Lys Ser Ser Glu Pro Val Val Ile Met
 3035 3040 3045
 Lys Arg Ser Leu Arg Thr Ser Ala Lys Arg Ile Glu Pro Ala Glu
 3050 3055 3060
 Glu Leu Asn Ser Asn Asp Met Lys Thr Asn Lys Glu Glu His Lys
 3065 3070 3075
 Leu Gln Asp Ser Val Pro Glu Asn Lys Gly Ile Ser Leu Arg Ser
 3080 3085 3090
 Arg Arg Gln Asp Lys Thr Glu Ala Glu Gln Gln Ile Thr Glu Val
 3095 3100 3105
 Phe Val Leu Ala Glu Arg Ile Glu Ile Asn Arg Asn Glu Lys Lys
 3110 3115 3120
 Pro Met Lys Thr Ser Pro Glu Met Asp Ile Gln Asn Pro Asp Asp
 3125 3130 3135
 Gly Ala Arg Lys Pro Ile Pro Arg Asp Lys Val Thr Glu Asn Lys
 3140 3145 3150
 Arg Cys Leu Arg Ser Ala Arg Gln Asn Glu Ser Ser Gln Pro Lys
 3155 3160 3165
 Val Ala Glu Glu Ser Gly Gly Gln Lys Ser Ala Lys Val Leu Met
 3170 3175 3180
 Gln Asn Gln Lys Gly Lys Gly Glu Ala Gly Asn Ser Asp Ser Met
 3185 3190 3195
 Cys Leu Arg Ser Arg Lys Thr Lys Ser Gln Pro Ala Ala Ser Thr
 3200 3205 3210

Leu Glu Ser Lys Ser Val Gln Arg Val Thr Arg Ser Val Lys Arg
3215 3220 3225

Cys Ala Glu Asn Pro Lys Lys Ala Glu Asp Asn Val Cys Val Lys
3230 3235 3240

Lys Ile Thr Thr Arg Ser His Arg Asp Ser Glu Asp Ile
3245 3250 3255

<210> 200
<211> 478
<212> PRT
<213> Homo sapiens

<400> 200

Met Ala Gly Val Glu Glu Val Ala Ala Ser Gly Ser His Leu Asn Gly
1 5 10 15

Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Ala Ala Ser Thr Ala Glu
20 25 30

Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Ser Lys Gly Pro
35 40 45

Ser Ala Ala Gly Glu Gln Glu Pro Asp Lys Glu Ser Gly Ala Ser Val
50 55 60

Asp Glu Val Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu
65 70 75 80

Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Asp Gly Ala Thr
85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
165 170 175

Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
195 200 205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
210 215 220

Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
225 230 235 240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Gln Tyr
 325 330 335
 Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
 435 440 445
 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Leu
 450 455 460
 Arg Pro Thr Cys Lys Glu Val Val Ser Arg Gly Asp Asp Tyr
 465 470 475
 <210> 201
 <211> 488
 <212> PRT
 <213> Homo sapiens
 <400> 201
 Met His Gly Arg Lys Asp Asp Ala Gln Lys Gln Pro Val Lys Asn Gln
 1 5 10 15
 Leu Gly Leu Asn Pro Gln Ser His Leu Pro Glu Leu Gln Leu Phe Gln
 20 25 30
 Ala Glu Gly Lys Ile Tyr Lys Tyr Asp His Met Glu Lys Ser Val Asn
 35 40 45

Ser Ser Ser Leu Val Ser Pro Pro Gln Arg Ile Ser Ser Thr Val Lys
 50 55 60
 Thr His Ile Ser His Ile Tyr Glu Cys Asn Phe Val Asp Ser Leu Phe
 65 70 75 80
 Thr Gln Lys Glu Lys Ala Asn Ile Gly Thr Glu His Tyr Lys Cys Asn
 85 90 95
 Glu Arg Gly Lys Ala Phe His Gln Gly Leu His Phe Thr Ile His Gln
 100 105 110
 Ile Ile His Thr Lys Glu Thr Gln Phe Lys Cys Asp Ile Cys Gly Lys
 115 120 125
 Ile Phe Asn Lys Lys Ser Asn Leu Ala Ser His Gln Arg Ile His Thr
 130 135 140
 Gly Glu Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Val Phe His Asn
 145 150 155 160
 Met Ser His Leu Ala Gln His Arg Arg Ile His Thr Gly Glu Lys Pro
 165 170 175
 Tyr Lys Cys Asn Glu Cys Gly Lys Val Phe Asn Gln Ile Ser His Leu
 180 185 190
 Ala Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Asn
 195 200 205
 Glu Cys Gly Lys Val Phe His Gln Ile Ser His Leu Ala Gln His Arg
 210 215 220
 Thr Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Lys Cys Gly Lys
 225 230 235 240
 Val Phe Ser Arg Asn Ser Tyr Leu Val Gln His Leu Ile Ile His Thr
 245 250 255
 Gly Glu Lys Pro Tyr Arg Cys Asn Val Cys Gly Lys Val Phe Ser His
 260 265 270
 Lys Ser Ser Leu Val Asn His Trp Arg Ile His Thr Gly Glu Lys Pro
 275 280 285
 Tyr Lys Cys Asn Glu Cys Gly Lys Val Phe Ser His Lys Ser Ser Leu
 290 295 300
 Val Asn His Trp Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Asn
 305 310 315 320
 Glu Cys Gly Lys Val Phe Ser Arg Asn Ser Tyr Leu Ala Gln His Leu
 325 330 335
 Ile Ile His Ala Gly Glu Lys Pro Tyr Lys Cys Asp Glu Cys Asp Lys
 340 345 350
 Ala Phe Ser Gln Asn Ser His Leu Val Gln His His Arg Ile His Thr

355 360 365
 Gly Glu Lys Pro Tyr Lys Cys Asp Glu Cys Gly Lys Val Phe Ser Gln
 370 375 380
 Asn Ser Tyr Leu Ala Tyr His Trp Arg Ile His Thr Gly Glu Lys Ala
 385 390 395 400
 Tyr Lys Cys Asn Glu Cys Gly Lys Val Phe Gly Leu Asn Ser Ser Leu
 405 410 415
 Ala His His Arg Lys Ile His Thr Gly Glu Lys Pro Phe Lys Cys Asn
 420 425 430
 Glu Cys Gly Lys Ala Phe Ser Met Arg Ser Ser Leu Thr Asn His His
 435 440 445
 Ala Ile His Thr Gly Glu Lys His Phe Lys Cys Asn Glu Cys Gly Lys
 450 455 460
 Leu Phe Arg Asp Asn Ser Tyr Leu Val Arg His Gln Arg Phe His Ala
 465 470 475 480
 Gly Lys Lys Ser Asn Thr Cys Asn
 485

<210> 202
 <211> 553
 <212> PRT
 <213> Homo sapiens

<400> 202

Met Leu Ser Val Arg Val Ala Ala Ala Val Val Arg Ala Leu Pro Arg
 1 5 10 15
 Arg Ala Gly Leu Val Ser Arg Asn Ala Leu Gly Ser Ser Phe Ile Ala
 20 25 30
 Ala Arg Asn Phe His Ala Ser Asn Thr His Leu Gln Lys Thr Gly Thr
 35 40 45
 Ala Glu Met Ser Ser Ile Leu Glu Glu Arg Ile Leu Gly Ala Asp Thr
 50 55 60
 Ser Val Asp Leu Glu Glu Thr Gly Arg Val Leu Ser Ile Gly Asp Gly
 65 70 75 80
 Ile Ala Arg Val His Gly Leu Arg Asn Val Gln Ala Glu Glu Met Val
 85 90 95
 Glu Phe Ser Ser Gly Leu Lys Gly Met Ser Leu Asn Leu Glu Pro Asp
 100 105 110
 Asn Val Gly Val Val Val Phe Gly Asn Asp Lys Leu Ile Lys Glu Gly
 115 120 125
 Asp Ile Val Lys Arg Thr Gly Ala Ile Val Asp Val Pro Val Gly Glu
 130 135 140
 Glu Leu Leu Gly Arg Val Val Asp Ala Leu Gly Asn Ala Ile Asp Gly

145 150 155 160
 Lys Gly Pro Ile Gly Ser Lys Thr Arg Arg Arg Val Gly Leu Lys Ala
 165 170 175
 Pro Gly Ile Ile Pro Arg Ile Ser Val Arg Glu Pro Met Gln Thr Gly
 180 185 190
 Ile Lys Ala Val Asp Ser Leu Val Pro Ile Gly Arg Gly Gln Arg Glu
 195 200 205
 Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr Ser Ile Ala Ile Asp
 210 215 220
 Thr Ile Ile Asn Gln Lys Arg Phe Asn Asp Gly Ser Asp Glu Lys Lys
 225 230 235 240
 Lys Leu Tyr Cys Ile Tyr Val Ala Ile Gly Gln Lys Arg Ser Thr Val
 245 250 255
 Ala Gln Leu Val Lys Arg Leu Thr Asp Ala Asp Ala Met Lys Tyr Thr
 260 265 270
 Ile Val Val Ser Ala Thr Ala Ser Asp Ala Ala Pro Leu Gln Tyr Leu
 275 280 285
 Ala Pro Tyr Ser Gly Cys Ser Met Gly Glu Tyr Phe Arg Asp Asn Gly
 290 295 300
 Lys His Ala Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala
 305 310 315 320
 Tyr Arg Gln Met Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala
 325 330 335
 Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala
 340 345 350
 Ala Lys Met Asn Asp Ala Phe Gly Gly Gly Ser Leu Thr Ala Leu Pro
 355 360 365
 Val Ile Glu Thr Gln Ala Gly Asp Val Ser Ala Tyr Ile Pro Thr Asn
 370 375 380
 Val Ile Ser Ile Thr Asp Gly Gln Ile Phe Leu Glu Thr Glu Leu Phe
 385 390 395 400
 Tyr Lys Gly Ile Arg Pro Ala Ile Asn Val Gly Leu Ser Val Ser Arg
 405 410 415
 Val Gly Ser Ala Ala Gln Thr Arg Ala Met Lys Gln Val Ala Gly Thr
 420 425 430
 Met Lys Leu Glu Leu Ala Gln Tyr Arg Glu Val Ala Ala Phe Ala Gln
 435 440 445
 Phe Gly Ser Asp Leu Asp Ala Ala Thr Gln Gln Leu Leu Ser Arg Gly
 450 455 460

Val Arg Leu Thr Glu Leu Leu Lys Gln Gly Gln Tyr Ser Pro Met Ala
465 470 475 480

Ile Glu Glu Gln Val Ala Val Ile Tyr Ala Gly Val Arg Gly Tyr Leu
485 490 495

Asp Lys Leu Glu Pro Ser Lys Ile Thr Lys Phe Glu Asn Ala Phe Leu
500 505 510

Ser His Val Val Ser Gln His Gln Ala Leu Leu Gly Thr Ile Arg Ala
515 520 525

Asp Gly Lys Ile Ser Glu Gln Ser Asp Ala Lys Leu Lys Glu Ile Val
530 535 540

Thr Asn Phe Leu Ala Gly Phe Glu Ala
545 550

<210> 203
<211> 462
<212> PRT
<213> Homo sapiens

<400> 203

Met Gly Lys Glu Lys Thr His Ile Asn Ile Val Val Ile Gly His Val
1 5 10 15

Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Cys Gly
20 25 30

Gly Ile Asp Lys Arg Thr Ile Glu Lys Phe Glu Lys Glu Ala Ala Glu
35 40 45

Met Gly Lys Gly Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
50 55 60

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ser Leu Trp Lys Phe
65 70 75 80

Glu Thr Ser Lys Tyr Tyr Val Thr Ile Ile Asp Ala Pro Gly His Arg
85 90 95

Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
100 105 110

Val Leu Ile Val Ala Ala Gly Val Gly Glu Phe Glu Ala Gly Ile Ser
115 120 125

Lys Asn Gly Gln Thr Arg Glu His Ala Leu Leu Ala Tyr Thr Leu Gly
130 135 140

Val Lys Gln Leu Ile Val Gly Val Asn Lys Met Asp Ser Thr Glu Pro
145 150 155 160

Pro Tyr Ser Gln Lys Arg Tyr Glu Glu Ile Val Lys Glu Val Ser Thr
165 170 175

Tyr Ile Lys Lys Ile Gly Tyr Asn Pro Asp Thr Val Ala Phe Val Pro
180 185 190

Ile Ser Gly Trp Asn Gly Asp Asn Met Leu Glu Pro Ser Ala Asn Met
195 200 205

Pro Trp Phe Lys Gly Trp Lys Val Thr Arg Lys Asp Gly Asn Ala Ser
210 215 220

Gly Thr Thr Leu Leu Glu Ala Val Asp Cys Ile Leu Pro Pro Thr Arg
225 230 235 240

Pro Thr Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile
245 250 255

Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu
260 265 270

Lys Pro Gly Met Val Val Thr Phe Ala Pro Val Asn Val Thr Thr Glu
275 280 285

Val Lys Ser Val Glu Met His His Glu Ala Leu Ser Glu Ala Leu Pro
290 295 300

Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Val
305 310 315 320

Arg Arg Gly Asn Val Ala Gly Asp Ser Lys Asn Asp Pro Pro Met Glu
325 330 335

Ala Ala Gly Phe Thr Ala Gln Val Ile Ile Leu Asn His Pro Gly Gln
340 345 350

Ile Ser Ala Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ala His Ile
355 360 365

Ala Cys Lys Phe Ala Glu Leu Lys Glu Lys Ile Asp Arg Arg Ser Gly
370 375 380

Lys Lys Leu Glu Asp Gly Pro Lys Phe Leu Lys Ser Gly Asp Ala Ala
385 390 395 400

Ile Val Asp Met Val Pro Gly Lys Pro Met Cys Val Glu Ser Phe Ser
405 410 415

Asp Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr
420 425 430

Val Ala Val Gly Val Ile Lys Ala Val Asp Lys Lys Ala Ala Gly Ala
435 440 445

Gly Lys Val Thr Lys Ser Ala Gln Lys Ala Gln Lys Ala Lys
450 455 460

<210> 204
<211> 1069
<212> PRT
<213> Homo sapiens

<400> 204

Met Leu Arg Met Arg Thr Ala Gly Trp Ala Arg Gly Trp Cys Leu Gly
1 5 10 15

Cys Cys Leu Leu Leu Pro Leu Ser Phe Ser Leu Ala Ala Ala Lys Gln
 20 25 30
 Leu Leu Arg Tyr Arg Leu Ala Glu Glu Gly Pro Ala Asp Val Arg Ile
 35 40 45
 Gly Asn Val Ala Ser Asp Leu Gly Ile Val Thr Gly Ser Gly Glu Val
 50 55 60
 Thr Phe Ser Leu Glu Ser Gly Ser Glu Tyr Leu Lys Ile Asp Asn Leu
 65 70 75 80
 Thr Gly Glu Leu Ser Thr Ser Glu Arg Arg Ile Asp Arg Glu Lys Leu
 85 90 95
 Pro Gln Cys Gln Met Ile Phe Asp Glu Asn Glu Cys Phe Leu Asp Phe
 100 105 110
 Glu Val Ser Val Ile Gly Pro Ser Gln Ser Trp Val Asp Leu Phe Glu
 115 120 125
 Gly Gln Val Ile Val Leu Asp Ile Asn Asp Asn Thr Pro Thr Phe Pro
 130 135 140
 Ser Pro Val Leu Thr Leu Thr Val Glu Glu Asn Arg Pro Val Gly Thr
 145 150 155 160
 Leu Tyr Leu Leu Pro Thr Ala Thr Asp Arg Asp Phe Gly Arg Asn Gly
 165 170 175
 Ile Glu Arg Tyr Glu Leu Leu Gln Glu Pro Gly Gly Gly Gly Ser Gly
 180 185 190
 Gly Glu Ser Arg Arg Ala Gly Ala Ala Asp Ser Ala Pro Tyr Pro Gly
 195 200 205
 Gly Gly Gly Asn Gly Ala Ser Gly Gly Gly Ser Gly Gly Ser Lys Arg
 210 215 220
 Arg Leu Asp Ala Ser Glu Gly Gly Gly Gly Thr Asn Pro Gly Gly Arg
 225 230 235 240
 Ser Ser Val Phe Glu Leu Gln Val Ala Asp Thr Pro Asp Gly Glu Lys
 245 250 255
 Gln Pro Gln Leu Ile Val Lys Gly Ala Leu Asp Arg Glu Gln Arg Asp
 260 265 270
 Ser Tyr Glu Leu Thr Leu Arg Val Arg Asp Gly Gly Asp Pro Pro Arg
 275 280 285
 Ser Ser Gln Ala Ile Leu Arg Val Leu Ile Thr Asp Val Asn Asp Asn
 290 295 300
 Ser Pro Arg Phe Glu Lys Ser Val Tyr Glu Ala Asp Leu Ala Glu Asn
 305 310 315 320
 Ser Ala Pro Gly Thr Pro Ile Leu Gln Leu Arg Ala Ala Asp Leu Asp
 325 330 335

Val Gly Val Asn Gly Gln Ile Glu Tyr Val Phe Gly Ala Ala Thr Glu
 340 345 350
 Ser Val Arg Arg Leu Leu Arg Leu Asp Glu Thr Ser Gly Trp Leu Ser
 355 360 365
 Val Leu His Arg Ile Asp Arg Glu Glu Val Asn Gln Leu Arg Phe Thr
 370 375 380
 Val Met Ala Arg Asp Arg Gly Gln Pro Pro Lys Thr Asp Lys Ala Thr
 385 390 395 400
 Val Val Leu Asn Ile Lys Asp Glu Asn Asp Asn Val Pro Ser Ile Glu
 405 410 415
 Ile Arg Lys Ile Gly Arg Ile Pro Leu Lys Asp Gly Val Ala Asn Val
 420 425 430
 Ala Glu Asp Val Leu Val Asp Thr Pro Ile Ala Leu Val Gln Val Ser
 435 440 445
 Asp Arg Asp Gln Gly Glu Asn Gly Val Val¹ Thr Cys Thr Val Val Gly
 450 455 460
 Asp Val Pro Phe Gln Leu Lys Pro Ala Ser Asp Thr Glu Gly Asp Gln
 465 470 475 480
 Asn Lys Lys Lys Tyr Phe Leu His Thr Ser Thr Pro Leu Asp Tyr Glu
 485 490 495
 Ala Thr Arg Glu Phe Asn Val Val Ile Val Ala Val Asp Ser Gly Ser
 500 505 510
 Pro Ser Leu Ser Ser Lys Asn Ser Leu Ile Val Lys Val Gly Asp Thr
 515 520 525
 Asn Asp Asn Pro Pro Met Phe Gly Gln Ser Val Val Glu Val Tyr Phe
 530 535 540
 Pro Glu Asn Asn Ile Pro Gly Glu Arg Val Ala Thr Val Leu Ala Thr
 545 550 555 560
 Asp Ala Asp Ser Gly Lys Asn Ala Glu Ile Ala Tyr Ser Leu Asp Ser
 565 570 575
 Ser Val Met Gly Ile Phe Ala Ile Asp Pro Asp Ser Gly Asp Ile Leu
 580 585 590
 Val Asn Thr Val Leu Asp Arg Glu Gln Thr Asp Arg Tyr Glu Phe Lys
 595 600 605
 Val Asn Ala Lys Asp Lys Gly Ile Pro Val Leu Gln Gly Ser Thr Thr
 610 615 620
 Val Ile Val Gln Val Ala Asp Lys Asn Asp Asn Asp Pro Lys Phe Met
 625 630 635 640
 Gln Asp Val Phe Thr Phe Tyr Val Lys Glu Asn Leu Gln Pro Asn Ser
 645 650 655

Pro Val Gly Met Val Thr Val Met Asp Ala Asp Lys Gly Arg Asn Ala
 660 665 670 .
 Glu Met Ser Leu Tyr Ile Glu Glu Asn Asn Asn Ile Phe Ser Ile Glu
 675 680 685
 Asn Asp Thr Gly Thr Ile Tyr Ser Thr Met Ser Phe Asp Arg Glu His
 690 695 700
 Gln Thr Thr Tyr Thr Phe Arg Val Lys Ala Val Asp Gly Gly Asp Pro
 705 710 715 720
 Pro Arg Ser Ala Thr Ala Thr Val Ser Leu Phe Val Met Asp Glu Asn
 725 730 735
 Asp Asn Ala Pro Thr Val Thr Leu Pro Lys Asn Ile Ser Tyr Thr Leu
 740 745 750
 Leu Pro Pro Ser Ser Asn Val Arg Thr Val Val Ala Thr Val Leu Ala
 755 760 765
 Thr Asp Ser Asp Asp Gly Ile Asn Ala Asp Leu Asn Tyr Ser Ile Val
 770 775 780
 Gly Gly Asn Pro Phe Lys Leu Phe Glu Ile Asp Pro Thr Ser Gly Val
 785 790 795 800
 Val Ser Leu Val Gly Lys Leu Thr Gln Lys His Tyr Gly Leu His Arg
 805 810 815
 Leu Val Val Gln Val Asn Asp Ser Gly Gln Pro Ser Gln Ser Thr Thr
 820 825 830
 Thr Val Val His Val Phe Val Asn Glu Ser Val Ser Asn Ala Thr Ala
 835 840 845
 Ile Asp Ser Gln Ile Ala Arg Ser Leu His Ile Pro Leu Thr Gln Asp
 850 855 860
 Ile Ala Gly Asp Pro Ser Tyr Glu Ile Ser Lys Gln Arg Leu Ser Ile
 865 870 875 880
 Val Ile Gly Val Val Ala Gly Ile Met Thr Val Ile Leu Ile Ile Leu
 885 890 895
 Ile Val Val Met Ala Arg Tyr Cys Arg Ser Lys Asn Lys Asn Gly Tyr
 900 905 910
 Glu Ala Gly Lys Lys Asp His Glu Asp Phe Phe Thr Pro Gln Gln His
 915 920 925
 Asp Lys Ser Lys Lys Pro Lys Lys Asp Lys Lys Asn Lys Lys Ser Lys
 930 935 940
 Gln Pro Leu Tyr Ser Ser Ile Val Thr Val Glu Ala Ser Lys Pro Asn
 945 950 955 960
 Gly Gln Arg Tyr Asp Ser Val Asn Glu Lys Leu Ser Asp Ser Pro Ser

965

970

975

Met Gly Arg Tyr Arg Ser Val Asn Gly Gly Pro Gly Ser Pro Asp Leu
 980 985 990

Ala Arg His Tyr Lys Ser Ser Ser Pro Leu Pro Thr Val Gln Leu His
 995 1000 1005

Pro Gln Ser Pro Thr Ala Gly Lys Lys His Gln Ala Val Gln Asp
 1010 1015 1020

Leu Pro Pro Ala Asn Thr Phe Val Gly Ala Gly Asp Asn Ile Ser
 1025 1030 1035

Ile Gly Ser Asp His Cys Ser Glu Tyr Ser Cys Gln Thr Asn Asn
 1040 1045 1050

Lys Tyr Ser Lys Gln Met Arg Leu His Pro Tyr Ile Thr Val Phe
 1055 1060 1065

Gly

<210> 205
 <211> 401
 <212> PRT
 <213> Homo sapiens

<400> 205

Met Ser Phe Ser Lys Thr His Ser Thr Ala Thr Met Pro Pro Pro Ile
 1 5 10 15

Asn Pro Ile Leu Ala Ser Leu Gln His Asn Ser Ile Leu Thr Pro Thr
 20 25 30

Arg Val Ser Ser Ser Ala Thr Lys Gln Lys Val Leu Ser Pro Pro His
 35 40 45

Ile Lys Ala Asp Phe Asn Leu Ala Asp Phe Glu Cys Glu Glu Asp Pro
 50 55 60

Phe Asp Asn Leu Glu Leu Lys Thr Ile Asp Glu Lys Glu Glu Leu Arg
 65 70 75 80

Asn Ile Leu Val Gly Thr Thr Gly Pro Ile Met Ala Gln Leu Leu Asp
 85 90 95

Asn Asn Leu Pro Arg Gly Gly Ser Gly Ser Val Leu Gln Asp Glu Glu
 100 105 110

Val Leu Ala Ser Leu Glu Arg Ala Thr Leu Asp Phe Lys Pro Leu His
 115 120 125

Lys Pro Asn Gly Phe Ile Thr Leu Pro Gln Leu Gly Asn Cys Glu Lys
 130 135 140

Met Ser Leu Ser Ser Lys Val Ser Leu Pro Pro Ile Pro Ala Val Ser
 145 150 155 160

Asn Ile Lys Ser Leu Ser Phe Pro Lys Leu Asp Ser Asp Asp Ser Asn

[illegible]

Ser

```
<210> 206
<211> 285
<212> PRT
<213> Homo sapiens
```

<400> 206

Met Glu Val Pro Pro Pro Asp Ala Gly Ser Phe Leu Cys Arg Ala Leu
1 5 10 15

Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
20 25 30

Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro

35 40 45
 Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys
 50 55 60
 Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala Asn Ile Cys Lys Thr
 65 70 75 80
 Ala Ala Thr Ala Gly Ile Ile Gly Trp Val Tyr Gly Gly Ile Pro Ala
 85 90 95
 Phe Ile His Ala Lys Gln Gln Tyr Ile Glu Gln Ser Gln Ala Glu Ile
 100 105 110
 Tyr His Asn Arg Phe Asp Ala Val Gln Ser Ala His Arg Ala Ala Thr
 115 120 125
 Arg Gly Phe Ile Arg Tyr Gly Trp Arg Trp Gly Trp Arg Thr Ala Val
 130 135 140
 Phe Val Thr Ile Phe Asn Thr Val Asn Thr Ser Leu Asn Val Tyr Arg
 145 150 155 160
 Asn Lys Asp Ala Leu Ser His Phe Val Ile Ala Gly Ala Val Thr Gly
 165 170 175
 Ser Leu Phe Arg Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly Gly
 180 185 190
 Ile Ile Gly Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met Ala
 195 200 205
 Phe Gln Lys Tyr Ser Gly Glu Thr Val Gln Glu Arg Lys Gln Lys Asp
 210 215 220
 Arg Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg Leu
 225 230 235 240
 Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Gln Glu
 245 250 255
 Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu Asn Leu
 260 265 270
 Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp
 275 280 285
 <210> 207
 <211> 212
 <212> PRT
 <213> Homo sapiens
 <400> 207
 Met Leu Asn Lys Val Leu Ser Arg Leu Gly Val Ala Gly Gln Trp Arg
 1 5 10 15
 Phe Val Asp Val Leu Gly Leu Glu Glu Glu Ser Leu Gly Ser Val Pro
 20 25 30
 Ala Pro Ala Cys Ala Leu Leu Leu Leu Phe Pro Leu Thr Ala Gln His

```

      35              40              45

Glu Asn Phe Arg Lys Lys Gln Ile Glu Glu Leu Lys Gly Gln Glu Val
 50              55              60

Ser Pro Lys Val Tyr Phe Met Lys Gln Thr Ile Gly Asn Ser Cys Gly
 65              70              75              80

Thr Ile Gly Leu Ile His Ala Val Ala Asn Asn Gln Asp Lys Leu Gly
      85              90              95

Phe Glu Asp Gly Ser Val Leu Lys Gln Phe Leu Ser Glu Thr Glu Lys
      100              105              110

Met Ser Pro Glu Asp Arg Ala Lys Cys Phe Glu Lys Asn Glu Ala Ile
      115              120              125

Gln Ala Ala His Asp Ala Val Ala Gln Glu Gly Gln Cys Arg Val Asp
      130              135              140

Asp Lys Val Asn Phe His Phe Ile Leu Phe Asn Asn Val Asp Gly His
      145              150              155              160

Leu Tyr Glu Leu Asp Gly Arg Met Pro Phe Pro Val Asn His Gly Ala
      165              170              175

Ser Ser Glu Asp Thr Leu Leu Lys Asp Ala Ala Lys Val Cys Arg Glu
      180              185              190

Phe Thr Glu Arg Glu Gln Gly Glu Val Arg Phe Ser Ala Val Ala Leu
      195              200              205

Cys Lys Ala Ala
      210

<210> 208
<211> 596
<212> PRT
<213> Homo sapiens

<400> 208

Met Ser Leu Ser Met Arg Asp Pro Val Ile Pro Gly Thr Ser Met Ala
 1              5              10              15

Tyr His Pro Phe Leu Pro His Arg Ala Pro Asp Phe Ala Met Ser Ala
      20              25              30

Val Leu Gly His Gln Pro Pro Phe Phe Pro Ala Leu Thr Leu Pro Pro
      35              40              45

Asn Gly Ala Ala Ala Leu Ser Leu Pro Gly Ala Leu Ala Lys Pro Ile
      50              55              60

Met Asp Gln Leu Val Gly Ala Ala Glu Thr Gly Ile Pro Phe Ser Ser
      65              70              75              80

Leu Gly Pro Gln Ala His Leu Arg Pro Leu Lys Thr Met Glu Pro Glu
      85              90              95

Glu Glu Val Glu Asp Asp Pro Lys Val His Leu Glu Ala Lys Glu Leu

```

100					105					110					
Trp	Asp	Gln	Phe	His	Lys	Arg	Gly	Thr	Glu	Met	Val	Ile	Thr	Lys	Ser
	115						120					125			
Gly	Arg	Arg	Met	Phe	Pro	Pro	Phe	Lys	Val	Arg	Cys	Ser	Gly	Leu	Asp
	130						135					140			
Lys	Lys	Ala	Lys	Tyr	Ile	Leu	Leu	Met	Asp	Ile	Ile	Ala	Ala	Asp	Asp
	145					150					155				160
Cys	Arg	Tyr	Lys	Phe	His	Asn	Ser	Arg	Trp	Met	Val	Ala	Gly	Lys	Ala
			165						170					175	
Asp	Pro	Glu	Met	Pro	Lys	Arg	Met	Tyr	Ile	His	Pro	Asp	Ser	Pro	Ala
			180					185						190	
Thr	Gly	Glu	Gln	Trp	Met	Ser	Lys	Val	Val	Thr	Phe	His	Lys	Leu	Lys
		195					200					205			
Leu	Thr	Asn	Asn	Ile	Ser	Asp	Lys	His	Gly	Phe	Thr	Leu	Ala	Phe	Pro
		210					215					220			
Ser	Asp	His	Ala	Thr	Trp	Gln	Gly	Asn	Tyr	Ser	Phe	Gly	Thr	Gln	Thr
	225					230					235				240
Ile	Leu	Asn	Ser	Met	His	Lys	Tyr	Gln	Pro	Arg	Phe	His	Ile	Val	Arg
			245						250					255	
Ala	Asn	Asp	Ile	Leu	Lys	Leu	Pro	Tyr	Ser	Thr	Phe	Arg	Thr	Tyr	Leu
		260						265						270	
Phe	Pro	Glu	Thr	Glu	Phe	Ile	Ala	Val	Thr	Ala	Tyr	Gln	Asn	Asp	Lys
		275					280					285			
Ile	Thr	Gln	Leu	Lys	Ile	Asp	Asn	Asn	Pro	Phe	Ala	Lys	Gly	Phe	Arg
	290					295					300				
Asp	Thr	Gly	Asn	Gly	Arg	Arg	Glu	Lys	Arg	Gln	Gln	Leu	Thr	Leu	Gln
	305					310					315				320
Ser	Met	Arg	Val	Phe	Asp	Glu	Arg	His	Lys	Lys	Glu	Asn	Gly	Thr	Ser
			325						330					335	
Asp	Glu	Ser	Ser	Ser	Glu	Gln	Ala	Ala	Phe	Asn	Cys	Phe	Ala	Gln	Ala
			340					345						350	
Ser	Ser	Pro	Ala	Ala	Ser	Thr	Val	Gly	Thr	Ser	Asn	Leu	Lys	Asp	Leu
		355					360					365			
Cys	Pro	Ser	Glu	Gly	Glu	Ser	Asp	Ala	Glu	Ala	Glu	Ser	Lys	Glu	Glu
	370					375					380				
His	Gly	Pro	Glu	Ala	Cys	Asp	Ala	Ala	Lys	Ile	Ser	Thr	Thr	Thr	Ser
	385					390					395				400
Glu	Glu	Pro	Cys	Arg	Asp	Lys	Gly	Ser	Pro	Ala	Val	Lys	Ala	His	Leu
			405						410					415	

Phe Ala Ala Glu Arg Pro Arg Asp Ser Gly Arg Leu Asp Lys Ala Ser
420 425 430

Pro Asp Ser Arg His Ser Pro Ala Thr Ile Ser Ser Ser Thr Arg Gly
435 440 445

Leu Gly Ala Glu Glu Arg Arg Ser Pro Val Arg Glu Gly Thr Ala Pro
450 455 460

Ala Lys Val Glu Glu Ala Arg Ala Leu Pro Gly Lys Glu Ala Phe Ala
465 470 475 480

Pro Leu Thr Val Gln Thr Asp Ala Ala Arg Ser Ser Val His Arg His
485 490 495

Pro Phe Arg Asn Leu Asn Thr Met Arg Pro Arg Leu Arg Tyr Ser Pro
500 505 510

Tyr Ser Ile Pro Val Pro Val Pro Asp Gly Ser Ser Leu Leu Thr Thr
515 520 525

Ala Leu Ala Ala Ser Pro Ala Ser Val Ala Val Asp Ser Gly Ser Glu
530 535 540

Leu Asn Ser Arg Ser Ser Thr Leu Ser Ser Ser Ser Met Ser Leu Ser
545 550 555 560

Pro Lys Leu Cys Ala Glu Lys Glu Ala Ala Thr Ser Glu Leu Gln Ser
565 570 575

Ile Gln Arg Leu Val Ser Gly Leu Glu Ala Lys Pro Asp Arg Ser Arg
580 585 590

Ser Ala Ser Pro
595

<210> 209
<211> 215
<212> PRT
<213> Homo sapiens

<400> 209

Met Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr
1 5 10 15

Ala Phe Phe Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro
20 25 30

Asp Ala Ser Val Asn Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg
35 40 45

Trp Lys Thr Met Ser Ala Lys Glu Lys Gly Lys Phe Glu Asp Met Ala
50 55 60

Lys Ala Asp Lys Ala Arg Tyr Glu Arg Glu Met Lys Thr Tyr Ile Pro
65 70 75 80

Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp Pro Asn Ala Pro Lys
85 90 95

Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr Arg Pro Lys
 100 105 110
 Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys Lys
 115 120 125
 Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro Tyr
 130 135 140
 Glu Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala
 145 150 155 160
 Ala Tyr Arg Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val Val
 165 170 175
 Lys Ala Glu Lys Ser Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu Glu
 180 185 190
 Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Asp Glu Asp Glu
 195 200 205
 Glu Glu Asp Asp Asp Asp Glu
 210 215
 <210> 210
 <211> 243
 <212> PRT
 <213> Homo sapiens
 <400> 210
 Met Ala Ala Ile Ala Ala Ser Glu Val Leu Val Asp Ser Ala Glu Glu
 1 5 10 15
 Gly Ser Leu Ala Ala Ala Ala Glu Leu Ala Ala Gln Lys Arg Glu Gln
 20 25 30
 Arg Leu Arg Lys Phe Arg Glu Leu His Leu Met Arg Asn Glu Ala Arg
 35 40 45
 Lys Leu Asn His Gln Glu Val Val Glu Glu Asp Lys Arg Leu Lys Leu
 50 55 60
 Pro Ala Asn Trp Glu Ala Lys Lys Ala Arg Leu Glu Trp Glu Leu Lys
 65 70 75 80
 Glu Glu Glu Lys Lys Lys Glu Cys Ala Ala Arg Gly Glu Asp Tyr Glu
 85 90 95
 Lys Val Lys Leu Leu Glu Ile Ser Ala Glu Asp Ala Glu Arg Trp Glu
 100 105 110
 Arg Lys Lys Lys Arg Lys Asn Pro Asp Leu Gly Phe Ser Asp Tyr Ala
 115 120 125
 Ala Ala Gln Leu Arg Gln Tyr His Arg Leu Thr Lys Gln Ile Lys Pro
 130 135 140
 Asp Met Glu Thr Tyr Glu Arg Leu Arg Glu Lys His Gly Glu Glu Phe
 145 150 155 160

Phe Pro Thr Ser Asn Ser Leu Leu His Gly Thr His Val Pro Ser Thr
165 170 175

Glu Glu Ile Asp Arg Met Val Ile Asp Leu Glu Lys Gln Ile Glu Lys
180 185 190

Arg Asp Lys Tyr Ser Arg Arg Arg Pro Tyr Asn Asp Asp Ala Asp Ile
195 200 205

Asp Tyr Ile Asn Glu Arg Asn Ala Lys Phe Asn Lys Lys Ala Glu Arg
210 215 220

Phe Tyr Gly Lys Tyr Thr Ala Glu Ile Lys Gln Asn Leu Glu Arg Gly
225 230 235 240

Thr Ala Val

<210> 211
<211> 479
<212> PRT
<213> Homo sapiens

<400> 211

Met Leu Gln Ile Asn Gln Met Phe Ser Val Gln Leu Ser Leu Gly Glu
1 5 10 15

Gln Thr Trp Glu Ser Glu Gly Ser Ser Ile Lys Lys Ala Gln Gln Ala
20 25 30

Val Ala Asn Lys Ala Leu Thr Glu Ser Thr Leu Pro Lys Pro Val Gln
35 40 45

Lys Pro Pro Lys Ser Asn Val Asn Asn Asn Pro Gly Ser Ile Thr Pro
50 55 60

Thr Val Glu Leu Asn Gly Leu Ala Met Lys Arg Gly Glu Pro Ala Ile
65 70 75 80

Tyr Arg Pro Leu Asp Pro Lys Pro Phe Pro Asn Tyr Arg Ala Asn Tyr
85 90 95

Asn Phe Arg Gly Met Tyr Asn Gln Arg Tyr His Cys Pro Val Pro Lys
100 105 110

Ile Phe Tyr Val Gln Leu Thr Val Gly Asn Asn Glu Phe Phe Gly Glu
115 120 125

Gly Lys Thr Arg Gln Ala Ala Arg His Asn Ala Ala Met Lys Ala Leu
130 135 140

Gln Ala Leu Gln Asn Glu Pro Ile Pro Glu Arg Ser Pro Gln Asn Gly
145 150 155 160

Glu Ser Gly Lys Asp Met Asp Asp Asp Lys Asp Ala Asn Lys Ser Glu
165 170 175

Ile Ser Leu Val Phe Glu Ile Ala Leu Lys Arg Asn Met Pro Val Ser
180 185 190

Phe Glu Val Ile Lys Glu Ser Gly Pro Pro His Met Lys Ser Phe Val
 195 200 205
 Thr Arg Val Ser Val Gly Glu Phe Ser Ala Glu Gly Glu Gly Asn Ser
 210 215 220
 Lys Lys Leu Ser Lys Lys Arg Ala Ala Thr Thr Val Leu Gln Glu Leu
 225 230 235 240
 Lys Lys Leu Pro Pro Leu Pro Val Val Glu Lys Pro Lys Leu Phe Phe
 245 250 255
 Lys Lys Arg Pro Lys Thr Ile Val Lys Ala Gly Pro Glu Tyr Gly Gln
 260 265 270
 Gly Met Asn Pro Ile Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys
 275 280 285
 Glu Lys Glu Pro Asp Tyr Val Leu Leu Ser Glu Arg Gly Met Pro Arg
 290 295 300
 Arg Arg Glu Phe Val Met Gln Val Lys Val Gly Asn Glu Val Ala Thr
 305 310 315 320
 Gly Thr Gly Pro Asn Lys Lys Ile Ala Lys Lys Asn Ala Ala Glu Ala
 325 330 335
 Met Leu Leu Gln Leu Gly Tyr Lys Ala Ser Thr Asn Leu Gln Asp Gln
 340 345 350
 Leu Glu Lys Thr Gly Glu Asn Lys Gly Trp Ser Gly Pro Lys Pro Gly
 355 360 365
 Phe Pro Glu Pro Thr Asn Asn Thr Pro Lys Gly Ile Leu His Leu Ser
 370 375 380
 Pro Asp Val Tyr Gln Glu Met Glu Ala Ser Arg His Lys Val Ile Ser
 385 390 395 400
 Gly Thr Thr Leu Gly Tyr Leu Ser Pro Lys Asp Met Asn Gln Pro Ser
 405 410 415
 Ser Ser Phe Phe Ser Ile Ser Pro Thr Ser Asn Ser Ser Ala Thr Ile
 420 425 430
 Ala Arg Glu Leu Leu Met Asn Gly Thr Ser Ser Thr Ala Glu Ala Ile
 435 440 445
 Gly Leu Lys Gly Ser Ser Pro Thr Pro Pro Cys Ser Pro Val Gln Pro
 450 455 460
 Ser Lys Gln Leu Glu Tyr Leu Ala Arg Ile Gln Gly Phe Gln Val
 465 470 475

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
17 October 2002 (17.10.2002)

PCT

(10) International Publication Number
WO 02/081638 A3

(51) International Patent Classification⁷: **C12N 15/12**,
15/11, C12Q 1/68, G01N 33/53, 33/48, C07K 16/00,
A01N 43/04, A61K 38/00, A01K 67/00

GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent
(BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
NE, SN, TD, TG).

(21) International Application Number: PCT/US02/10824

Declarations under Rule 4.17:

(22) International Filing Date: 8 April 2002 (08.04.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/281,731 6 April 2001 (06.04.2001) US
60/281,732 6 April 2001 (06.04.2001) US

— as to applicant's entitlement to apply for and be granted
a patent (Rule 4.17(ii)) for the following designations AE,
AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI,
GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG,
KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK,
MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG,
SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA,
ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ,
TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ,
MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE,
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR),
OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW,
ML, MR, NE, SN, TD, TG)

— as to the applicant's entitlement to claim the priority of the
earlier application (Rule 4.17(iii)) for the following desig-
nations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY,
BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC,
EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN,
IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV,
MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT,
RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA,
UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS,
MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent
(AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent
(AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU,
MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI,
CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)
— of inventorship (Rule 4.17(iv)) for US only

(71) Applicant (for all designated States except US): **ORI-
GENE TECHNOLOGIES, INC** [US/US]; 6 Taft Court,
Suite 100, Rockville, MD 20850 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **SUN, Zairen**
[CN/US]; 1083 Copperstone Court, Rockville, MD 20852
(US). **JAY, Gilbert** [US/US]; 5801 Nicholson Lane, North
Bethesda, MD 20852 (US).

(74) Agent: **LEBOVITZ, Richard, M.**; Origene Technologies,
Inc., 6 Taft Court, Suite 100, Rockville, MD 20850 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK,
SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA,
ZW.

Published:

— with international search report

(88) Date of publication of the international search report:
27 February 2003

(84) Designated States (regional): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),
European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR,

For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

(54) Title: **PROSTATE CANCER EXPRESSION PROFILES**

(57) Abstract: The present invention relates to all facets of novel polynucleotides, the polypeptides they encode, antibodies and specific binding partners thereto, and their applications to research, diagnosis, drug discovery, therapy, clinical medicine, forensic science and medicine, etc. The polynucleotides are differentially-regulated in prostate cancer and are therefore useful in variety of ways, including, but not limited to, as molecular markers, as drug targets, and for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, determining predisposition to, etc., diseases and conditions, to prostate cancer.



WO 02/081638 A3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/10824

A. CLASSIFICATION OF SUBJECT MATTER		
IPC(7) : C12N 15/12, 15/11; C12Q 1/68; G01N 33/53, 33/48; C07K 16/00; A01N 43/04; A61K 38/00; A01K 67/00		
US CL : 536/23.5, 23.1; 435/6, 7.1, 91.2; 514/12, 44; 530/387.1; 800/9		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) U.S. : 536/23.5, 23.1; 435/6, 7.1, 91.2; 514/12, 44; 530/387.1; 800/9		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) Compugen (nucleic acid and amino acid sequence databases): SEQ ID NOs: 2 and 141.		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	HORREVOETS et al, Vascular endothelial genes that are responsive to tumor necrosis factor-alpha in vitro are expressed in atherosclerotic lesions, including inhibitor of apoptosis protein-1, stannin, and two novel genes, Blood, 15 May 1999, Vol. 93, No. 10, pages 3418-3431, see entire document.	26
<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents:		
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	
"B" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family	
"P" document published prior to the international filing date but later than the <small>national filing date</small>		
Date of the actual completion of the international search 15 July 2002 (15.07.2002)	Date of mailing of the international search report 08 OCT 2002	
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer <i>Valerie Bell Harris for</i> James Martinell Telephone No. (703) 308-0196	

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/10824

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claim Nos.: 23 and 25
because they relate to subject matter not required to be searched by this Authority, namely:
Claims 23 and 25 are drawn to displays of information.
2. ☒ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
Each of the claims depends from a plurality of other claims and not in the alternative.
3. ☒ Claim Nos.: 2,5,8 and 17
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: Please See Continuation Sheet

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/10824

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

The claims are directed to 211 independent, distinct, and unrelated nucleic acid and polypeptide sequences that do not share a common technical feature. Accordingly, there are 211 Groups of inventions, one for each independent, distinct, and unrelated nucleic acid and polypeptide sequence.

The inventions listed as Groups 1-211 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: the application does not disclose how any of the sequences relates to any of the other sequences.

Continuation of Box II Item 4:

1, 3, 4, 7, 9-16, 18-22, 24, and 26 insofar as they relate to SEQ ID NOs: 2 and 141.